



## Full wwPDB EM Validation Report ⓘ

Mar 5, 2026 – 08:02 PM UTC

PDB ID : 9GNI / pdb\_00009gni  
EMDB ID : EMD-51471  
Title : NONO/SFPQ filament: composite structure  
Authors : Rasmussen, T.; Bottcher, B.  
Deposited on : 2024-09-03  
Resolution : 3.90 Å (reported)  
Based on initial models : 9GLC, 6WMZ, 9GLD

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

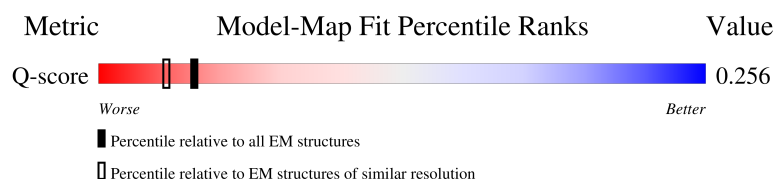
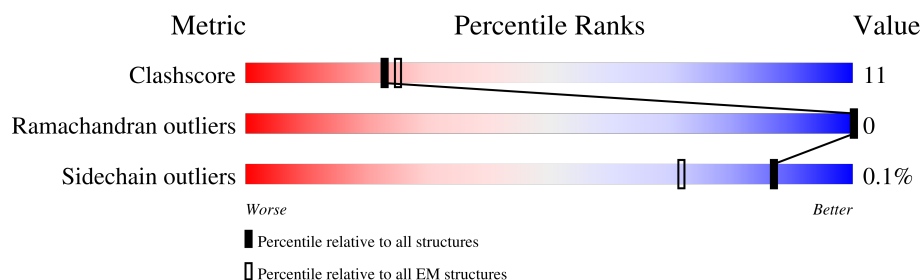
EMDB validation analysis : 0.0.1.dev132  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:  
*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.




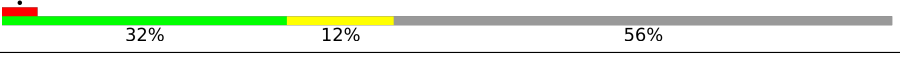



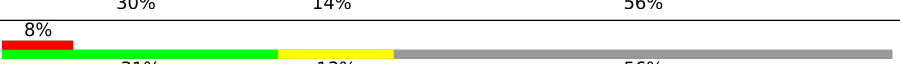
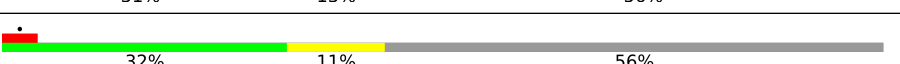



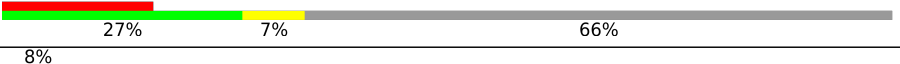
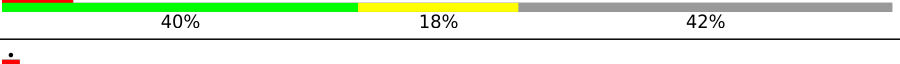
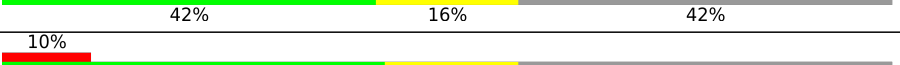
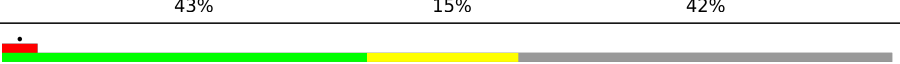
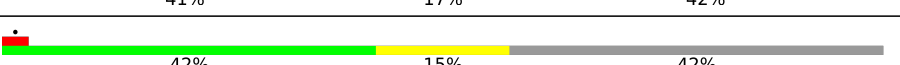
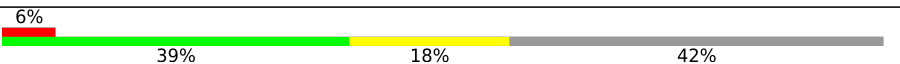
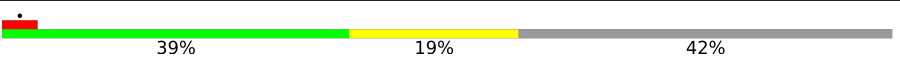
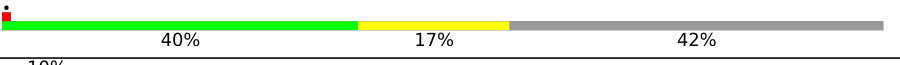
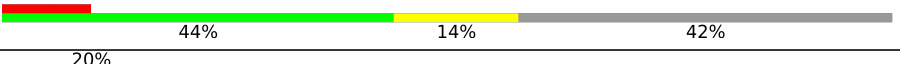

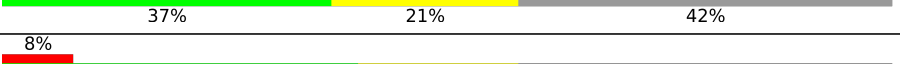
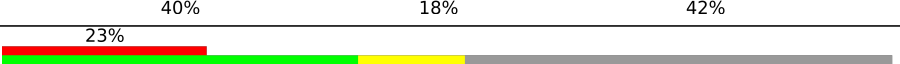
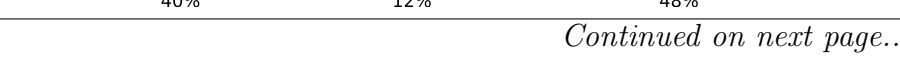


Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	8855 ( 3.40 - 4.40 )

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion  $< 40\%$ ). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	AA	703	
1	AC	703	
1	AE	703	
1	AG	703	

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Mol	Chain	Length	Quality of chain
1	BA	703	
1	BC	703	
1	BE	703	
1	BG	703	
1	CA	703	
1	CC	703	
1	CE	703	
1	CG	703	
1	DA	703	
1	DC	703	
1	DE	703	
1	DG	703	
2	AB	472	
2	AD	472	
2	AF	472	
2	AH	472	
2	BB	472	
2	BD	472	
2	BF	472	
2	BH	472	
2	CB	472	
2	CD	472	
2	CF	472	
2	CH	472	
2	DB	472	

*Continued on next page...*

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Mol	Chain	Length	Quality of chain
2	DD	472	<div><div><div></div><div></div><div></div></div><div>7%37%21%42%</div></div>
2	DF	472	<div><div><div></div><div></div><div></div></div><div>34%44%14%42%</div></div>
2	DH	472	<div><div><div></div><div></div><div></div></div><div>20%41%17%42%</div></div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 74499 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	AA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	AC	304	Total	C	N	O	S	0	0
			2527	1561	469	482	15		
1	AE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	AG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BC	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	BG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CA	275	Total	C	N	O	S	0	0
			2251	1405	406	429	11		
1	CC	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CE	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	CG	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	DA	308	Total	C	N	O	S	0	0
			2560	1581	473	491	15		
1	DC	276	Total	C	N	O	S	0	0
			2262	1411	410	430	11		
1	DG	239	Total	C	N	O	S	0	0
			1932	1215	339	371	7		
1	DE	236	Total	C	N	O	S	0	0
			1901	1195	334	365	7		

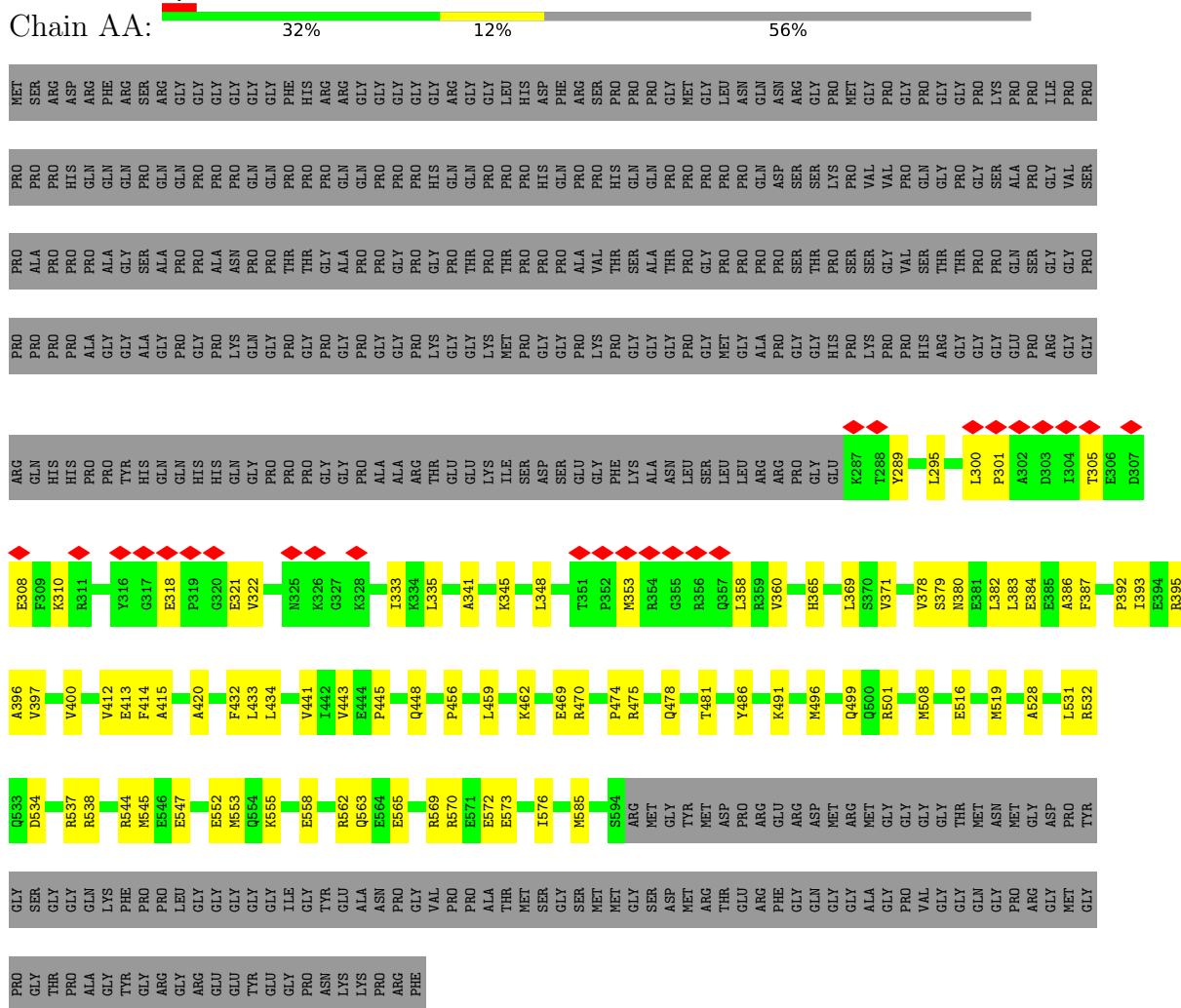
- Molecule 2 is a protein called Non-POU domain-containing octamer-binding protein isoform X2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	AB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	AH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	BH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CB	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CD	243	Total	C	N	O	S	0	0
			1979	1246	355	368	10		
2	CF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	CH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DB	244	Total	C	N	O	S	0	0
			1987	1252	356	369	10		
2	DD	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DH	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		
2	DF	273	Total	C	N	O	S	0	0
			2250	1408	413	416	13		

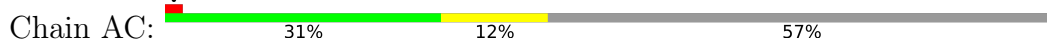
### 3 Residue-property plots

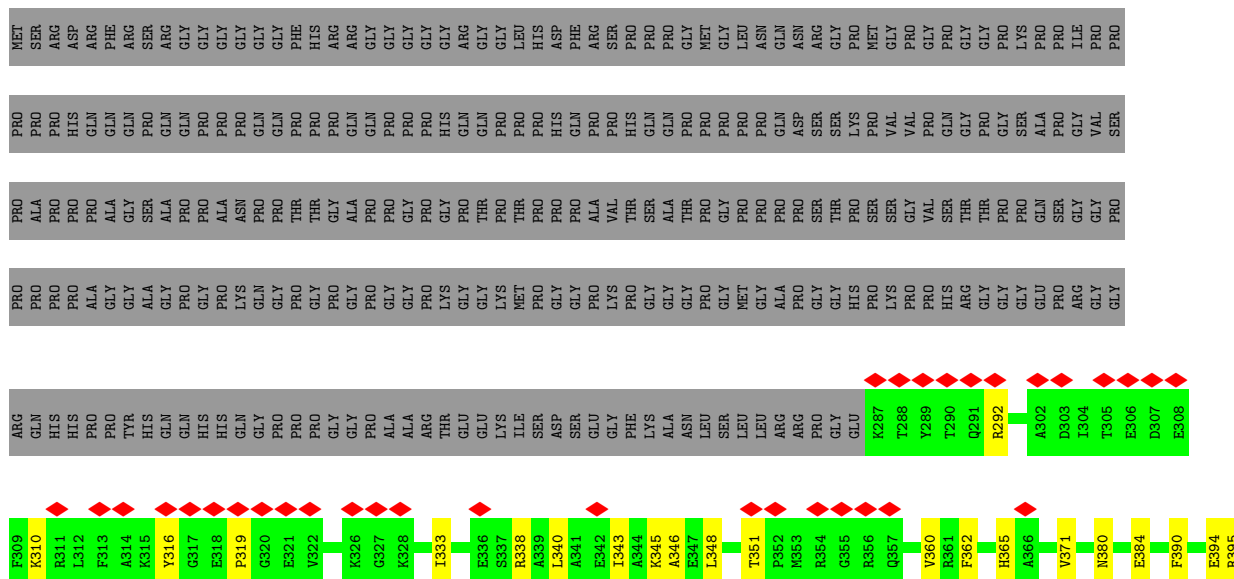
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)

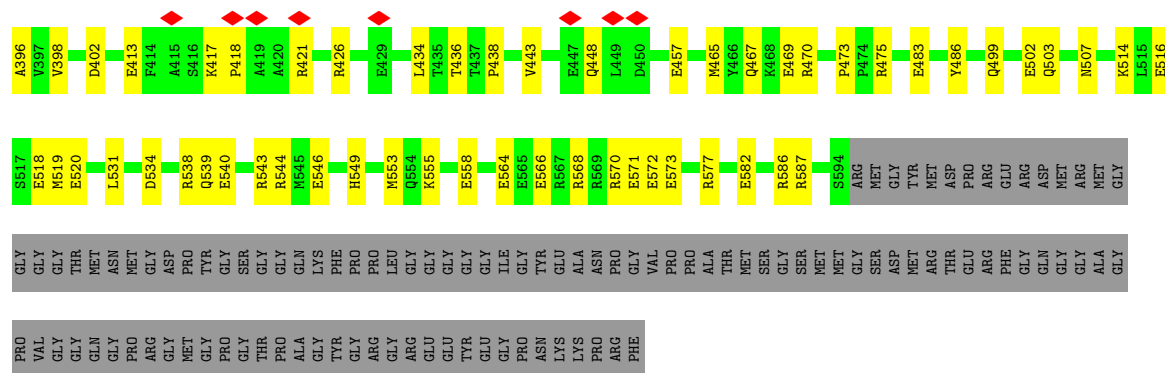


- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)

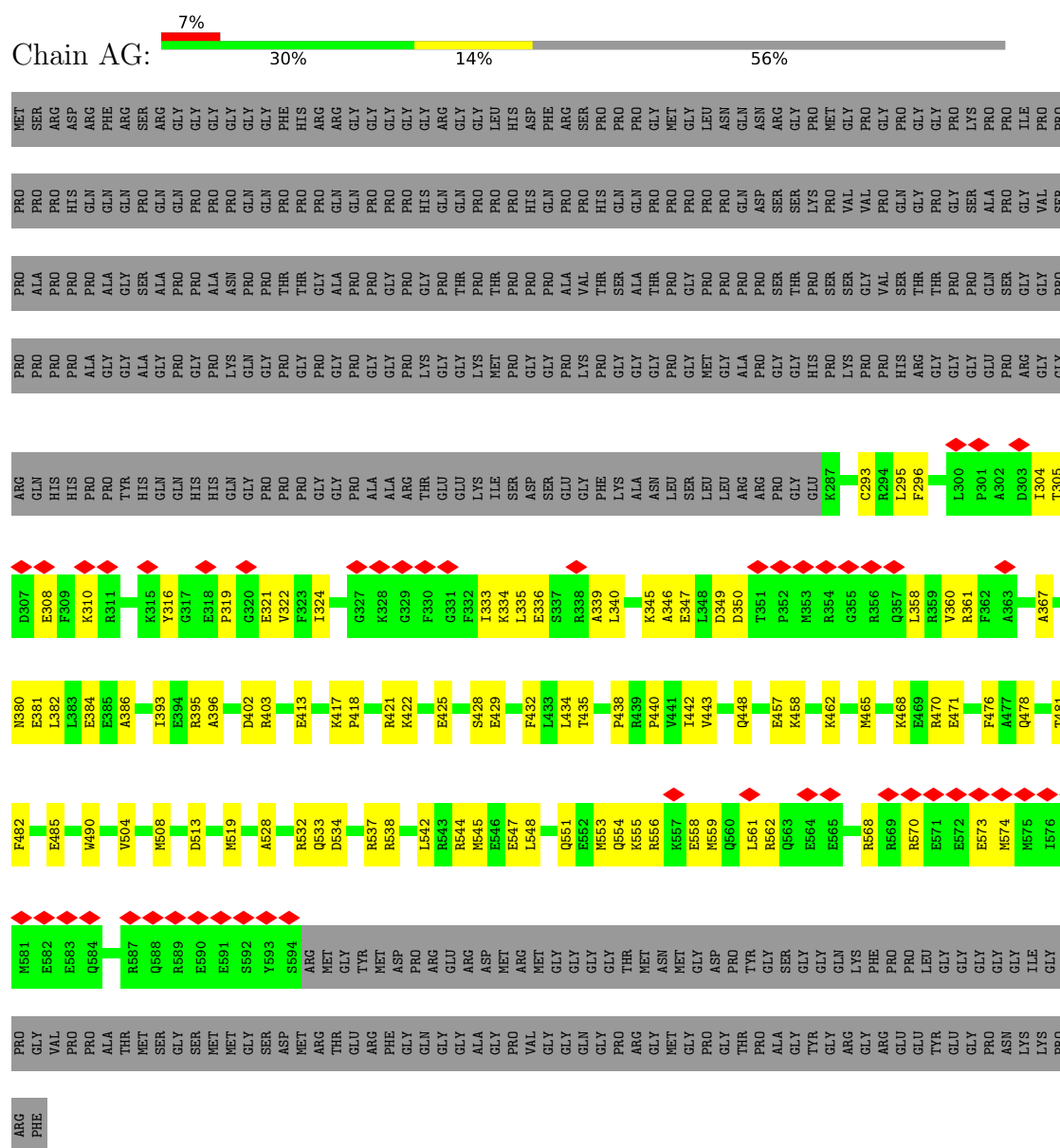





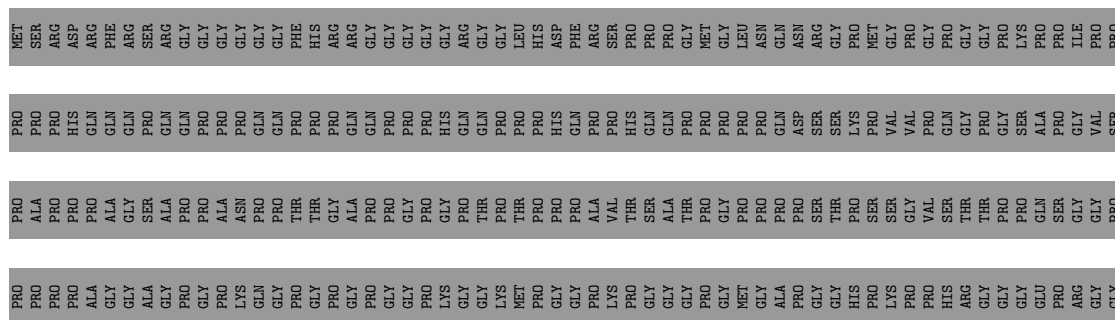
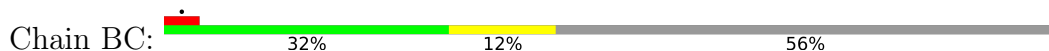
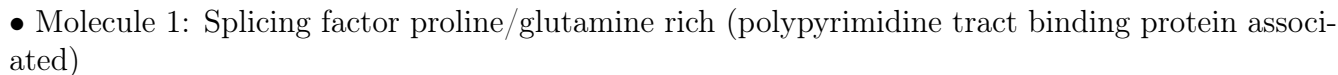


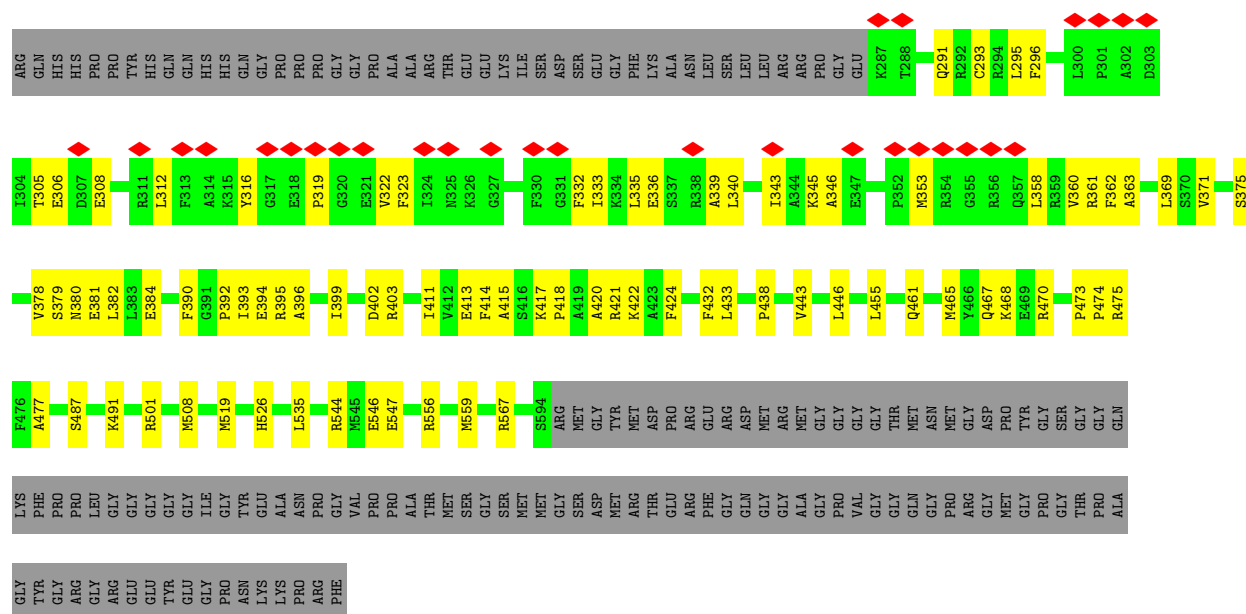


- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)

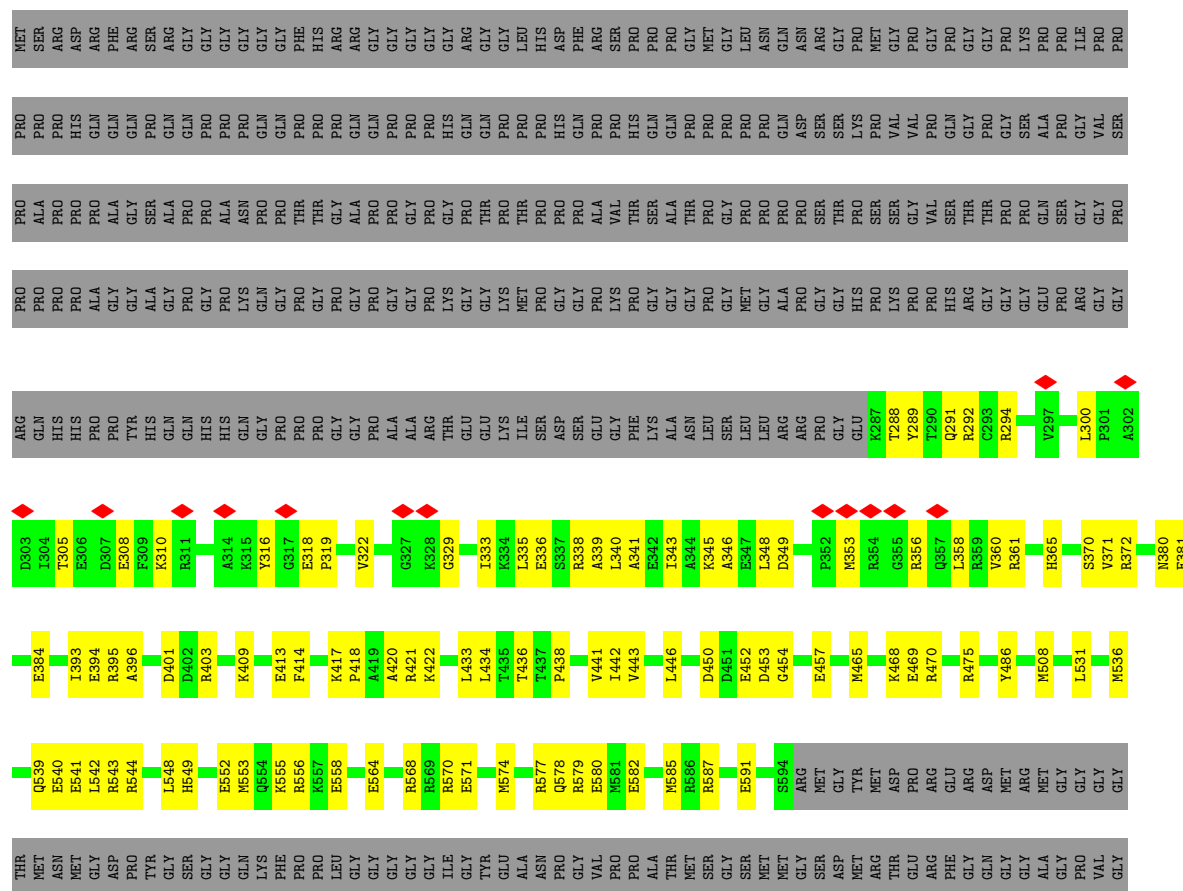
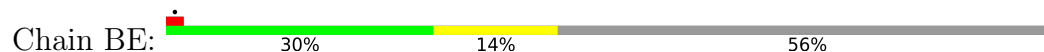


- Chain BA: 





- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)

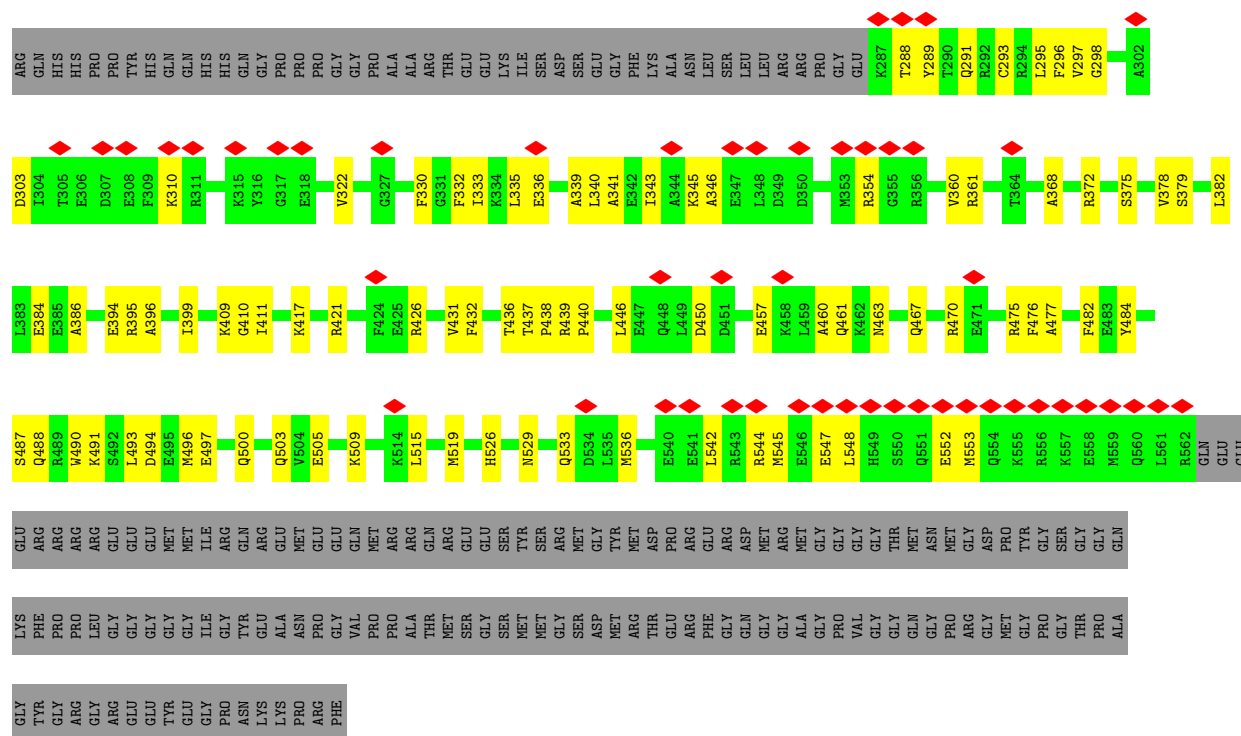






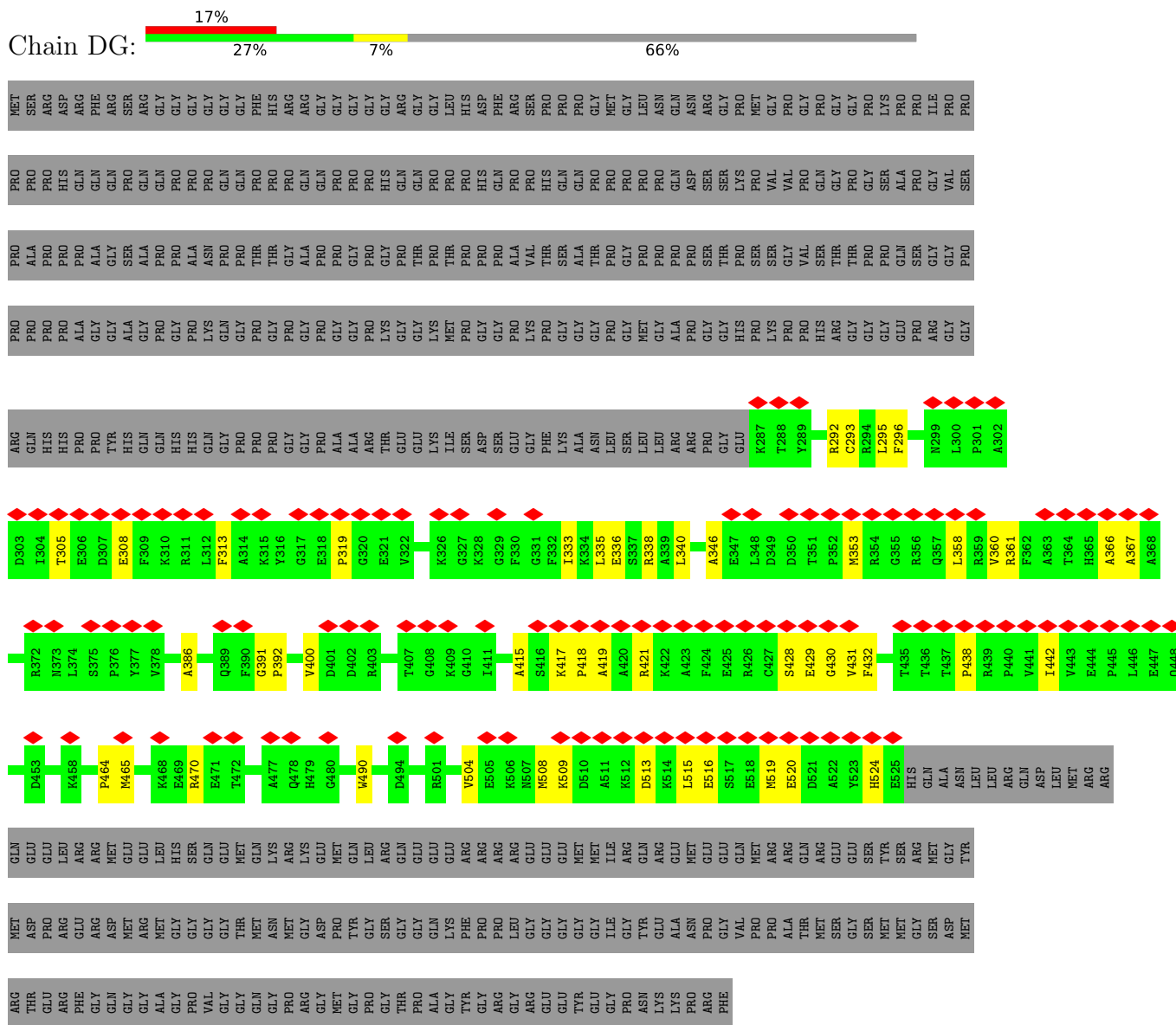








- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)



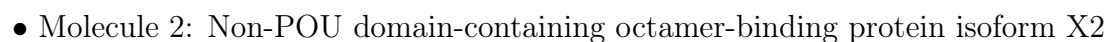
- Molecule 1: Splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)



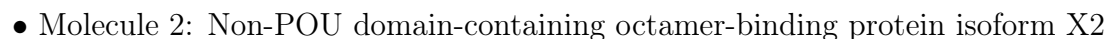




Frequency	Percentage
Daily	41%
Weekly	17%
Monthly	42%



Frequency	Percentage
Daily	42%
Weekly	15%
Monthly	42%

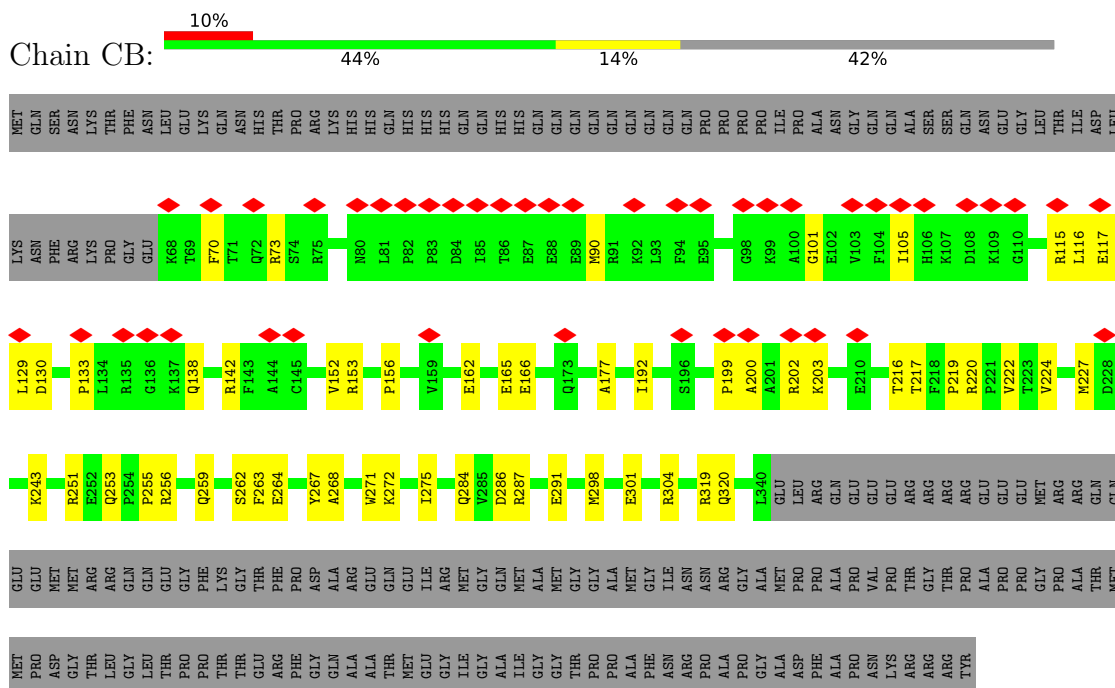


Frequency	Percentage
Very often	6%
Often	39%
Sometimes	18%
Never	42%

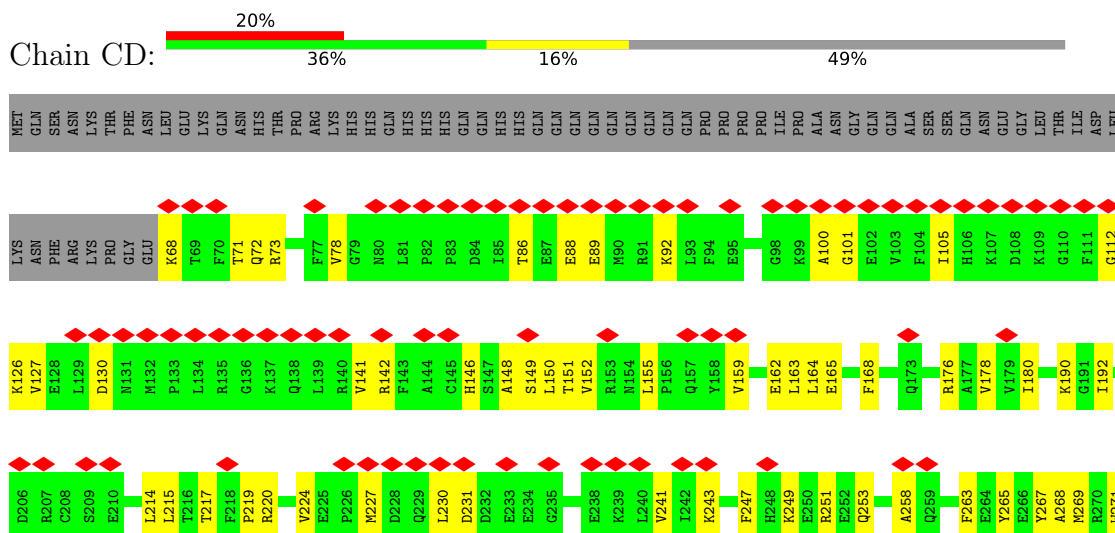




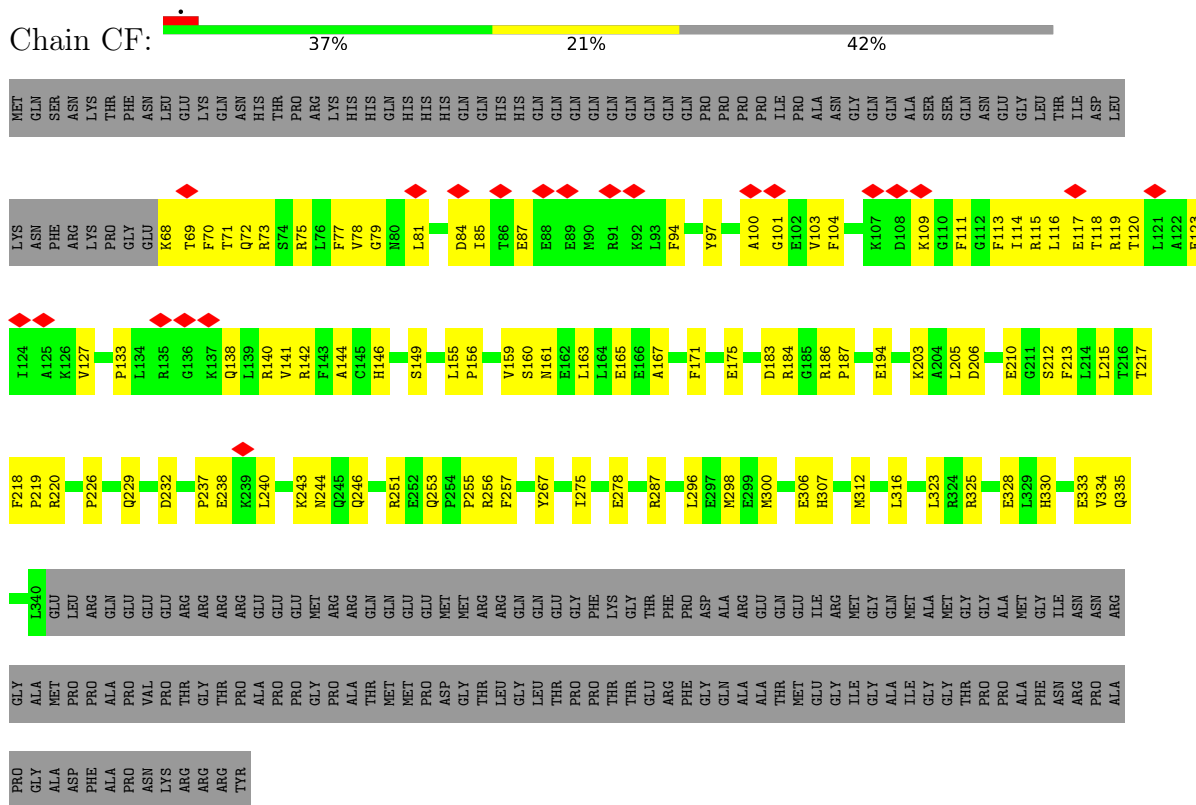
- Molecule 2: Non-POU domain-containing octamer-binding protein isoform X2



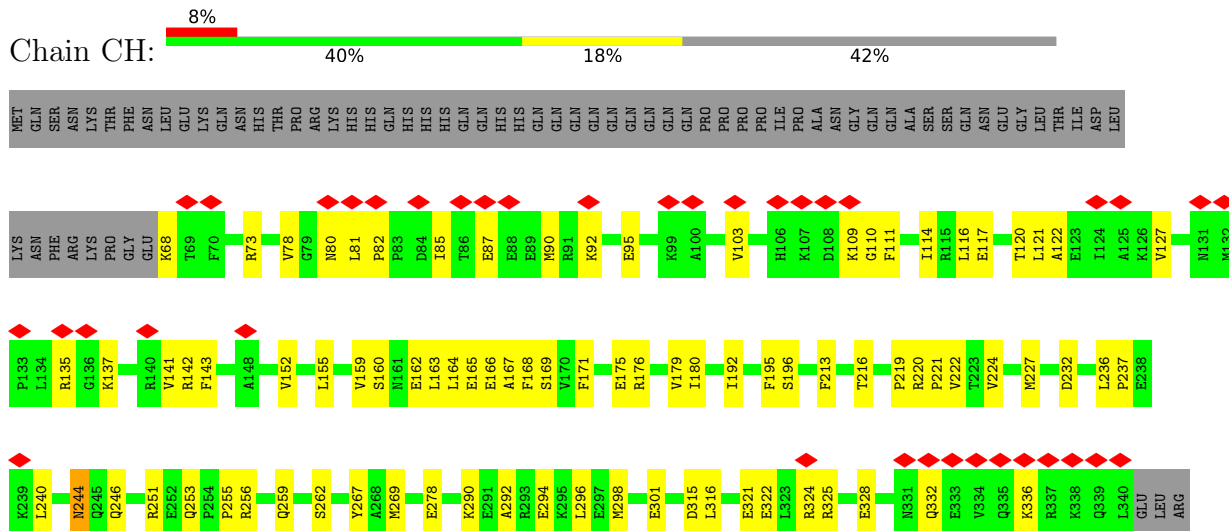
- Molecule 2: Non-POU domain-containing octamer-binding protein isoform X2



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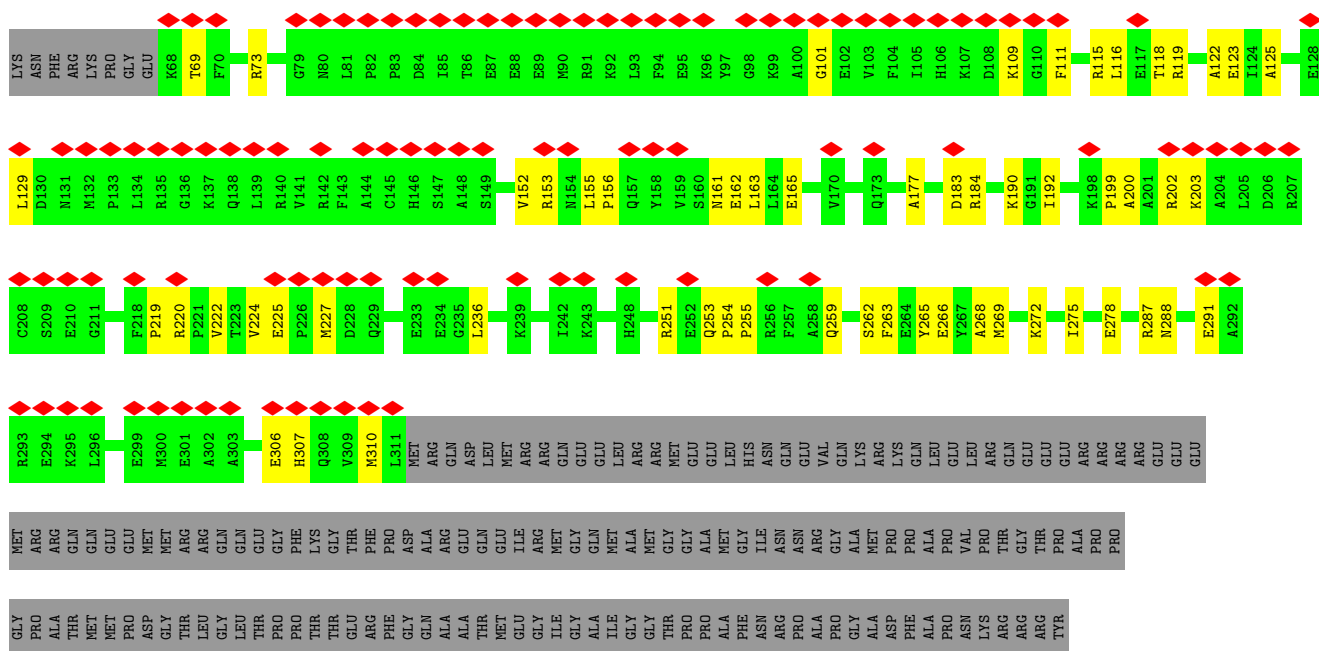


[illegible]

- Molecule 2: Non-POU domain-containing octamer-binding protein isoform X2



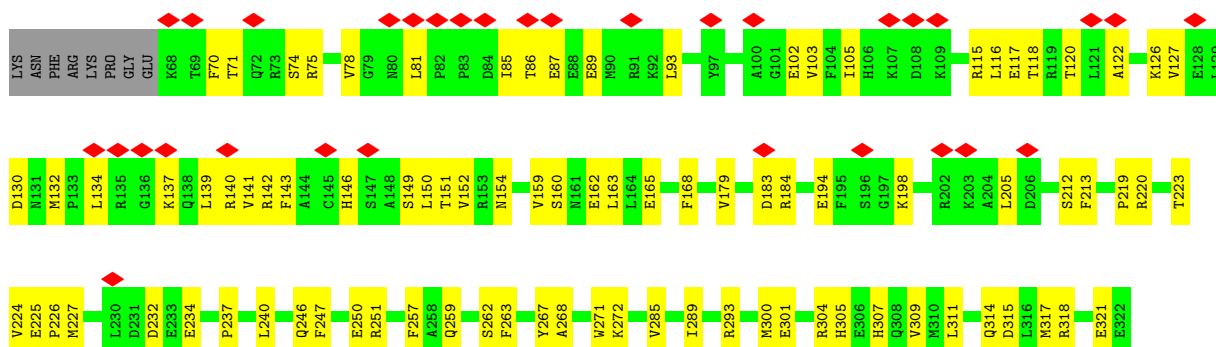
MET	GLN	SER	ASN	LYS	THR	PHE	ASN	LEU	GLU	GLY	GLN	ASN	HIS	THR	ARG	LYS	HIS	HIS	HIS	HIS	GLN	GLN	GLN	GLN	GLN	GLN	PRO	PRO	PRO	PRO	ILE	ALA	ALA	ASN	GLY	GLY	GLN	GLN	ALA	SER	SER	ASN	GLN	GLN	GLU	GLY	THR	ILE	ASP	ASP
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- Molecule 2: Non-POU domain-containing octamer-binding protein isoform X2



MET	GLN	SER	ASN	LYS	THR	PHE	ASN	LEU	GLU	LYS	GLN	ASN	HIS	THR	ARG	LYS	HIS	HIS	HIS	HIS	GLN	GLN	GLN	GLN	GLN	GLN	GLN	PRO	PRO	PRO	PRO	ILE	ALA	ALA	ASN	GLY	GLN	GLN	GLN	ALA	SER	SER	ASN	GLN	GLN	GLU	GLY	THR	ILE	ASP	ASP
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[illegible]

## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	2974535	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	70	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1400	Depositor
Magnification	130000	Depositor
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	85.165	Depositor
Minimum map value	-51.683	Depositor
Average map value	-0.012	Depositor
Map value standard deviation	1.132	Depositor
Recommended contour level	5	Depositor
Map size (Å)	484.352, 484.352, 484.352	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.946, 0.946, 0.946	Depositor

## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	AA	0.16	0/2601	0.34	0/3476
1	AC	0.19	0/2567	0.38	0/3430
1	AE	0.13	0/2601	0.32	0/3476
1	AG	0.16	0/2601	0.37	0/3476
1	BA	0.17	0/2601	0.34	0/3476
1	BC	0.17	0/2601	0.34	0/3476
1	BE	0.17	0/2601	0.36	0/3476
1	BG	0.16	0/2601	0.35	0/3476
1	CA	0.13	0/2291	0.30	0/3071
1	CC	0.12	0/2601	0.30	0/3476
1	CE	0.16	0/2601	0.33	0/3476
1	CG	0.14	0/2601	0.32	0/3476
1	DA	0.11	0/2601	0.29	0/3476
1	DC	0.14	0/2302	0.30	0/3085
1	DE	0.11	0/1937	0.28	0/2603
1	DG	0.09	0/1970	0.25	0/2648
2	AB	0.15	0/2289	0.35	0/3065
2	AD	0.20	0/2289	0.39	0/3065
2	AF	0.11	0/2289	0.31	0/3065
2	AH	0.18	0/2289	0.35	0/3065
2	BB	0.16	0/2289	0.33	0/3065
2	BD	0.17	0/2289	0.34	0/3065
2	BF	0.21	0/2289	0.39	0/3065
2	BH	0.18	0/2289	0.33	0/3065
2	CB	0.11	0/2289	0.29	0/3065
2	CD	0.11	0/2017	0.30	0/2707
2	CF	0.17	0/2289	0.35	0/3065
2	CH	0.16	0/2289	0.31	0/3065
2	DB	0.15	0/2025	0.31	0/2718
2	DD	0.11	0/2289	0.34	0/3065
2	DF	0.11	0/2289	0.33	0/3065
2	DH	0.10	0/2289	0.29	0/3065
All	All	0.15	0/75766	0.33	0/101408

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	AA	2560	0	2521	70	0
1	AC	2527	0	2496	70	0
1	AE	2560	0	2521	65	0
1	AG	2560	0	2521	86	0
1	BA	2560	0	2521	59	0
1	BC	2560	0	2521	69	0
1	BE	2560	0	2521	81	0
1	BG	2560	0	2521	80	0
1	CA	2251	0	2227	39	0
1	CC	2560	0	2521	80	0
1	CE	2560	0	2521	77	0
1	CG	2560	0	2521	58	0
1	DA	2560	0	2521	46	0
1	DC	2262	0	2240	67	0
1	DE	1901	0	1881	34	0
1	DG	1932	0	1903	37	0
2	AB	2250	0	2256	66	0
2	AD	2250	0	2256	65	0
2	AF	2250	0	2256	50	0
2	AH	2250	0	2256	65	0
2	BB	2250	0	2256	58	0
2	BD	2250	0	2256	76	0
2	BF	2250	0	2256	68	0
2	BH	2250	0	2256	67	0
2	CB	2250	0	2256	47	0
2	CD	1979	0	1974	55	0
2	CF	2250	0	2256	77	0
2	CH	2250	0	2256	63	0
2	DB	1987	0	1985	38	0
2	DD	2250	0	2256	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	DF	2250	0	2256	47	0
2	DH	2250	0	2256	64	0
All	All	74499	0	74021	1658	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

All (1658) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DH:129:LEU:HA	2:DH:132:MET:HE3	1.58	0.86
1:BE:452:GLU:HA	2:BF:176:ARG:HH22	1.41	0.85
1:BE:292:ARG:HD2	1:BE:395:ARG:HD2	1.57	0.85
1:BC:339:ALA:HB1	2:BD:127:VAL:HG13	1.59	0.84
2:CF:186:ARG:HE	2:CF:187:PRO:HD2	1.42	0.82
1:AA:371:VAL:HG12	1:AA:443:VAL:HG12	1.61	0.82
1:AG:382:LEU:HD21	2:AH:251:ARG:HH12	1.43	0.81
2:AB:198:LYS:HB2	2:AB:202:ARG:HH21	1.44	0.81
1:AG:417:LYS:HB3	1:AG:421:ARG:HH21	1.46	0.79
2:BH:184:ARG:HD2	2:BH:186:ARG:HE	1.48	0.79
1:AG:533:GLN:HB3	1:AG:537:ARG:HH12	1.47	0.79
2:DF:73:ARG:HH21	2:DF:176:ARG:HB3	1.46	0.79
1:AA:508:MET:HE1	2:AB:278:GLU:HB2	1.65	0.79
1:BE:555:LYS:NZ	1:CC:581:MET:SD	2.56	0.78
2:BB:73:ARG:HH12	2:BB:194:GLU:HG2	1.46	0.78
1:BC:465:MET:HG2	1:BC:468:LYS:HE3	1.64	0.77
1:BA:575:MET:HE3	2:CH:298:MET:HE2	1.66	0.77
1:BE:570:ARG:HD2	1:CC:570:ARG:HH11	1.50	0.77
1:BC:508:MET:HE3	2:BD:278:GLU:HA	1.66	0.77
2:BD:326:MET:SD	1:CC:524:HIS:NE2	2.57	0.77
1:CE:345:LYS:HD3	1:CE:362:PHE:HE1	1.50	0.77
1:BE:371:VAL:HG12	1:BE:443:VAL:HG22	1.67	0.76
1:CE:373:ASN:HD22	2:CF:275:ILE:HD11	1.49	0.76
2:CH:152:VAL:HG12	2:CH:224:VAL:HG12	1.68	0.75
2:BH:244:ASN:OD1	2:BH:246:GLN:NE2	2.20	0.74
2:BH:87:GLU:HG3	2:BH:103:VAL:HG11	1.69	0.74
1:BE:465:MET:HG3	1:BE:468:LYS:HE3	1.68	0.74
1:BG:438:PRO:HG2	2:BH:267:TYR:CD2	2.22	0.74
1:DE:386:ALA:HB1	1:DE:432:PHE:HZ	1.51	0.74
2:DB:165:GLU:HG2	2:DB:177:ALA:HB3	1.70	0.74
2:BD:237:PRO:HG2	2:BD:240:LEU:HD13	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AD:100:ALA:HB1	2:AD:114:ILE:HD11	1.70	0.73
1:BG:555:LYS:NZ	1:DA:585:MET:SD	2.61	0.72
2:CB:165:GLU:HG2	2:CB:177:ALA:HB3	1.68	0.72
1:BC:417:LYS:HB3	1:BC:421:ARG:HH21	1.53	0.72
2:CF:140:ARG:HH21	2:CF:142:ARG:HH22	1.38	0.72
2:BD:100:ALA:HB1	2:BD:114:ILE:HD11	1.71	0.72
2:CD:251:ARG:NH1	2:CD:253:GLN:O	2.23	0.71
1:AC:389:GLN:OE1	2:AD:256:ARG:NH1	2.22	0.71
2:BH:256:ARG:HH22	2:BH:264:GLU:HG3	1.55	0.71
1:CC:417:LYS:HB3	1:CC:421:ARG:HH21	1.55	0.71
1:AG:533:GLN:HB3	1:AG:537:ARG:NH1	2.05	0.71
1:DC:346:ALA:HB1	2:DD:120:THR:HG23	1.71	0.71
1:CA:340:LEU:HD23	1:CA:343:ILE:HD11	1.71	0.71
1:DC:297:VAL:HG13	1:DC:360:VAL:HG22	1.72	0.71
2:DH:192:ILE:HG23	2:DH:227:MET:HE1	1.73	0.70
2:BB:68:LYS:NZ	2:BB:69:THR:O	2.23	0.70
1:BE:570:ARG:HD2	1:CC:570:ARG:NH1	2.06	0.70
1:DC:470:ARG:HH12	2:DD:163:LEU:HD21	1.56	0.70
1:AC:438:PRO:HG2	2:AD:267:TYR:HD2	1.54	0.70
1:CC:399:ILE:HG12	1:CC:410:GLY:HA2	1.72	0.70
1:AC:379:SER:HB2	2:AD:236:LEU:O	1.91	0.70
2:AD:105:ILE:HD13	2:AD:112:GLY:HA3	1.74	0.70
1:CE:294:ARG:NH2	1:CE:321:GLU:OE2	2.25	0.70
2:BD:313:ARG:NH2	1:CC:546:GLU:OE1	2.24	0.69
2:AB:70:PHE:O	2:AB:115:ARG:NH1	2.26	0.69
2:BD:78:VAL:HG22	2:BD:141:VAL:HG13	1.75	0.69
2:CH:192:ILE:HG23	2:CH:227:MET:HE1	1.72	0.69
2:AH:184:ARG:HD3	2:AH:186:ARG:HH21	1.56	0.69
2:DH:100:ALA:HB1	2:DH:114:ILE:HD11	1.74	0.69
1:DE:431:VAL:HG21	2:DF:269:MET:HE1	1.73	0.69
1:AG:339:ALA:HB1	2:AH:127:VAL:HG13	1.75	0.69
2:AD:313:ARG:NH2	1:BC:546:GLU:OE2	2.26	0.68
1:DE:436:THR:HG22	2:DF:253:GLN:HG3	1.75	0.68
1:DC:395:ARG:NH1	2:DD:232:ASP:O	2.27	0.68
1:CG:367:ALA:HB2	1:CG:417:LYS:HD3	1.75	0.68
1:AC:442:ILE:HG13	2:AD:275:ILE:HG21	1.75	0.68
2:BB:73:ARG:HE	2:BB:176:ARG:HH11	1.42	0.68
2:AB:119:ARG:NE	2:AB:123:GLU:OE2	2.27	0.68
2:AD:318:ARG:HH22	2:AD:319:ARG:HE	1.40	0.68
1:DA:475:ARG:HG3	1:DA:477:ALA:H	1.57	0.68
2:AB:306:GLU:OE2	1:DA:549:HIS:NE2	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:361:ARG:NH2	1:BE:450:ASP:OD2	2.27	0.68
1:BG:378:VAL:HG21	1:BG:434:LEU:HD23	1.74	0.68
1:CE:470:ARG:NH2	2:CF:163:LEU:HB2	2.09	0.68
1:AC:470:ARG:NH2	2:AD:166:GLU:OE1	2.24	0.67
2:AD:237:PRO:HG2	2:AD:240:LEU:HD13	1.75	0.67
1:AE:571:GLU:OE2	1:BC:567:ARG:NH1	2.27	0.67
1:AG:346:ALA:HB1	2:AH:120:THR:HG23	1.76	0.67
2:BF:119:ARG:NE	2:BF:123:GLU:OE2	2.28	0.67
1:CC:579:ARG:HB3	2:CF:298:MET:HE1	1.75	0.67
1:BE:291:GLN:OE1	1:BE:365:HIS:ND1	2.27	0.67
1:AC:436:THR:HG21	2:AD:252:GLU:HB2	1.76	0.67
1:AC:417:LYS:HB3	1:AC:421:ARG:HH21	1.58	0.67
2:DD:140:ARG:NH2	2:DD:234:GLU:OE2	2.27	0.67
2:AB:116:LEU:HD12	2:AB:122:ALA:HA	1.75	0.67
1:DC:339:ALA:HB1	2:DD:127:VAL:HG13	1.76	0.67
1:DA:475:ARG:NH2	1:DA:483:GLU:OE1	2.27	0.67
2:DB:156:PRO:HA	2:DB:220:ARG:HH21	1.59	0.67
1:AE:434:LEU:HA	2:AF:255:PRO:HB3	1.76	0.67
2:AF:131:ASN:O	2:AF:138:GLN:NE2	2.27	0.67
1:AG:296:PHE:N	1:AG:361:ARG:O	2.26	0.67
2:DD:126:LYS:HE3	2:DD:143:PHE:HD1	1.60	0.67
1:AA:300:LEU:HD23	1:AA:353:MET:HE1	1.76	0.67
1:DE:504:VAL:HG22	1:DE:508:MET:HE1	1.78	0.66
2:AB:301:GLU:OE2	1:BG:586:ARG:NH2	2.28	0.66
2:BH:74:SER:HA	2:BH:119:ARG:HD3	1.78	0.66
1:CE:470:ARG:NH2	2:CF:160:SER:OG	2.28	0.66
1:BC:340:LEU:HD23	1:BC:343:ILE:HD12	1.75	0.66
2:DH:324:ARG:NH1	2:DH:328:GLU:OE2	2.28	0.66
2:AF:75:ARG:NH2	2:AF:102:GLU:OE2	2.28	0.66
2:AF:152:VAL:HG12	2:AF:224:VAL:HG22	1.76	0.66
2:AF:186:ARG:HD2	2:AF:187:PRO:HD2	1.76	0.66
1:BC:371:VAL:HG12	1:BC:443:VAL:HG12	1.77	0.66
2:CB:101:GLY:HA3	2:CB:115:ARG:HE	1.60	0.66
2:DH:244:ASN:N	2:DH:244:ASN:HD22	1.93	0.66
1:AG:295:LEU:HD22	1:AG:360:VAL:HG12	1.77	0.66
2:DF:314:GLN:HA	2:DF:317:MET:SD	2.36	0.66
1:AC:303:ASP:HB3	1:AC:354:ARG:HH22	1.59	0.66
1:DC:379:SER:HB3	1:DC:382:LEU:HD23	1.77	0.66
1:AA:491:LYS:NZ	2:AB:209:SER:O	2.29	0.66
2:BD:150:LEU:HD11	2:BD:201:ALA:HB1	1.78	0.66
2:AD:116:LEU:HD22	2:AD:122:ALA:HA	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:455:LEU:HD11	1:CC:459:LEU:HD22	1.77	0.65
1:CE:384:GLU:HG2	1:CE:396:ALA:HB3	1.79	0.65
1:CE:535:LEU:HD11	2:DF:320:GLN:HG3	1.78	0.65
1:DG:367:ALA:HB2	1:DG:417:LYS:HD3	1.77	0.65
2:DH:149:SER:OG	2:DH:227:MET:SD	2.53	0.65
1:BA:475:ARG:NH2	1:BA:483:GLU:OE1	2.27	0.65
2:BH:146:HIS:O	2:BH:229:GLN:NE2	2.30	0.65
2:BH:100:ALA:HB1	2:BH:114:ILE:HD11	1.77	0.65
1:DA:377:TYR:O	2:DB:251:ARG:NH2	2.29	0.65
1:DG:516:GLU:HA	1:DG:519:MET:HE2	1.79	0.65
1:AA:501:ARG:NH2	2:AB:286:ASP:OD1	2.29	0.65
2:BH:251:ARG:HH22	2:BH:254:PRO:HA	1.61	0.65
2:DH:251:ARG:HH22	2:DH:255:PRO:HD3	1.60	0.65
2:AB:89:GLU:OE2	2:AB:135:ARG:NH1	2.29	0.65
1:AC:336:GLU:HB3	1:AC:340:LEU:HD12	1.79	0.65
1:AG:556:ARG:HH22	2:DH:301:GLU:HB2	1.60	0.65
1:BC:470:ARG:NH2	2:BD:166:GLU:OE2	2.30	0.65
2:CH:87:GLU:HG3	2:CH:103:VAL:HG11	1.78	0.65
2:CH:324:ARG:NH1	2:CH:328:GLU:OE2	2.30	0.65
1:BG:411:ILE:HD13	1:BG:446:LEU:HD13	1.78	0.65
1:BG:367:ALA:HB2	1:BG:417:LYS:HD3	1.78	0.65
1:CA:483:GLU:HG3	2:CB:219:PRO:HB3	1.79	0.65
1:DE:475:ARG:HG2	1:DE:477:ALA:H	1.62	0.65
1:AG:293:CYS:HB2	1:AG:335:LEU:HB2	1.79	0.64
1:BC:501:ARG:NH2	2:BD:286:ASP:OD1	2.30	0.64
1:BE:442:ILE:HD13	2:BF:275:ILE:HG21	1.79	0.64
1:DC:417:LYS:HB3	1:DC:421:ARG:HH21	1.58	0.64
1:AC:545:MET:SD	2:DD:309:VAL:HG22	2.37	0.64
1:BA:367:ALA:HB2	1:BA:417:LYS:HD3	1.77	0.64
1:CA:377:TYR:O	2:CB:251:ARG:NH2	2.30	0.64
1:BE:574:MET:HE1	1:BE:577:ARG:NH1	2.12	0.64
2:CF:104:PHE:HB3	2:CF:113:PHE:HB2	1.78	0.64
2:AB:324:ARG:NH2	2:DH:327:GLU:HB3	2.12	0.64
2:BH:140:ARG:NH2	2:BH:234:GLU:OE2	2.30	0.64
1:BE:549:HIS:NE2	2:CF:306:GLU:OE1	2.31	0.64
1:CE:566:GLU:OE2	1:CE:570:ARG:NH1	2.30	0.64
2:CF:146:HIS:O	2:CF:229:GLN:NE2	2.31	0.64
1:CG:319:PRO:HB3	1:CG:333:ILE:HD11	1.80	0.64
2:AH:167:ALA:HB1	2:AH:213:PHE:HZ	1.62	0.64
1:BC:392:PRO:HG2	1:BC:415:ALA:HB3	1.78	0.64
1:DC:493:LEU:O	1:DC:497:GLU:HG2	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BD:116:LEU:HD22	2:BD:122:ALA:HA	1.79	0.64
2:AH:116:LEU:HD12	2:AH:122:ALA:HA	1.80	0.63
1:BE:564:GLU:OE1	1:BE:568:ARG:NH2	2.31	0.63
2:CB:152:VAL:HG12	2:CB:224:VAL:HG22	1.80	0.63
1:AG:336:GLU:HB2	1:AG:340:LEU:HD12	1.80	0.63
2:AH:321:GLU:OE2	2:AH:324:ARG:NH2	2.31	0.63
1:BC:361:ARG:HH21	1:BC:363:ALA:HA	1.62	0.63
1:BA:371:VAL:HG12	1:BA:443:VAL:HG22	1.81	0.63
1:BE:292:ARG:O	1:BE:338:ARG:NH1	2.32	0.63
2:DH:146:HIS:O	2:DH:229:GLN:NE2	2.31	0.63
2:DF:297:GLU:HA	2:DF:300:MET:HE3	1.79	0.63
1:BA:575:MET:HE2	2:CH:294:GLU:HG3	1.78	0.63
2:BF:159:VAL:HG23	2:BF:163:LEU:HD22	1.79	0.63
1:CE:466:TYR:HE1	1:CE:470:ARG:HE	1.45	0.63
1:BE:438:PRO:HG2	2:BF:267:TYR:CD2	2.33	0.63
1:AE:395:ARG:HG2	1:AE:413:GLU:HG2	1.80	0.63
1:AC:346:ALA:HB1	2:AD:120:THR:HG23	1.79	0.63
2:BF:324:ARG:HH12	2:BF:328:GLU:HG2	1.64	0.63
1:CE:370:SER:HB2	1:CE:446:LEU:HD13	1.79	0.63
2:CD:71:THR:HG22	2:CD:73:ARG:H	1.64	0.62
2:BH:126:LYS:HE3	2:BH:142:ARG:HA	1.82	0.62
1:CA:371:VAL:HG12	1:CA:443:VAL:HG12	1.81	0.62
2:CD:152:VAL:HG12	2:CD:224:VAL:HG22	1.80	0.62
1:AC:384:GLU:HB2	1:AC:393:ILE:HG21	1.81	0.62
2:BD:81:LEU:HB3	2:BD:85:ILE:HD13	1.82	0.62
2:BB:216:THR:HG22	2:BB:217:THR:H	1.64	0.62
1:DC:293:CYS:HB3	1:DC:335:LEU:H	1.63	0.62
2:AB:216:THR:HG22	2:AB:217:THR:H	1.64	0.62
2:AD:133:PRO:HA	2:AD:138:GLN:HA	1.81	0.62
2:BB:253:GLN:OE1	2:BB:256:ARG:NE	2.32	0.62
1:BC:346:ALA:HB1	2:BD:120:THR:HG23	1.81	0.62
1:BG:584:GLN:O	1:BG:587:ARG:HG3	1.99	0.62
1:CC:346:ALA:HB1	2:CD:120:THR:HG23	1.81	0.62
1:CG:312:LEU:HD11	1:CG:353:MET:HE1	1.81	0.62
1:DC:303:ASP:HB3	1:DC:354:ARG:HH22	1.64	0.62
1:BE:393:ILE:HD11	1:BE:396:ALA:HB2	1.80	0.61
2:CF:73:ARG:NH2	2:CF:194:GLU:OE2	2.33	0.61
1:AC:319:PRO:HB3	1:AC:333:ILE:HD11	1.82	0.61
1:AG:371:VAL:HG22	1:AG:443:VAL:HG12	1.82	0.61
2:BF:71:THR:HG23	2:BF:73:ARG:H	1.65	0.61
2:CF:146:HIS:HD2	2:CF:149:SER:HB2	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BA:579:ARG:HB2	2:CH:298:MET:HE1	1.82	0.61
2:AB:90:MET:HE1	2:AB:114:ILE:HG21	1.83	0.61
2:AB:117:GLU:HG3	2:AB:118:THR:HG23	1.83	0.61
1:AE:316:TYR:HB3	1:AE:340:LEU:HD22	1.81	0.61
2:AF:77:PHE:HB2	2:AF:144:ALA:HB2	1.82	0.61
1:BC:384:GLU:HB2	1:BC:393:ILE:HG21	1.83	0.61
2:CH:90:MET:HE2	2:CH:114:ILE:HG13	1.83	0.61
1:AA:459:LEU:HA	1:AA:462:LYS:HG3	1.82	0.61
2:CB:116:LEU:HD12	2:CB:122:ALA:HA	1.83	0.61
2:CH:321:GLU:OE2	2:CH:324:ARG:NH2	2.34	0.61
2:DB:155:LEU:HD23	2:DB:222:VAL:HG11	1.83	0.61
2:AB:319:ARG:HH12	1:DA:538:ARG:HE	1.48	0.61
2:BF:116:LEU:HD22	2:BF:122:ALA:HA	1.83	0.61
2:CF:119:ARG:NE	2:CF:123:GLU:OE2	2.32	0.61
1:DE:434:LEU:HA	2:DF:255:PRO:HB3	1.82	0.61
1:AC:508:MET:SD	1:AC:512:LYS:NZ	2.74	0.61
1:BE:346:ALA:HB1	2:BF:120:THR:HG23	1.81	0.61
2:DH:296:LEU:O	2:DH:300:MET:HE3	2.01	0.61
1:BG:296:PHE:N	1:BG:361:ARG:O	2.34	0.60
1:BG:434:LEU:HD13	1:BG:441:VAL:HG21	1.82	0.60
1:AG:382:LEU:HD21	2:AH:251:ARG:NH1	2.15	0.60
2:BH:238:GLU:OE1	2:BH:238:GLU:N	2.30	0.60
2:DB:116:LEU:HD12	2:DB:122:ALA:HA	1.82	0.60
2:BF:87:GLU:HG3	2:BF:103:VAL:HG11	1.82	0.60
1:CG:346:ALA:HB1	2:CH:120:THR:HG23	1.83	0.60
1:BG:293:CYS:SG	1:BG:335:LEU:N	2.73	0.60
1:BG:339:ALA:HB1	2:BH:127:VAL:HG13	1.83	0.60
1:DG:438:PRO:HG2	2:DH:267:TYR:HD2	1.66	0.60
1:AC:380:ASN:HD21	2:AD:235:GLY:HA3	1.65	0.60
2:BF:146:HIS:ND1	2:BF:194:GLU:OE1	2.34	0.60
1:AA:585:MET:HE2	1:CG:552:GLU:OE1	2.01	0.60
2:BF:104:PHE:HB3	2:BF:113:PHE:HB2	1.83	0.60
2:BH:162:GLU:HA	2:BH:165:GLU:HG2	1.84	0.60
1:AA:570:ARG:HE	1:CG:570:ARG:HD3	1.66	0.60
1:AE:564:GLU:OE1	1:AE:568:ARG:NH2	2.35	0.60
2:BB:287:ARG:NH1	1:CG:568:ARG:HE	2.00	0.60
2:BD:78:VAL:HG13	2:BD:141:VAL:HG22	1.83	0.60
1:CA:503:GLN:HA	1:CA:506:LYS:HG2	1.84	0.60
1:CE:371:VAL:HG12	1:CE:443:VAL:HG22	1.83	0.60
2:DB:153:ARG:HH12	2:DB:225:GLU:HB2	1.66	0.60
1:AE:365:HIS:CE1	1:AE:413:GLU:HB2	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:336:GLU:HB3	1:BC:340:LEU:HD12	1.83	0.60
1:BG:306:GLU:HG3	1:BG:322:VAL:HG11	1.83	0.60
2:BD:324:ARG:HH12	2:BD:328:GLU:HG2	1.66	0.60
1:BE:305:THR:HG23	1:BE:308:GLU:H	1.67	0.60
1:DE:438:PRO:HG2	2:DF:267:TYR:HD2	1.66	0.60
1:AA:396:ALA:HB2	1:AA:412:VAL:HG23	1.84	0.59
1:AA:558:GLU:OE2	1:AA:562:ARG:NH2	2.34	0.59
2:BF:146:HIS:O	2:BF:229:GLN:NE2	2.35	0.59
1:BG:438:PRO:HG2	2:BH:267:TYR:HD2	1.65	0.59
1:AA:491:LYS:NZ	2:AB:211:GLY:O	2.34	0.59
2:CD:142:ARG:NH2	2:CD:231:ASP:OD2	2.35	0.59
1:CG:449:LEU:HD13	2:CH:180:ILE:HG21	1.83	0.59
2:DB:306:GLU:O	2:DB:310:MET:HG3	2.01	0.59
2:DH:244:ASN:OD1	2:DH:246:GLN:NE2	2.33	0.59
2:AD:87:GLU:HG3	2:AD:103:VAL:HG11	1.85	0.59
1:BC:316:TYR:HB3	1:BC:340:LEU:HD22	1.84	0.59
1:CG:336:GLU:HB3	1:CG:340:LEU:HD12	1.84	0.59
1:AE:531:LEU:HB3	2:BF:323:LEU:HD12	1.84	0.59
2:BB:138:GLN:HB3	2:BB:140:ARG:HH22	1.66	0.59
2:BD:152:VAL:HG12	2:BD:224:VAL:HG22	1.83	0.59
1:CE:292:ARG:HD2	1:CE:395:ARG:HD3	1.84	0.59
1:CE:549:HIS:NE2	2:DF:306:GLU:OE1	2.34	0.59
2:BB:119:ARG:NE	2:BB:123:GLU:OE2	2.36	0.59
1:CC:475:ARG:HG2	1:CC:477:ALA:H	1.66	0.59
2:DB:125:ALA:O	2:DB:129:LEU:HB2	2.03	0.59
2:DD:314:GLN:HA	2:DD:317:MET:SD	2.43	0.59
1:AE:436:THR:HG22	2:AF:253:GLN:HG3	1.83	0.59
1:CC:469:GLU:OE2	2:CD:217:THR:OG1	2.21	0.59
2:CD:180:ILE:HB	2:CD:190:LYS:HG3	1.85	0.59
2:DB:272:LYS:HA	2:DB:275:ILE:HG12	1.84	0.59
2:BH:105:ILE:HD13	2:BH:112:GLY:HA3	1.83	0.59
1:AE:573:GLU:OE2	1:AE:577:ARG:NH2	2.36	0.59
2:BF:206:ASP:OD1	2:BF:207:ARG:N	2.35	0.59
1:BG:574:MET:HE3	1:DA:563:GLN:CD	2.27	0.59
1:CG:366:ALA:HB3	1:CG:417:LYS:HZ2	1.66	0.59
1:BG:371:VAL:HG22	1:BG:443:VAL:HG12	1.85	0.59
1:CC:431:VAL:HG22	2:CD:272:LYS:HE3	1.84	0.59
2:CD:276:GLU:OE2	2:CD:280:GLN:NE2	2.36	0.59
1:CE:542:LEU:HB2	2:DF:312:MET:HE1	1.83	0.59
2:DD:237:PRO:HG2	2:DD:240:LEU:HD13	1.83	0.59
1:BE:335:LEU:HD12	1:BE:341:ALA:HA	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DG:400:VAL:HB	2:DH:231:ASP:HB3	1.85	0.58
2:BF:238:GLU:OE1	2:BF:238:GLU:N	2.33	0.58
1:CE:342:GLU:HA	1:CE:345:LYS:HG2	1.85	0.58
2:DH:321:GLU:OE2	2:DH:324:ARG:NH2	2.35	0.58
2:CH:116:LEU:HD12	2:CH:122:ALA:HA	1.86	0.58
2:CD:150:LEU:HD21	2:CD:205:LEU:HB2	1.86	0.58
2:DH:244:ASN:HD22	2:DH:244:ASN:H	1.51	0.58
1:CA:555:LYS:HG2	1:CA:559:MET:HE1	1.85	0.58
2:AB:152:VAL:HG12	2:AB:224:VAL:HG22	1.84	0.58
1:BA:483:GLU:HG2	2:BB:219:PRO:HB3	1.85	0.58
1:BC:379:SER:HB3	1:BC:382:LEU:HD23	1.85	0.58
2:BD:119:ARG:HH22	2:BD:143:PHE:HB3	1.68	0.58
1:BG:384:GLU:HB2	1:BG:393:ILE:HG21	1.85	0.58
2:BH:70:PHE:O	2:BH:115:ARG:NH1	2.37	0.58
2:DB:119:ARG:NE	2:DB:123:GLU:OE2	2.36	0.58
2:DD:150:LEU:HA	2:DD:226:PRO:HA	1.86	0.58
1:AC:293:CYS:HB3	1:AC:335:LEU:H	1.69	0.58
2:CB:216:THR:HG22	2:CB:217:THR:H	1.69	0.58
1:DC:438:PRO:HG2	2:DD:267:TYR:CD2	2.38	0.58
2:DD:85:ILE:HG12	2:DD:105:ILE:HG21	1.84	0.58
1:AG:386:ALA:HB1	1:AG:432:PHE:HZ	1.68	0.58
1:BA:534:ASP:OD2	2:CB:319:ARG:NH2	2.33	0.58
1:BA:587:ARG:HH12	1:BA:591:GLU:HB2	1.68	0.58
2:BH:116:LEU:HD12	2:BH:122:ALA:HA	1.86	0.58
2:CB:156:PRO:HA	2:CB:220:ARG:HH21	1.69	0.58
1:CE:508:MET:HE3	2:CF:278:GLU:HA	1.86	0.58
1:DG:428:SER:OG	1:DG:429:GLU:OE1	2.22	0.58
1:AA:538:ARG:HG3	2:BB:319:ARG:NH2	2.18	0.58
1:BE:571:GLU:OE2	1:CC:567:ARG:NH1	2.37	0.58
2:BF:183:ASP:OD1	2:BF:184:ARG:N	2.37	0.58
1:DC:493:LEU:O	1:DC:496:MET:HG3	2.02	0.58
1:DG:431:VAL:HG22	2:DH:272:LYS:HE3	1.86	0.58
2:AB:126:LYS:HE3	2:AB:142:ARG:HA	1.86	0.57
2:BH:244:ASN:N	2:BH:244:ASN:HD22	2.00	0.57
1:CC:339:ALA:HB1	2:CD:127:VAL:HG13	1.85	0.57
1:CE:311:ARG:HH11	1:CE:312:LEU:HD23	1.69	0.57
2:AD:75:ARG:HH11	2:AD:115:ARG:HH21	1.50	0.57
2:DH:87:GLU:HG3	2:DH:103:VAL:HG11	1.86	0.57
1:AG:402:ASP:OD1	1:AG:403:ARG:NH1	2.38	0.57
1:BE:536:MET:HE3	1:BE:536:MET:HA	1.86	0.57
2:DF:237:PRO:HG2	2:DF:240:LEU:HD23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:291:GLN:NE2	1:BC:394:GLU:OE2	2.36	0.57
1:CC:359:ARG:NH1	1:CC:453:ASP:OD2	2.36	0.57
2:CH:155:LEU:HD23	2:CH:222:VAL:HG11	1.87	0.57
1:AA:565:GLU:OE2	1:AA:569:ARG:NH2	2.37	0.57
1:BE:508:MET:HA	1:BE:508:MET:HE2	1.86	0.57
2:CH:175:GLU:OE2	2:CH:196:SER:OG	2.21	0.57
1:AC:449:LEU:HD13	2:AD:180:ILE:HD12	1.86	0.57
2:CB:287:ARG:O	2:CB:291:GLU:HG2	2.04	0.57
2:AF:105:ILE:HD13	2:AF:112:GLY:HA3	1.87	0.57
1:BA:306:GLU:HG3	1:BA:322:VAL:HG11	1.87	0.57
2:BF:216:THR:HG22	2:BF:217:THR:H	1.70	0.57
1:BG:536:MET:HE3	1:BG:536:MET:HA	1.87	0.57
2:BD:175:GLU:OE2	2:BD:196:SER:OG	2.21	0.57
2:BF:92:LYS:HA	2:BF:95:GLU:HB2	1.87	0.57
1:AE:438:PRO:HG2	2:AF:267:TYR:CD2	2.40	0.57
2:CB:130:ASP:OD2	2:CB:142:ARG:NH2	2.36	0.57
1:CC:336:GLU:HB3	1:CC:340:LEU:HD12	1.85	0.57
1:CE:438:PRO:HG2	2:CF:267:TYR:CD2	2.39	0.57
2:AH:126:LYS:HE3	2:AH:142:ARG:HA	1.87	0.57
1:AC:528:ALA:O	1:AC:532:ARG:HG2	2.05	0.56
1:BE:316:TYR:HB3	1:BE:340:LEU:HD22	1.85	0.56
1:DA:372:ARG:HA	1:DA:409:LYS:HA	1.87	0.56
2:DH:116:LEU:HD12	2:DH:122:ALA:HA	1.86	0.56
1:AA:552:GLU:OE1	1:CG:585:MET:HE2	2.06	0.56
1:CG:555:LYS:O	1:CG:558:GLU:HG3	2.05	0.56
2:DB:153:ARG:HG3	2:DB:190:LYS:HG2	1.87	0.56
1:AA:392:PRO:HG2	1:AA:415:ALA:HB3	1.86	0.56
1:AC:341:ALA:O	1:AC:345:LYS:HG2	2.05	0.56
1:AE:514:LYS:NZ	1:AE:518:GLU:OE2	2.38	0.56
1:BA:403:ARG:O	1:BA:405:ARG:NH1	2.38	0.56
2:BH:119:ARG:HD2	2:BH:122:ALA:HB3	1.87	0.56
1:CC:431:VAL:HG11	2:CD:268:ALA:HB1	1.86	0.56
1:DC:431:VAL:HG11	2:DD:268:ALA:HB1	1.86	0.56
1:DG:336:GLU:HB3	1:DG:340:LEU:HD12	1.87	0.56
2:AB:68:LYS:NZ	2:AB:174:VAL:O	2.38	0.56
1:AC:532:ARG:O	1:AC:536:MET:HG2	2.04	0.56
1:BE:345:LYS:HA	1:BE:360:VAL:HG11	1.87	0.56
1:AG:568:ARG:HH21	2:DB:287:ARG:HD3	1.70	0.56
1:CE:528:ALA:O	1:CE:532:ARG:HG2	2.05	0.56
1:BA:470:ARG:NH2	2:BB:166:GLU:OE1	2.30	0.56
2:AB:200:ALA:HA	2:AB:203:LYS:HE2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BD:89:GLU:HB3	2:BD:90:MET:HE2	1.88	0.56
1:BE:539:GLN:HG2	2:CF:316:LEU:HD11	1.88	0.56
2:BH:101:GLY:HA3	2:BH:115:ARG:HB3	1.87	0.56
2:BH:146:HIS:CE1	2:BH:194:GLU:HB3	2.41	0.56
1:CA:526:HIS:CG	2:CB:263:PHE:HB2	2.41	0.56
1:DG:515:LEU:HD11	2:DH:274:LEU:HD13	1.88	0.56
1:BA:534:ASP:OD1	1:BA:537:ARG:NH2	2.39	0.56
1:BE:339:ALA:O	1:BE:343:ILE:HG12	2.06	0.56
1:CA:372:ARG:HA	1:CA:409:LYS:HA	1.88	0.56
2:CD:68:LYS:O	2:CD:71:THR:OG1	2.24	0.56
2:CF:133:PRO:HA	2:CF:138:GLN:HA	1.88	0.56
1:AE:540:GLU:OE2	1:AE:544:ARG:NH1	2.37	0.56
2:BD:82:PRO:HD3	2:BD:137:LYS:HZ1	1.71	0.56
2:AB:155:LEU:HD23	2:AB:222:VAL:HG11	1.87	0.55
1:AG:508:MET:HE3	2:AH:278:GLU:HB2	1.88	0.55
1:BG:293:CYS:HB2	1:BG:335:LEU:HB2	1.87	0.55
1:BG:528:ALA:O	1:BG:532:ARG:HG2	2.06	0.55
1:DG:442:ILE:HD11	2:DH:272:LYS:HG2	1.88	0.55
1:CC:442:ILE:HG13	2:CD:275:ILE:HG21	1.87	0.55
1:DC:368:ALA:HB1	1:DC:411:ILE:HD11	1.88	0.55
2:DD:246:GLN:O	2:DD:250:GLU:HG2	2.06	0.55
1:BA:463:ASN:OD1	1:BA:466:TYR:N	2.40	0.55
1:BA:535:LEU:HD11	2:CB:320:GLN:HG2	1.87	0.55
2:BF:146:HIS:CE1	2:BF:194:GLU:HB3	2.42	0.55
2:AB:214:LEU:HD11	2:AB:219:PRO:HA	1.88	0.55
1:CE:300:LEU:HD22	1:CE:309:PHE:HZ	1.71	0.55
1:CE:436:THR:HA	2:CF:253:GLN:HE21	1.72	0.55
1:AE:340:LEU:HD23	1:AE:343:ILE:HD11	1.87	0.55
2:BH:321:GLU:OE2	2:BH:324:ARG:NH2	2.39	0.55
2:BB:152:VAL:HG12	2:BB:224:VAL:HG22	1.89	0.55
1:AA:295:LEU:HD22	1:AA:345:LYS:HD3	1.86	0.55
1:BC:381:GLU:O	1:BC:384:GLU:HG2	2.07	0.55
1:CE:380:ASN:O	1:CE:384:GLU:HG3	2.07	0.55
1:DE:436:THR:HA	2:DF:253:GLN:HE21	1.70	0.55
1:AG:306:GLU:HG3	1:AG:322:VAL:HG11	1.88	0.55
1:BC:295:LEU:HD21	1:BC:345:LYS:HE2	1.88	0.55
1:BG:486:TYR:OH	2:BH:296:LEU:O	2.24	0.55
1:CA:289:TYR:OH	1:CA:318:GLU:O	2.24	0.55
1:CC:368:ALA:HB1	1:CC:411:ILE:HD11	1.89	0.55
1:DC:470:ARG:HH22	2:DD:163:LEU:HD22	1.72	0.55
2:AB:256:ARG:HH22	2:AB:264:GLU:HG3	1.70	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:501:ARG:NH2	2:CD:286:ASP:OD1	2.39	0.54
2:CF:244:ASN:ND2	2:CF:246:GLN:OE1	2.40	0.54
1:AG:305:THR:HG23	1:AG:308:GLU:H	1.72	0.54
1:BE:486:TYR:OH	2:BF:296:LEU:O	2.25	0.54
2:BF:72:GLN:OE1	2:BF:115:ARG:NH2	2.39	0.54
1:BG:436:THR:HG21	2:BH:252:GLU:HB2	1.89	0.54
1:DA:482:PHE:HB2	2:DB:307:HIS:CE1	2.42	0.54
1:AA:508:MET:CE	2:AB:278:GLU:HB2	2.37	0.54
1:BA:342:GLU:HA	1:BA:345:LYS:HG2	1.89	0.54
2:CD:307:HIS:HA	2:CD:310:MET:HE2	1.89	0.54
1:DG:438:PRO:HG2	2:DH:267:TYR:CD2	2.43	0.54
2:AB:176:ARG:HE	2:AB:178:VAL:HG21	1.71	0.54
1:AG:551:GLN:O	1:AG:554:GLN:HG3	2.07	0.54
2:CB:90:MET:HE1	2:CB:105:ILE:HD11	1.89	0.54
2:CB:200:ALA:HA	2:CB:203:LYS:HE2	1.88	0.54
2:DF:131:ASN:O	2:DF:138:GLN:NE2	2.40	0.54
2:AB:131:ASN:HA	2:AB:140:ARG:HH21	1.73	0.54
1:CC:291:GLN:NE2	1:CC:394:GLU:OE2	2.41	0.54
1:DA:335:LEU:HD12	1:DA:341:ALA:HA	1.89	0.54
1:BE:531:LEU:HB3	2:CF:323:LEU:HD12	1.89	0.54
2:CB:162:GLU:OE1	2:CB:162:GLU:N	2.40	0.54
1:CE:373:ASN:ND2	2:CF:275:ILE:HD11	2.22	0.54
1:CE:515:LEU:O	2:CF:267:TYR:OH	2.25	0.54
1:CG:343:ILE:HD11	2:CH:127:VAL:HG11	1.89	0.54
2:DD:126:LYS:HE2	2:DD:142:ARG:HA	1.90	0.54
1:AA:305:THR:HG23	1:AA:308:GLU:H	1.72	0.54
1:AC:395:ARG:NE	1:AC:413:GLU:OE1	2.38	0.54
2:BD:101:GLY:N	2:BD:115:ARG:O	2.38	0.54
2:BD:279:LYS:O	2:BD:279:LYS:HD3	2.08	0.54
1:CE:417:LYS:HZ1	1:CE:421:ARG:HH21	1.55	0.54
2:CH:259:GLN:O	2:CH:262:SER:OG	2.24	0.54
2:DD:285:VAL:O	2:DD:289:ILE:HG12	2.07	0.54
2:DD:321:GLU:OE2	2:DD:324:ARG:NH2	2.41	0.54
1:AC:295:LEU:HD22	1:AC:345:LYS:HD3	1.90	0.54
1:BC:339:ALA:O	1:BC:343:ILE:HG13	2.08	0.54
1:BC:343:ILE:HD11	2:BD:127:VAL:HG11	1.90	0.54
1:BG:399:ILE:HG21	2:BH:230:LEU:HD13	1.90	0.54
2:CH:73:ARG:HH22	2:CH:176:ARG:HH21	1.55	0.54
2:DD:78:VAL:HG22	2:DD:141:VAL:HG13	1.90	0.54
1:AC:501:ARG:NH2	2:AD:286:ASP:OD1	2.40	0.54
2:AD:161:ASN:O	2:AD:165:GLU:HG3	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CF:78:VAL:HG13	2:CF:141:VAL:HG22	1.90	0.54
1:CG:534:ASP:O	1:CG:538:ARG:HG2	2.08	0.54
1:DA:305:THR:HG23	1:DA:308:GLU:H	1.72	0.54
2:DF:78:VAL:HG13	2:DF:141:VAL:HG22	1.90	0.54
1:BE:574:MET:SD	1:CC:563:GLN:NE2	2.81	0.54
1:AA:301:PRO:HD3	1:AA:353:MET:HE3	1.90	0.53
2:AD:90:MET:SD	2:AD:103:VAL:HG13	2.48	0.53
2:AD:101:GLY:N	2:AD:115:ARG:O	2.40	0.53
2:AH:312:MET:HE1	1:BG:542:LEU:HA	1.89	0.53
2:BF:97:TYR:HB3	2:BF:121:LEU:HD12	1.89	0.53
1:DA:544:ARG:O	1:DA:547:GLU:HG3	2.08	0.53
1:DG:431:VAL:HG11	2:DH:268:ALA:HB1	1.89	0.53
1:AC:515:LEU:O	2:AD:267:TYR:OH	2.27	0.53
2:AH:146:HIS:O	2:AH:229:GLN:NE2	2.40	0.53
1:BA:395:ARG:HH22	2:BB:233:GLU:HA	1.71	0.53
1:BE:577:ARG:O	1:BE:580:GLU:HG3	2.07	0.53
1:DA:481:THR:HG23	1:DA:484:TYR:H	1.73	0.53
2:DD:301:GLU:OE2	2:DD:304:ARG:NH2	2.41	0.53
2:DH:238:GLU:O	2:DH:243:LYS:NZ	2.36	0.53
1:CG:428:SER:OG	1:CG:429:GLU:OE1	2.26	0.53
1:DG:366:ALA:HB3	1:DG:417:LYS:HZ2	1.73	0.53
1:DE:361:ARG:NH2	1:DE:450:ASP:OD2	2.41	0.53
1:BG:353:MET:HE1	1:BG:358:LEU:HB2	1.91	0.53
1:CA:515:LEU:O	1:CA:519:MET:HE3	2.09	0.53
1:CC:518:GLU:O	1:CC:519:MET:HE2	2.09	0.53
1:CC:544:ARG:O	1:CC:547:GLU:HG3	2.07	0.53
1:DA:289:TYR:OH	1:DA:318:GLU:O	2.26	0.53
1:AG:442:ILE:HD13	2:AH:275:ILE:HG21	1.91	0.53
1:BC:353:MET:HG3	1:BC:358:LEU:HD13	1.91	0.53
1:CA:469:GLU:HG3	2:CB:216:THR:HG21	1.90	0.53
1:CE:461:GLN:HA	1:CE:466:TYR:HD2	1.74	0.53
1:AC:432:PHE:HD1	2:AD:257:PHE:HE1	1.56	0.53
2:AD:73:ARG:HG2	2:AD:119:ARG:HH11	1.74	0.53
1:BA:346:ALA:HB1	2:BB:120:THR:HG23	1.90	0.53
1:BC:369:LEU:HD11	1:BC:424:PHE:HB2	1.90	0.53
1:BG:478:GLN:O	1:BG:481:THR:HG22	2.09	0.53
1:CC:559:MET:O	1:CC:563:GLN:HG2	2.08	0.53
2:AD:287:ARG:NH1	1:AE:568:ARG:HH12	2.06	0.53
2:BB:101:GLY:HA3	2:BB:115:ARG:HB3	1.91	0.53
1:BC:399:ILE:HG21	2:BD:230:LEU:HD13	1.91	0.53
2:BH:284:GLN:OE1	2:BH:287:ARG:NH2	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BC:487:SER:O	1:BC:491:LYS:HG2	2.09	0.53
2:DD:305:HIS:O	2:DD:309:VAL:HG23	2.09	0.53
2:DH:220:ARG:NH1	2:DH:221:PRO:O	2.41	0.53
1:AG:421:ARG:HG3	1:AG:422:LYS:HD3	1.91	0.53
2:CB:298:MET:HE3	2:CB:298:MET:HA	1.91	0.53
1:DC:497:GLU:OE2	2:DD:289:ILE:HD12	2.09	0.53
1:BG:424:PHE:HA	1:BG:443:VAL:HG21	1.91	0.53
1:CC:490:TRP:NE1	2:CD:219:PRO:O	2.42	0.53
1:CE:316:TYR:HB3	1:CE:340:LEU:HD22	1.91	0.53
1:CG:306:GLU:HG3	1:CG:322:VAL:HG11	1.90	0.53
1:AA:470:ARG:NH1	2:AB:166:GLU:OE2	2.42	0.52
1:AE:549:HIS:NE2	2:BF:306:GLU:OE1	2.41	0.52
1:CA:470:ARG:NH2	2:CB:166:GLU:OE2	2.42	0.52
1:CE:486:TYR:OH	2:CF:296:LEU:O	2.27	0.52
1:CG:417:LYS:HB3	1:CG:421:ARG:HH21	1.73	0.52
1:DA:296:PHE:HD2	1:DA:361:ARG:HB2	1.73	0.52
1:DA:392:PRO:HG2	1:DA:415:ALA:HB3	1.90	0.52
2:DB:259:GLN:O	2:DB:262:SER:OG	2.25	0.52
1:DC:436:THR:HB	2:DD:250:GLU:HA	1.91	0.52
1:DG:431:VAL:HG21	2:DH:269:MET:HE1	1.90	0.52
2:AB:75:ARG:HD3	2:AB:113:PHE:CZ	2.44	0.52
2:AB:319:ARG:NH2	1:DA:534:ASP:OD2	2.40	0.52
2:BD:70:PHE:O	2:BD:115:ARG:NH1	2.36	0.52
1:BE:541:GLU:OE2	1:BE:544:ARG:NH2	2.43	0.52
2:CB:119:ARG:NE	2:CB:123:GLU:OE2	2.42	0.52
1:CE:292:ARG:HB3	1:CE:338:ARG:HH11	1.73	0.52
2:AH:78:VAL:HG22	2:AH:141:VAL:HG13	1.91	0.52
2:BB:89:GLU:OE2	2:BB:135:ARG:NH1	2.42	0.52
1:BG:540:GLU:O	1:BG:543:ARG:HG3	2.09	0.52
1:AA:519:MET:HE1	2:AB:267:TYR:HE2	1.74	0.52
2:AB:259:GLN:O	2:AB:262:SER:OG	2.27	0.52
2:AF:120:THR:O	2:AF:124:ILE:HG12	2.09	0.52
2:BB:105:ILE:HD13	2:BB:112:GLY:HA3	1.92	0.52
1:BA:297:VAL:HG22	1:BA:360:VAL:HG12	1.91	0.52
1:CC:305:THR:HG23	1:CC:308:GLU:H	1.74	0.52
1:CG:564:GLU:OE2	1:CG:567:ARG:NH2	2.41	0.52
1:AA:469:GLU:HB3	2:AB:216:THR:HG21	1.92	0.52
2:AB:327:GLU:OE2	1:DA:524:HIS:NE2	2.43	0.52
1:AE:546:GLU:OE2	2:BF:313:ARG:NH1	2.43	0.52
1:BA:436:THR:HG22	2:BB:253:GLN:HG3	1.91	0.52
1:BC:438:PRO:HG2	2:BD:267:TYR:CD2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CA:518:GLU:O	1:CA:519:MET:HE2	2.09	0.52
1:CG:305:THR:HG23	1:CG:308:GLU:H	1.74	0.52
1:AE:520:GLU:OE2	2:BF:338:LYS:NZ	2.42	0.52
2:AH:159:VAL:HG23	2:AH:163:LEU:HD23	1.91	0.52
1:BA:340:LEU:HA	1:BA:343:ILE:HG22	1.91	0.52
1:BE:542:LEU:HA	2:CF:312:MET:HE1	1.92	0.52
1:BG:421:ARG:O	1:BG:425:GLU:HG2	2.10	0.52
2:BH:237:PRO:HG2	2:BH:240:LEU:HG	1.91	0.52
2:AF:72:GLN:OE1	2:AF:115:ARG:NH2	2.43	0.52
1:BE:555:LYS:NZ	1:CC:585:MET:SD	2.64	0.52
2:BH:97:TYR:HA	2:BH:121:LEU:HD23	1.90	0.52
1:CA:438:PRO:HG2	2:CB:267:TYR:CD2	2.44	0.52
1:CC:577:ARG:O	1:CC:580:GLU:HG3	2.09	0.52
1:CE:335:LEU:HD12	1:CE:341:ALA:HA	1.91	0.52
2:DB:69:THR:HG22	2:DB:118:THR:HG22	1.92	0.52
1:AA:335:LEU:HD12	1:AA:341:ALA:HA	1.92	0.52
2:CD:301:GLU:OE2	2:CD:304:ARG:NH2	2.42	0.52
1:DC:322:VAL:HG22	1:DC:333:ILE:HG12	1.92	0.52
1:DG:509:LYS:NZ	1:DG:513:ASP:OD2	2.42	0.52
1:AC:375:SER:O	1:AC:378:VAL:HG12	2.10	0.52
2:AH:175:GLU:HB2	2:AH:194:GLU:HG3	1.90	0.52
1:BC:293:CYS:HB3	1:BC:335:LEU:H	1.74	0.52
1:BC:380:ASN:ND2	2:BD:234:GLU:O	2.43	0.52
1:BE:475:ARG:NH2	2:BF:216:THR:O	2.35	0.52
2:BH:167:ALA:HB1	2:BH:213:PHE:CE2	2.45	0.52
1:DC:519:MET:HE1	2:DD:267:TYR:CE1	2.45	0.52
1:DE:316:TYR:HB3	1:DE:340:LEU:HD22	1.92	0.52
1:DE:371:VAL:HG12	1:DE:443:VAL:HG12	1.92	0.52
2:BD:85:ILE:HG23	2:BD:105:ILE:HD12	1.92	0.51
2:CB:199:PRO:HA	2:CB:202:ARG:HG2	1.91	0.51
1:AA:289:TYR:OH	1:AA:318:GLU:O	2.28	0.51
1:CC:548:LEU:O	1:CC:552:GLU:HG2	2.09	0.51
2:CF:161:ASN:O	2:CF:165:GLU:HG3	2.10	0.51
1:CG:339:ALA:HB1	2:CH:127:VAL:HG13	1.93	0.51
1:DG:353:MET:HE1	1:DG:358:LEU:HD22	1.92	0.51
2:CH:166:GLU:O	2:CH:169:SER:OG	2.25	0.51
2:DB:200:ALA:HA	2:DB:203:LYS:HE2	1.92	0.51
1:DC:386:ALA:HB1	1:DC:432:PHE:HZ	1.74	0.51
2:DD:75:ARG:NH2	2:DD:102:GLU:OE2	2.41	0.51
1:DG:392:PRO:HG2	1:DG:415:ALA:HB3	1.92	0.51
1:AA:379:SER:OG	1:AA:380:ASN:N	2.43	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:516:GLU:HA	1:AA:519:MET:HE3	1.92	0.51
1:AE:457:GLU:OE1	1:AE:457:GLU:N	2.38	0.51
1:AG:544:ARG:O	1:AG:547:GLU:HG3	2.10	0.51
2:BD:182:ASP:OD1	2:BD:186:ARG:N	2.38	0.51
2:DD:321:GLU:O	2:DD:325:ARG:HG2	2.10	0.51
1:AE:582:GLU:OE2	1:BC:556:ARG:NH2	2.40	0.51
2:BF:161:ASN:ND2	2:BF:178:VAL:HG23	2.25	0.51
2:CD:72:GLN:HE22	2:CD:148:ALA:HB3	1.74	0.51
2:CF:183:ASP:OD1	2:CF:184:ARG:N	2.44	0.51
1:CG:392:PRO:HG2	1:CG:415:ALA:HB3	1.92	0.51
1:DC:457:GLU:HA	1:DC:460:ALA:HB3	1.92	0.51
1:CE:570:ARG:O	1:CE:574:MET:HG3	2.10	0.51
1:CG:386:ALA:HB1	1:CG:432:PHE:HZ	1.76	0.51
2:DH:140:ARG:NH2	2:DH:234:GLU:OE2	2.44	0.51
1:DC:399:ILE:HG12	1:DC:410:GLY:HA2	1.92	0.51
1:CE:434:LEU:HA	2:CF:255:PRO:HB3	1.93	0.51
2:CF:94:PHE:CE1	2:CF:116:LEU:HD22	2.46	0.51
2:CH:81:LEU:N	2:CH:110:GLY:O	2.34	0.51
2:DH:163:LEU:HG	2:DH:215:LEU:HD12	1.93	0.51
2:DH:265:TYR:O	2:DH:269:MET:HG2	2.10	0.51
1:DE:379:SER:HB2	1:DE:382:LEU:HD13	1.91	0.51
1:AC:461:GLN:O	1:AC:467:GLN:NE2	2.44	0.51
1:BE:508:MET:SD	2:BF:278:GLU:HB2	2.51	0.51
2:DH:244:ASN:H	2:DH:244:ASN:ND2	2.09	0.51
2:DF:150:LEU:HD12	2:DF:226:PRO:HA	1.93	0.51
2:AB:294:GLU:OE2	1:BG:579:ARG:NH1	2.44	0.51
2:AD:70:PHE:CE1	2:AD:117:GLU:HA	2.46	0.51
2:AD:318:ARG:NH2	2:AD:319:ARG:HE	2.09	0.51
2:AH:207:ARG:NH1	2:AH:211:GLY:HA3	2.26	0.51
1:BE:587:ARG:O	1:BE:591:GLU:HG2	2.10	0.51
1:CE:374:LEU:HB3	1:CE:378:VAL:HG21	1.93	0.51
1:CE:436:THR:HG22	2:CF:253:GLN:HG3	1.91	0.51
2:AB:104:PHE:HB3	2:AB:113:PHE:HB3	1.92	0.50
2:AF:104:PHE:O	2:AF:113:PHE:N	2.40	0.50
1:AG:316:TYR:OH	1:AG:347:GLU:OE1	2.29	0.50
1:BA:486:TYR:CE2	2:BB:300:MET:HE1	2.46	0.50
1:AA:353:MET:O	1:AA:353:MET:HG3	2.10	0.50
2:AB:125:ALA:O	2:AB:129:LEU:HB2	2.11	0.50
1:AE:469:GLU:OE2	2:AF:217:THR:OG1	2.29	0.50
2:BD:287:ARG:HH12	1:BE:568:ARG:NH2	2.09	0.50
1:BE:436:THR:HG22	2:BF:253:GLN:HG3	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:395:ARG:NH2	2:CF:232:ASP:O	2.44	0.50
1:AE:543:ARG:HH11	1:AE:544:ARG:HH12	1.60	0.50
2:BF:161:ASN:HD21	2:BF:178:VAL:HG23	1.77	0.50
1:BG:534:ASP:O	1:BG:538:ARG:HG2	2.11	0.50
1:CC:490:TRP:HB3	2:CD:220:ARG:HH11	1.77	0.50
1:DA:389:GLN:OE1	1:DA:389:GLN:N	2.38	0.50
2:AB:269:MET:HE2	2:AB:269:MET:HA	1.94	0.50
1:AG:293:CYS:SG	1:AG:335:LEU:N	2.85	0.50
2:BH:73:ARG:HD3	2:BH:119:ARG:HG2	1.93	0.50
1:CA:296:PHE:HD2	1:CA:361:ARG:HB3	1.77	0.50
1:CC:487:SER:HA	1:CC:490:TRP:HD1	1.76	0.50
1:CG:438:PRO:HG2	2:CH:267:TYR:CD2	2.46	0.50
1:DC:296:PHE:HD2	1:DC:361:ARG:HB3	1.76	0.50
1:AA:528:ALA:HB1	1:AA:532:ARG:HH12	1.76	0.50
2:AD:288:ASN:O	2:AD:291:GLU:HG3	2.11	0.50
1:BC:323:PHE:HB3	1:BC:332:PHE:HB2	1.94	0.50
2:BH:77:PHE:HD2	2:BH:142:ARG:HB2	1.77	0.50
2:CF:256:ARG:HG2	2:CF:257:PHE:O	2.11	0.50
1:CG:295:LEU:HD22	1:CG:360:VAL:HG12	1.93	0.50
1:DA:559:MET:O	1:DA:563:GLN:HG2	2.11	0.50
2:DD:205:LEU:HD12	2:DD:224:VAL:HG13	1.93	0.50
2:DD:315:ASP:O	2:DD:318:ARG:HG3	2.12	0.50
1:AA:534:ASP:OD1	1:AA:537:ARG:NH2	2.45	0.50
2:AB:90:MET:HA	2:AB:93:LEU:HG	1.94	0.50
1:AC:463:ASN:O	1:AC:467:GLN:NE2	2.44	0.50
1:AE:371:VAL:HG12	1:AE:443:VAL:HG12	1.93	0.50
2:AF:153:ARG:O	2:AF:222:VAL:HG13	2.12	0.50
1:CG:419:ALA:HA	1:CG:422:LYS:HG2	1.93	0.50
2:DD:247:PHE:O	2:DD:251:ARG:N	2.37	0.50
1:DG:295:LEU:HD22	1:DG:360:VAL:HG12	1.94	0.50
2:DH:332:GLN:HG2	2:DH:336:LYS:HE3	1.94	0.50
2:CD:100:ALA:HB1	2:CD:114:ILE:HD11	1.92	0.50
2:CD:159:VAL:HA	2:CD:163:LEU:HD23	1.94	0.50
2:DH:73:ARG:O	2:DH:119:ARG:NH1	2.45	0.50
1:DE:335:LEU:HD12	1:DE:341:ALA:HA	1.93	0.50
1:AE:555:LYS:O	1:AE:558:GLU:HG3	2.11	0.50
2:BB:238:GLU:O	2:BB:243:LYS:NZ	2.39	0.50
1:BG:428:SER:OG	1:BG:429:GLU:OE1	2.29	0.50
1:CC:375:SER:O	1:CC:378:VAL:HG12	2.12	0.50
1:DG:305:THR:HG23	1:DG:308:GLU:H	1.76	0.50
2:AH:167:ALA:HB1	2:AH:213:PHE:CZ	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BB:97:TYR:HB3	2:BB:121:LEU:HD21	1.94	0.50
2:BH:259:GLN:O	2:BH:262:SER:OG	2.27	0.50
1:CA:335:LEU:HD12	1:CA:341:ALA:HA	1.94	0.50
2:CH:220:ARG:NH1	2:CH:221:PRO:O	2.45	0.50
2:CH:251:ARG:NH2	2:CH:253:GLN:O	2.45	0.50
2:CH:255:PRO:O	2:CH:256:ARG:NE	2.45	0.50
1:DC:372:ARG:HB3	1:DC:409:LYS:HZ3	1.76	0.50
1:DC:553:MET:N	1:DC:553:MET:HE2	2.27	0.50
1:AG:319:PRO:HB3	1:AG:333:ILE:HD11	1.94	0.49
1:AG:465:MET:HA	1:AG:468:LYS:HG2	1.94	0.49
2:AH:315:ASP:OD1	2:AH:316:LEU:N	2.45	0.49
1:BA:335:LEU:HD12	1:BA:341:ALA:HA	1.94	0.49
2:BB:125:ALA:O	2:BB:129:LEU:HB2	2.12	0.49
2:BF:256:ARG:HG2	2:BF:257:PHE:O	2.12	0.49
1:CA:400:VAL:HG12	1:CA:406:SER:HA	1.93	0.49
2:CD:73:ARG:O	2:CD:119:ARG:NH1	2.44	0.49
1:CE:292:ARG:O	1:CE:338:ARG:NH1	2.45	0.49
2:CF:238:GLU:O	2:CF:243:LYS:NZ	2.37	0.49
1:CG:469:GLU:HB3	2:CH:216:THR:HG23	1.94	0.49
1:AC:544:ARG:O	1:AC:547:GLU:HG3	2.12	0.49
1:AE:394:GLU:HB3	1:AE:413:GLU:HG3	1.93	0.49
1:DC:505:GLU:O	1:DC:509:LYS:HG2	2.11	0.49
1:AG:545:MET:HE1	2:DH:309:VAL:HG22	1.94	0.49
1:BA:396:ALA:HB2	1:BA:412:VAL:HG23	1.94	0.49
2:BF:78:VAL:HG13	2:BF:141:VAL:HG12	1.93	0.49
2:BH:244:ASN:HD22	2:BH:244:ASN:H	1.61	0.49
1:AA:486:TYR:CE2	2:AB:300:MET:HE1	2.47	0.49
1:AE:467:GLN:OE1	1:AE:467:GLN:N	2.42	0.49
1:BG:296:PHE:HB3	1:BG:361:ARG:HB3	1.94	0.49
2:DH:244:ASN:N	2:DH:244:ASN:ND2	2.61	0.49
1:AA:544:ARG:HG3	1:AA:545:MET:HE2	1.94	0.49
1:AG:528:ALA:O	1:AG:532:ARG:HG2	2.12	0.49
2:BD:73:ARG:HE	2:BD:119:ARG:HG2	1.77	0.49
2:CH:117:GLU:HB3	2:CH:121:LEU:HD12	1.94	0.49
1:DA:383:LEU:HD23	1:DA:396:ALA:HB1	1.95	0.49
1:DC:500:GLN:O	1:DC:503:GLN:HG2	2.12	0.49
1:AC:426:ARG:HG2	2:AD:257:PHE:HZ	1.77	0.49
2:AH:244:ASN:ND2	2:AH:246:GLN:HE21	2.10	0.49
2:BB:269:MET:N	2:BB:269:MET:HE2	2.28	0.49
2:BF:104:PHE:O	2:BF:113:PHE:N	2.40	0.49
2:BH:126:LYS:O	2:BH:130:ASP:HB2	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CB:73:ARG:HG2	2:CB:119:ARG:HD3	1.95	0.49
1:CE:466:TYR:OH	1:CE:470:ARG:NH2	2.45	0.49
2:CF:75:ARG:NH1	2:CF:113:PHE:HB3	2.27	0.49
2:CH:109:LYS:HE3	2:CH:111:PHE:HE2	1.76	0.49
1:DA:295:LEU:HD22	1:DA:345:LYS:HD3	1.95	0.49
1:DA:301:PRO:HD3	1:DA:353:MET:HE3	1.94	0.49
1:DA:553:MET:HE2	1:DA:553:MET:HA	1.95	0.49
1:DC:336:GLU:HB3	1:DC:340:LEU:HD12	1.94	0.49
1:AC:475:ARG:NH2	2:AD:216:THR:O	2.40	0.49
2:BF:216:THR:HG22	2:BF:217:THR:N	2.28	0.49
1:CA:392:PRO:HG2	1:CA:415:ALA:HB3	1.95	0.49
2:CF:94:PHE:CZ	2:CF:116:LEU:HD22	2.47	0.49
1:DE:380:ASN:O	1:DE:384:GLU:HG3	2.13	0.49
1:AE:553:MET:HE2	1:AE:553:MET:HA	1.94	0.49
2:AH:119:ARG:HD2	2:AH:122:ALA:HB3	1.94	0.49
2:AH:126:LYS:O	2:AH:130:ASP:HB2	2.13	0.49
1:BG:296:PHE:O	1:BG:361:ARG:N	2.45	0.49
2:BH:218:PHE:CE1	2:BH:300:MET:HE1	2.48	0.49
2:CF:72:GLN:HE21	2:CF:75:ARG:HD2	1.77	0.49
2:CF:206:ASP:O	2:CF:210:GLU:HG3	2.12	0.49
1:CG:569:ARG:O	1:CG:572:GLU:HG3	2.12	0.49
1:DE:380:ASN:OD1	1:DE:381:GLU:N	2.45	0.49
1:AA:348:LEU:HB3	1:AA:358:LEU:HD23	1.95	0.49
1:AA:538:ARG:HG3	2:BB:319:ARG:HH21	1.76	0.49
1:AE:475:ARG:HG2	2:AF:214:LEU:HD11	1.94	0.49
1:BE:414:PHE:HB2	1:BE:420:ALA:HB2	1.95	0.49
1:BG:418:PRO:O	1:BG:421:ARG:HG2	2.13	0.49
1:CC:515:LEU:HD21	2:CD:271:TRP:HE1	1.77	0.49
1:CE:382:LEU:HD21	2:CF:251:ARG:HD3	1.95	0.49
2:CF:100:ALA:HB1	2:CF:114:ILE:HD11	1.94	0.49
2:AB:203:LYS:HB2	2:AB:207:ARG:HH12	1.77	0.49
1:AG:553:MET:HE2	1:AG:553:MET:N	2.27	0.49
2:BB:78:VAL:HG13	2:BB:141:VAL:HG22	1.94	0.49
2:BB:150:LEU:HD21	2:BB:205:LEU:HD12	1.94	0.49
1:BE:349:ASP:OD1	1:BE:360:VAL:N	2.42	0.49
2:CD:265:TYR:O	2:CD:269:MET:HG2	2.12	0.49
2:CH:332:GLN:HG2	2:CH:336:LYS:HE3	1.95	0.49
1:DA:569:ARG:O	1:DA:572:GLU:HG3	2.12	0.49
1:AA:400:VAL:HG23	2:AB:231:ASP:HB3	1.95	0.48
1:AC:434:LEU:HA	2:AD:255:PRO:HB3	1.95	0.48
1:BC:295:LEU:HD22	1:BC:360:VAL:HG12	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BD:247:PHE:HD1	2:BD:250:GLU:HB2	1.78	0.48
1:DC:461:GLN:O	1:DC:467:GLN:NE2	2.46	0.48
2:AB:288:ASN:O	2:AB:291:GLU:HG3	2.13	0.48
2:AD:251:ARG:HH22	2:AD:254:PRO:HA	1.78	0.48
2:AF:238:GLU:O	2:AF:243:LYS:NZ	2.45	0.48
1:AG:367:ALA:HB2	1:AG:417:LYS:HE2	1.94	0.48
1:AG:508:MET:HE1	2:AH:277:MET:CE	2.42	0.48
1:BG:475:ARG:NH2	1:BG:483:GLU:OE2	2.35	0.48
2:BH:216:THR:HG22	2:BH:218:PHE:H	1.78	0.48
1:CC:310:LYS:HE3	1:CC:322:VAL:HG21	1.95	0.48
2:CF:71:THR:OG1	2:CF:175:GLU:OE1	2.31	0.48
2:DF:180:ILE:HG12	2:DF:191:GLY:HA2	1.94	0.48
2:BD:259:GLN:O	2:BD:262:SER:OG	2.24	0.48
1:CE:300:LEU:O	1:CE:356:ARG:NH1	2.45	0.48
2:CF:155:LEU:HD21	2:CF:159:VAL:HG11	1.95	0.48
2:CH:269:MET:HA	2:CH:269:MET:HE2	1.95	0.48
1:DC:291:GLN:NE2	1:DC:394:GLU:OE2	2.45	0.48
1:DG:504:VAL:O	1:DG:508:MET:HG2	2.13	0.48
1:AG:393:ILE:HD11	1:AG:396:ALA:HB2	1.96	0.48
2:DH:101:GLY:N	2:DH:115:ARG:O	2.35	0.48
1:AC:293:CYS:HB3	1:AC:335:LEU:N	2.29	0.48
1:AC:544:ARG:HD2	1:AC:545:MET:N	2.29	0.48
2:AD:322:GLU:HG3	2:AD:325:ARG:HH21	1.78	0.48
1:AG:534:ASP:O	1:AG:538:ARG:HG2	2.14	0.48
1:BC:475:ARG:HG2	1:BC:477:ALA:H	1.78	0.48
1:CA:501:ARG:NH2	2:CB:286:ASP:OD1	2.45	0.48
1:AE:384:GLU:HG2	1:AE:396:ALA:HB3	1.95	0.48
1:AE:470:ARG:O	1:AE:470:ARG:HG3	2.12	0.48
2:AH:162:GLU:HA	2:AH:165:GLU:HG2	1.95	0.48
2:BD:214:LEU:HD23	2:BD:219:PRO:HA	1.94	0.48
2:BD:329:LEU:O	2:BD:332:GLN:HG2	2.13	0.48
1:BG:559:MET:O	1:BG:563:GLN:HG2	2.14	0.48
2:CF:94:PHE:CE1	2:CF:97:TYR:HB2	2.48	0.48
1:DC:544:ARG:O	1:DC:547:GLU:HG3	2.14	0.48
2:AD:152:VAL:HG12	2:AD:224:VAL:HG22	1.96	0.48
1:CE:369:LEU:HD13	1:CE:445:PRO:HA	1.94	0.48
2:AF:256:ARG:HG2	2:AF:257:PHE:O	2.14	0.48
1:AG:457:GLU:OE2	2:AH:162:GLU:HB2	2.14	0.48
1:BA:553:MET:HE2	1:BA:553:MET:HA	1.96	0.48
1:BE:418:PRO:O	1:BE:422:LYS:HG2	2.14	0.48
2:CH:162:GLU:HA	2:CH:165:GLU:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DH:85:ILE:HD11	2:DH:90:MET:HG2	1.96	0.48
1:DE:375:SER:HB3	1:DE:378:VAL:HG13	1.95	0.48
1:DE:384:GLU:HG2	1:DE:396:ALA:HB3	1.95	0.48
1:AC:531:LEU:HD13	2:DD:323:LEU:HD13	1.96	0.48
1:BA:296:PHE:HE2	1:BA:359:ARG:HH22	1.62	0.48
1:BG:545:MET:HA	1:BG:545:MET:HE2	1.96	0.48
2:CF:81:LEU:HD13	2:CF:85:ILE:HG12	1.95	0.48
1:DG:319:PRO:HB3	1:DG:333:ILE:HD11	1.95	0.48
1:DE:386:ALA:HB1	1:DE:432:PHE:CZ	2.41	0.48
1:AC:380:ASN:OD1	2:AD:236:LEU:N	2.47	0.48
1:AC:438:PRO:HG2	2:AD:267:TYR:CD2	2.44	0.48
1:AG:428:SER:OG	1:AG:429:GLU:OE1	2.30	0.48
2:BB:183:ASP:OD1	2:BB:184:ARG:N	2.47	0.48
2:BD:184:ARG:HG2	2:BD:186:ARG:NH1	2.29	0.48
1:BG:369:LEU:HD21	1:BG:424:PHE:HB2	1.96	0.48
1:BG:555:LYS:NZ	1:DA:581:MET:SD	2.87	0.48
2:CB:259:GLN:O	2:CB:262:SER:OG	2.31	0.48
1:CC:435:THR:HG22	1:CC:436:THR:H	1.77	0.48
1:CC:532:ARG:O	1:CC:536:MET:HG2	2.14	0.48
1:CG:370:SER:HB3	1:CG:444:GLU:HG2	1.96	0.48
2:AD:329:LEU:HA	2:AD:332:GLN:HG2	1.95	0.47
1:AE:499:GLN:O	1:AE:502:GLU:HG3	2.14	0.47
1:AG:438:PRO:HG2	2:AH:267:TYR:CD2	2.49	0.47
2:BF:253:GLN:OE1	2:BF:256:ARG:NE	2.47	0.47
1:BG:381:GLU:O	1:BG:384:GLU:HG2	2.13	0.47
1:CE:339:ALA:O	1:CE:343:ILE:HG12	2.14	0.47
1:CG:515:LEU:O	2:CH:267:TYR:OH	2.29	0.47
1:BA:568:ARG:HH12	2:CH:290:LYS:NZ	2.11	0.47
2:DF:312:MET:O	2:DF:316:LEU:HD23	2.15	0.47
1:AC:557:LYS:HE3	1:AC:561:LEU:HD21	1.96	0.47
2:AD:255:PRO:O	2:AD:256:ARG:NE	2.47	0.47
2:BB:256:ARG:HG2	2:BB:257:PHE:O	2.13	0.47
1:BG:534:ASP:O	1:BG:537:ARG:HG2	2.13	0.47
1:CC:289:TYR:O	1:CC:289:TYR:CG	2.66	0.47
1:DE:486:TYR:OH	2:DF:296:LEU:HG	2.15	0.47
1:AC:569:ARG:O	1:AC:572:GLU:HG2	2.15	0.47
2:AF:308:GLN:O	2:AF:312:MET:HG2	2.14	0.47
2:AH:199:PRO:HA	2:AH:202:ARG:NH1	2.30	0.47
2:BB:206:ASP:O	2:BB:210:GLU:HG3	2.14	0.47
1:BG:309:PHE:CE2	1:BG:333:ILE:HB	2.49	0.47
2:CB:271:TRP:O	2:CB:275:ILE:HG12	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CC:386:ALA:HB1	1:CC:432:PHE:HZ	1.79	0.47
1:CE:346:ALA:HB1	2:CF:120:THR:HA	1.96	0.47
2:CF:68:LYS:NZ	2:CF:175:GLU:O	2.28	0.47
1:DG:504:VAL:HG13	1:DG:508:MET:HE3	1.96	0.47
1:AA:538:ARG:NH1	2:BB:319:ARG:HH22	2.13	0.47
1:AC:475:ARG:HG3	1:AC:477:ALA:H	1.80	0.47
2:AF:117:GLU:HB2	2:AF:121:LEU:HD22	1.96	0.47
2:AH:247:PHE:O	2:AH:251:ARG:HG2	2.15	0.47
1:BA:290:THR:HG1	1:BA:293:CYS:HG	1.61	0.47
1:BA:374:LEU:HD13	1:BA:378:VAL:HG21	1.95	0.47
1:BE:452:GLU:OE1	2:BF:176:ARG:NH1	2.47	0.47
1:DC:494:ASP:OD2	2:DD:223:THR:OG1	2.27	0.47
2:DH:162:GLU:HA	2:DH:165:GLU:HG2	1.97	0.47
2:DF:236:LEU:O	2:DF:236:LEU:HD12	2.15	0.47
1:AA:395:ARG:HH22	2:AB:233:GLU:HA	1.79	0.47
2:AD:320:GLN:HG2	1:BC:535:LEU:HD11	1.95	0.47
1:AE:346:ALA:HB1	2:AF:120:THR:HG23	1.97	0.47
1:AG:304:ILE:HG13	1:AG:324:ILE:HD11	1.96	0.47
1:AG:386:ALA:HB1	1:AG:432:PHE:CZ	2.48	0.47
1:AG:421:ARG:O	1:AG:425:GLU:HG2	2.15	0.47
1:BC:455:LEU:HD13	2:BD:181:VAL:HG21	1.95	0.47
2:BD:243:LYS:HD3	2:BD:247:PHE:HD2	1.79	0.47
1:CC:490:TRP:HB3	2:CD:220:ARG:NH1	2.30	0.47
2:CD:241:VAL:HG12	2:CD:243:LYS:H	1.78	0.47
1:CG:471:GLU:OE1	1:CG:471:GLU:N	2.47	0.47
1:DG:386:ALA:HB1	1:DG:432:PHE:CE2	2.50	0.47
2:DF:90:MET:HE2	2:DF:114:ILE:HD13	1.97	0.47
1:BA:321:GLU:O	1:BA:333:ILE:HA	2.15	0.47
1:BA:418:PRO:O	1:BA:422:LYS:HG2	2.15	0.47
1:BE:450:ASP:OD2	1:BE:453:ASP:HB3	2.14	0.47
1:BE:540:GLU:OE2	1:BE:543:ARG:NH2	2.48	0.47
2:BF:106:HIS:CG	2:BF:109:LYS:HE2	2.50	0.47
2:BH:101:GLY:N	2:BH:115:ARG:O	2.36	0.47
1:CC:386:ALA:HB1	1:CC:432:PHE:CZ	2.49	0.47
1:CE:544:ARG:O	1:CE:547:GLU:HG3	2.15	0.47
2:CF:104:PHE:O	2:CF:113:PHE:N	2.44	0.47
1:CG:534:ASP:O	1:CG:537:ARG:HG2	2.14	0.47
2:CH:152:VAL:HG11	2:CH:168:PHE:CZ	2.49	0.47
2:DB:73:ARG:HE	2:DB:119:ARG:HD3	1.80	0.47
1:DC:426:ARG:HG2	2:DD:257:PHE:CZ	2.50	0.47
1:DC:482:PHE:HB2	2:DD:307:HIS:CG	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:335:LEU:HG	1:AC:341:ALA:HA	1.97	0.47
2:AF:287:ARG:HA	2:AF:287:ARG:HD2	1.75	0.47
1:BE:582:GLU:OE2	1:CC:556:ARG:NH2	2.36	0.47
1:AG:417:LYS:HB2	1:AG:418:PRO:HD3	1.97	0.47
2:BD:337:ARG:HG3	2:BD:338:LYS:HE2	1.97	0.47
1:BE:417:LYS:HZ3	1:BE:421:ARG:HB2	1.80	0.47
1:CG:293:CYS:HB2	1:CG:335:LEU:HB2	1.96	0.47
2:CH:164:LEU:HD11	2:CH:179:VAL:HG13	1.97	0.47
1:DE:402:ASP:OD1	1:DE:402:ASP:N	2.46	0.47
2:AD:119:ARG:HG2	2:AD:123:GLU:OE2	2.15	0.47
1:BC:319:PRO:HB3	1:BC:333:ILE:HD11	1.96	0.47
2:BD:298:MET:HE1	1:BE:579:ARG:HD3	1.95	0.47
1:BG:370:SER:N	1:BG:444:GLU:O	2.42	0.47
1:CC:461:GLN:O	1:CC:467:GLN:NE2	2.48	0.47
1:DC:295:LEU:O	1:DC:332:PHE:HA	2.15	0.47
1:AA:553:MET:HE2	1:AA:553:MET:HA	1.97	0.46
1:AE:310:LYS:HE2	1:AE:319:PRO:HG2	1.97	0.46
2:AF:307:HIS:CD2	2:AF:310:MET:HE3	2.49	0.46
1:AG:378:VAL:HG23	1:AG:382:LEU:HD22	1.96	0.46
2:BD:148:ALA:HB1	2:BD:195:PHE:HB2	1.96	0.46
1:BG:295:LEU:HD22	1:BG:360:VAL:HG12	1.95	0.46
1:BG:316:TYR:HB3	1:BG:340:LEU:HD11	1.96	0.46
1:CA:434:LEU:HA	2:CB:255:PRO:HB3	1.96	0.46
1:CA:475:ARG:NH1	2:CB:216:THR:O	2.48	0.46
2:CB:238:GLU:O	2:CB:243:LYS:NZ	2.42	0.46
2:CF:87:GLU:HG3	2:CF:103:VAL:HG11	1.96	0.46
1:CG:293:CYS:SG	1:CG:335:LEU:N	2.79	0.46
1:DA:548:LEU:O	1:DA:552:GLU:HG2	2.15	0.46
2:DB:152:VAL:HG12	2:DB:224:VAL:HG22	1.98	0.46
2:DB:199:PRO:HA	2:DB:202:ARG:HG2	1.97	0.46
1:DE:379:SER:HA	2:DF:236:LEU:HD11	1.98	0.46
1:AE:486:TYR:CE2	2:AF:300:MET:HE1	2.50	0.46
1:BE:289:TYR:OH	1:BE:318:GLU:O	2.29	0.46
1:BE:555:LYS:O	1:BE:558:GLU:HG3	2.16	0.46
2:BF:238:GLU:O	2:BF:243:LYS:NZ	2.47	0.46
2:CD:78:VAL:HG22	2:CD:141:VAL:HG13	1.97	0.46
2:DB:268:ALA:O	2:DB:272:LYS:HG2	2.14	0.46
1:DE:491:LYS:NZ	2:DF:209:SER:O	2.40	0.46
2:DF:126:LYS:HE3	2:DF:143:PHE:HB2	1.96	0.46
1:AC:555:LYS:O	1:AC:558:GLU:HG2	2.15	0.46
2:AD:241:VAL:HG12	2:AD:243:LYS:H	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AG:296:PHE:O	1:AG:361:ARG:N	2.47	0.46
1:AG:440:PRO:HG3	2:AH:272:LYS:HG3	1.97	0.46
1:AG:476:PHE:HZ	2:AH:171:PHE:HZ	1.63	0.46
2:AH:77:PHE:HD2	2:AH:142:ARG:HB2	1.80	0.46
1:BE:453:ASP:OD1	1:BE:454:GLY:N	2.48	0.46
2:BF:78:VAL:HA	2:BF:141:VAL:HG12	1.97	0.46
1:CE:296:PHE:HD2	1:CE:361:ARG:HB2	1.80	0.46
1:CE:465:MET:HA	1:CE:468:LYS:HG2	1.98	0.46
1:CE:534:ASP:OD2	1:CE:538:ARG:NH2	2.48	0.46
1:DG:292:ARG:HH21	1:DG:338:ARG:HD3	1.80	0.46
2:DH:151:THR:N	2:DH:225:GLU:O	2.41	0.46
1:AA:544:ARG:O	1:AA:547:GLU:HG3	2.15	0.46
2:AF:116:LEU:HD12	2:AF:122:ALA:HA	1.98	0.46
1:BA:303:ASP:O	1:BA:354:ARG:NH1	2.36	0.46
1:BC:465:MET:HE1	2:BD:158:TYR:CE2	2.50	0.46
2:BH:244:ASN:ND2	2:BH:247:PHE:H	2.13	0.46
1:CE:430:GLY:HA3	2:CF:257:PHE:HE2	1.80	0.46
1:CE:583:GLU:OE2	1:CE:587:ARG:NH2	2.49	0.46
1:CG:465:MET:HG2	1:CG:468:LYS:HD3	1.97	0.46
2:AF:166:GLU:O	2:AF:169:SER:OG	2.34	0.46
2:AH:164:LEU:HB3	2:AH:177:ALA:HB1	1.98	0.46
2:BB:73:ARG:HE	2:BB:176:ARG:NH1	2.09	0.46
1:BE:556:ARG:NH2	1:CC:582:GLU:OE2	2.43	0.46
1:BG:379:SER:OG	1:BG:380:ASN:N	2.48	0.46
2:CH:315:ASP:OD1	2:CH:316:LEU:N	2.49	0.46
1:DC:343:ILE:HD11	2:DD:127:VAL:HG11	1.98	0.46
2:DH:276:GLU:OE2	2:DH:280:GLN:NE2	2.47	0.46
2:AB:198:LYS:HG3	2:AB:199:PRO:HD3	1.98	0.46
2:AD:180:ILE:HG13	2:AD:188:SER:HB3	1.98	0.46
1:AG:448:GLN:N	1:AG:448:GLN:OE1	2.48	0.46
1:BG:469:GLU:O	2:BH:216:THR:HG23	2.16	0.46
1:CE:373:ASN:HD22	2:CF:275:ILE:CD1	2.25	0.46
2:CH:92:LYS:O	2:CH:95:GLU:HG2	2.16	0.46
2:CH:159:VAL:HA	2:CH:163:LEU:HD12	1.97	0.46
1:DA:483:GLU:HG2	2:DB:219:PRO:HB3	1.97	0.46
1:DG:346:ALA:HB1	2:DH:120:THR:HG23	1.98	0.46
2:DF:151:THR:HA	2:DF:227:MET:HE2	1.97	0.46
2:DF:333:GLU:HA	2:DF:336:LYS:HG2	1.98	0.46
1:BA:562:ARG:O	1:BA:565:GLU:HG3	2.16	0.46
2:BB:117:GLU:HB3	2:BB:121:LEU:HD13	1.97	0.46
1:BC:544:ARG:O	1:BC:547:GLU:HG3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BE:457:GLU:HB3	2:BF:162:GLU:OE1	2.16	0.46
2:BH:315:ASP:OD1	2:BH:316:LEU:N	2.48	0.46
1:CA:544:ARG:O	1:CA:547:GLU:HG3	2.15	0.46
1:CA:556:ARG:HA	1:CA:559:MET:HE2	1.98	0.46
2:CB:284:GLN:HA	2:CB:287:ARG:HD2	1.97	0.46
1:CE:289:TYR:OH	1:CE:318:GLU:O	2.27	0.46
1:DA:463:ASN:OD1	1:DA:466:TYR:N	2.49	0.46
2:DD:71:THR:HG23	2:DD:74:SER:H	1.79	0.46
2:DD:134:LEU:HD22	2:DD:139:LEU:HD11	1.97	0.46
2:DF:297:GLU:O	2:DF:300:MET:HG2	2.16	0.46
2:AB:205:LEU:HD23	2:AB:224:VAL:HG12	1.97	0.46
1:AC:369:LEU:O	1:AC:412:VAL:HG12	2.16	0.46
2:AD:109:LYS:HB3	2:AD:111:PHE:CE2	2.51	0.46
2:BF:156:PRO:HA	2:BF:220:ARG:HH21	1.80	0.46
2:BF:287:ARG:HH11	2:BF:290:LYS:HD3	1.79	0.46
1:BG:418:PRO:HA	1:BG:421:ARG:HE	1.81	0.46
1:BG:573:GLU:O	1:BG:576:ILE:HG22	2.15	0.46
1:CG:379:SER:OG	1:CG:380:ASN:N	2.48	0.46
2:AD:287:ARG:NH1	1:AE:564:GLU:OE2	2.49	0.46
1:AE:346:ALA:HB2	2:AF:123:GLU:OE1	2.16	0.46
1:BG:573:GLU:OE2	1:BG:577:ARG:NH2	2.48	0.46
1:CA:453:ASP:OD1	1:CA:453:ASP:N	2.47	0.46
1:CC:322:VAL:HG22	1:CC:333:ILE:HG12	1.98	0.46
1:CC:433:LEU:HD12	2:CD:258:ALA:HB2	1.98	0.46
1:DC:341:ALA:O	1:DC:345:LYS:HG2	2.16	0.46
1:DC:386:ALA:HB1	1:DC:432:PHE:CZ	2.50	0.46
2:AB:157:GLN:HB2	2:AB:158:TYR:CE1	2.51	0.46
2:AD:247:PHE:O	2:AD:251:ARG:N	2.49	0.46
1:AG:349:ASP:OD1	1:AG:350:ASP:N	2.48	0.46
1:AG:504:VAL:O	1:AG:508:MET:HG2	2.16	0.46
1:BA:475:ARG:HG3	1:BA:477:ALA:H	1.81	0.46
2:BD:82:PRO:HG2	2:BD:135:ARG:HH21	1.81	0.46
1:BG:398:VAL:HA	1:BG:410:GLY:HA2	1.98	0.46
2:CD:198:LYS:HE2	2:CD:198:LYS:HB3	1.81	0.46
1:DC:310:LYS:HE3	1:DC:322:VAL:HG21	1.97	0.46
1:DG:296:PHE:N	1:DG:361:ARG:O	2.46	0.46
1:AA:414:PHE:HB2	1:AA:420:ALA:HB2	1.99	0.45
2:AF:315:ASP:O	2:AF:319:ARG:HG3	2.16	0.45
2:BD:247:PHE:O	2:BD:251:ARG:N	2.45	0.45
1:DC:529:ASN:O	1:DC:533:GLN:HG2	2.16	0.45
2:DD:126:LYS:O	2:DD:130:ASP:HB2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:DD:134:LEU:N	2:DD:137:LYS:O	2.47	0.45
2:AB:131:ASN:HA	2:AB:140:ARG:NH2	2.31	0.45
2:AD:162:GLU:O	2:AD:166:GLU:HG3	2.16	0.45
2:AF:150:LEU:HD11	2:AF:201:ALA:HB1	1.98	0.45
1:AG:558:GLU:O	1:AG:561:LEU:HG	2.15	0.45
2:BB:138:GLN:HB3	2:BB:140:ARG:NH2	2.31	0.45
1:BE:348:LEU:O	1:BE:358:LEU:HD23	2.16	0.45
2:BH:332:GLN:HA	2:BH:335:GLN:OE1	2.16	0.45
1:CE:556:ARG:NH1	2:DF:298:MET:O	2.49	0.45
1:CG:371:VAL:HG22	1:CG:443:VAL:HG12	1.98	0.45
1:CG:487:SER:O	1:CG:491:LYS:HG2	2.16	0.45
1:DC:431:VAL:HG13	1:DC:440:PRO:HB3	1.99	0.45
2:DH:215:LEU:H	2:DH:215:LEU:HD23	1.80	0.45
1:AA:569:ARG:O	1:AA:572:GLU:HG3	2.16	0.45
2:AD:126:LYS:O	2:AD:130:ASP:HB2	2.16	0.45
1:AG:350:ASP:N	1:AG:358:LEU:O	2.48	0.45
1:BE:553:MET:HE2	1:BE:553:MET:HA	1.98	0.45
2:CB:268:ALA:O	2:CB:272:LYS:HG2	2.16	0.45
1:CC:436:THR:OG1	2:CD:249:LYS:O	2.30	0.45
1:DA:496:MET:O	1:DA:499:GLN:HG2	2.16	0.45
2:DD:146:HIS:CE1	2:DD:194:GLU:HB2	2.51	0.45
1:DG:465:MET:N	1:DG:465:MET:SD	2.89	0.45
1:DG:490:TRP:NE1	2:DH:219:PRO:O	2.49	0.45
2:DH:269:MET:HE2	2:DH:269:MET:N	2.30	0.45
1:AA:386:ALA:HB1	1:AA:432:PHE:HZ	1.80	0.45
2:AB:207:ARG:NH1	2:AB:207:ARG:HB2	2.31	0.45
1:AE:292:ARG:HB3	1:AE:338:ARG:HH11	1.82	0.45
1:AE:539:GLN:HG2	2:BF:316:LEU:HD11	1.99	0.45
2:AH:216:THR:HG22	2:AH:218:PHE:H	1.80	0.45
1:BC:461:GLN:O	1:BC:467:GLN:NE2	2.41	0.45
2:BF:325:ARG:HA	2:BF:328:GLU:HG3	1.99	0.45
2:BH:311:LEU:HD23	2:BH:311:LEU:HA	1.82	0.45
1:CC:510:ASP:O	1:CC:514:LYS:HG2	2.16	0.45
1:DC:298:GLY:HA2	1:DC:330:PHE:CD1	2.51	0.45
2:DD:116:LEU:HD22	2:DD:122:ALA:HA	1.96	0.45
2:DD:159:VAL:HG13	2:DD:179:VAL:HG21	1.98	0.45
2:DH:305:HIS:O	2:DH:309:VAL:HG23	2.16	0.45
2:AD:70:PHE:N	2:AD:117:GLU:O	2.47	0.45
2:AF:119:ARG:NE	2:AF:123:GLU:OE2	2.49	0.45
2:AH:246:GLN:HA	2:AH:249:LYS:HE3	1.98	0.45
1:BC:519:MET:HE1	2:BD:267:TYR:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BD:140:ARG:HB3	2:BD:140:ARG:NH1	2.31	0.45
2:BF:205:LEU:HD11	2:BF:226:PRO:HD3	1.97	0.45
2:CD:155:LEU:HD13	2:CD:159:VAL:HG21	1.98	0.45
1:CE:482:PHE:HB2	2:CF:307:HIS:ND1	2.32	0.45
1:DC:411:ILE:HD13	1:DC:446:LEU:HD22	1.98	0.45
2:DF:277:MET:SD	2:DF:281:GLN:NE2	2.89	0.45
2:AF:104:PHE:HB3	2:AF:113:PHE:HB2	1.98	0.45
1:AG:508:MET:HE1	2:AH:277:MET:HE2	1.98	0.45
1:BG:508:MET:HG3	2:BH:278:GLU:CD	2.42	0.45
1:CE:292:ARG:CD	1:CE:395:ARG:HD3	2.46	0.45
1:CG:380:ASN:HD21	2:CH:236:LEU:H	1.63	0.45
2:CH:81:LEU:HD13	2:CH:85:ILE:HG12	1.97	0.45
2:DD:87:GLU:HG3	2:DD:103:VAL:HG11	1.99	0.45
1:DG:293:CYS:SG	1:DG:335:LEU:N	2.84	0.45
2:AB:133:PRO:HA	2:AB:138:GLN:HA	1.99	0.45
1:AG:478:GLN:O	1:AG:481:THR:OG1	2.30	0.45
2:AH:182:ASP:OD1	2:AH:186:ARG:N	2.46	0.45
2:BD:241:VAL:HG12	2:BD:243:LYS:H	1.82	0.45
1:DC:475:ARG:HG3	1:DC:477:ALA:H	1.81	0.45
2:DD:198:LYS:HB3	2:DD:198:LYS:HE2	1.78	0.45
1:AA:531:LEU:HB3	2:BB:323:LEU:HD12	1.97	0.45
1:BA:345:LYS:HD2	1:BA:362:PHE:CZ	2.52	0.45
1:BC:305:THR:HG23	1:BC:308:GLU:H	1.80	0.45
1:BE:470:ARG:HG3	1:BE:470:ARG:O	2.17	0.45
1:BE:585:MET:HE2	1:CC:552:GLU:OE1	2.17	0.45
1:CC:293:CYS:HB3	1:CC:335:LEU:H	1.81	0.45
1:CC:339:ALA:O	1:CC:343:ILE:HG13	2.17	0.45
1:CC:384:GLU:HB3	1:CC:396:ALA:HB3	1.98	0.45
2:CF:70:PHE:CZ	2:CF:117:GLU:HG3	2.51	0.45
2:CH:142:ARG:NH1	2:CH:143:PHE:H	2.15	0.45
1:AA:434:LEU:HD13	1:AA:441:VAL:HG21	1.99	0.45
2:AD:322:GLU:O	2:AD:325:ARG:HG3	2.16	0.45
1:AE:473:PRO:O	1:AE:475:ARG:NH1	2.48	0.45
1:AG:470:ARG:NH1	2:AH:163:LEU:HD13	2.32	0.45
1:BA:490:TRP:CD1	2:BB:221:PRO:HD2	2.52	0.45
1:BC:414:PHE:HD2	1:BC:420:ALA:HA	1.82	0.45
1:BE:548:LEU:O	1:BE:552:GLU:HG2	2.17	0.45
1:BG:457:GLU:HB2	2:BH:162:GLU:CD	2.42	0.45
1:BG:552:GLU:CD	1:DA:585:MET:HE2	2.41	0.45
2:BH:317:MET:O	2:BH:320:GLN:HG3	2.17	0.45
2:AB:73:ARG:HH12	2:AB:176:ARG:HH11	1.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:AB:78:VAL:HG13	2:AB:141:VAL:HG22	1.99	0.45
1:AE:566:GLU:OE2	1:AE:570:ARG:NH1	2.50	0.45
1:BC:411:ILE:HD13	1:BC:446:LEU:HD13	1.99	0.45
1:BE:292:ARG:HB3	1:BE:338:ARG:HH11	1.82	0.45
1:BE:574:MET:SD	1:CC:563:GLN:OE1	2.75	0.45
2:BH:167:ALA:HB1	2:BH:213:PHE:HE2	1.81	0.45
2:BH:330:HIS:O	2:BH:333:GLU:HG3	2.17	0.45
1:CA:438:PRO:HG2	2:CB:267:TYR:HD2	1.82	0.45
2:CD:214:LEU:HD23	2:CD:219:PRO:HA	1.99	0.45
2:CD:215:LEU:HD23	2:CD:215:LEU:H	1.82	0.45
1:AE:519:MET:HE1	2:AF:267:TYR:CZ	2.52	0.44
1:AG:458:LYS:O	1:AG:462:LYS:HG2	2.17	0.44
2:AH:238:GLU:O	2:AH:243:LYS:NZ	2.43	0.44
1:CC:560:GLN:O	1:CC:563:GLN:HB2	2.17	0.44
1:DC:526:HIS:ND1	2:DD:263:PHE:HB2	2.31	0.44
1:DE:369:LEU:HD21	1:DE:424:PHE:HB2	1.98	0.44
2:AB:206:ASP:OD1	2:AB:207:ARG:N	2.50	0.44
2:AH:228:ASP:OD1	2:AH:228:ASP:N	2.47	0.44
1:BA:369:LEU:O	1:BA:412:VAL:HG12	2.17	0.44
1:CA:500:GLN:O	1:CA:503:GLN:HG3	2.17	0.44
1:CE:400:VAL:HG12	1:CE:406:SER:HA	2.00	0.44
2:DB:265:TYR:O	2:DB:269:MET:HG2	2.17	0.44
1:DC:487:SER:O	1:DC:491:LYS:HG2	2.17	0.44
1:DC:542:LEU:HA	1:DC:545:MET:HG2	1.99	0.44
2:DF:192:ILE:HG12	2:DF:194:GLU:OE1	2.17	0.44
1:AC:292:ARG:HD2	1:AC:395:ARG:HD3	1.99	0.44
1:AC:395:ARG:NH2	1:AC:413:GLU:OE2	2.50	0.44
1:AC:434:LEU:HD23	1:AC:441:VAL:HG21	1.99	0.44
2:AF:288:ASN:O	2:AF:291:GLU:HG3	2.16	0.44
1:AG:310:LYS:HE3	1:AG:322:VAL:HG21	2.00	0.44
1:AG:438:PRO:HG2	2:AH:267:TYR:HD2	1.81	0.44
2:BB:247:PHE:CE1	2:BB:251:ARG:HG3	2.53	0.44
1:BG:585:MET:HE2	1:DA:552:GLU:OE1	2.18	0.44
2:CF:330:HIS:O	2:CF:333:GLU:HG3	2.16	0.44
1:CG:508:MET:HE1	2:CH:278:GLU:HA	1.98	0.44
1:DC:375:SER:O	1:DC:378:VAL:HG12	2.17	0.44
2:DD:162:GLU:HA	2:DD:165:GLU:HB3	2.00	0.44
2:AD:75:ARG:HH11	2:AD:115:ARG:NH2	2.15	0.44
1:AG:418:PRO:O	1:AG:422:LYS:HG2	2.16	0.44
1:BC:380:ASN:HD21	2:BD:235:GLY:HA3	1.82	0.44
2:CH:80:ASN:O	2:CH:137:LYS:NZ	2.28	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DG:313:PHE:CZ	1:DG:333:ILE:HG21	2.52	0.44
1:AA:369:LEU:HD12	1:AA:445:PRO:HA	1.99	0.44
1:AE:345:LYS:HA	1:AE:360:VAL:HG11	1.99	0.44
1:AG:375:SER:O	1:AG:378:VAL:HG12	2.18	0.44
1:AG:476:PHE:HZ	2:AH:171:PHE:CZ	2.35	0.44
1:BC:306:GLU:HG3	1:BC:322:VAL:HG11	2.00	0.44
1:BE:365:HIS:CD2	1:BE:413:GLU:HB3	2.53	0.44
1:BG:549:HIS:O	1:BG:552:GLU:HB2	2.17	0.44
2:BH:334:VAL:O	2:BH:337:ARG:HG2	2.18	0.44
2:CB:153:ARG:O	2:CB:222:VAL:HG13	2.17	0.44
2:CB:256:ARG:HH22	2:CB:264:GLU:HG3	1.83	0.44
1:DA:406:SER:OG	2:DB:236:LEU:HD11	2.18	0.44
2:DD:325:ARG:HA	2:DD:328:GLU:HG3	1.98	0.44
1:AC:345:LYS:HE3	1:AC:360:VAL:HG12	2.00	0.44
1:AC:350:ASP:N	1:AC:358:LEU:O	2.49	0.44
2:AH:71:THR:HG23	2:AH:74:SER:H	1.83	0.44
2:AH:75:ARG:HH11	2:AH:113:PHE:HB3	1.83	0.44
1:BC:438:PRO:HG2	2:BD:267:TYR:HD2	1.80	0.44
1:BE:370:SER:HB2	1:BE:446:LEU:HD13	1.98	0.44
2:BF:333:GLU:HA	2:BF:336:LYS:HG2	1.99	0.44
2:CF:77:PHE:HB2	2:CF:144:ALA:HB2	2.00	0.44
1:DA:508:MET:HE1	2:DB:278:GLU:HA	2.00	0.44
2:DD:311:LEU:HD12	2:DD:311:LEU:HA	1.87	0.44
1:AC:306:GLU:HG3	1:AC:322:VAL:HG11	1.99	0.44
1:AG:395:ARG:NH1	2:AH:232:ASP:O	2.48	0.44
1:BC:395:ARG:NH2	1:BC:413:GLU:OE2	2.46	0.44
1:BC:402:ASP:OD1	1:BC:403:ARG:N	2.51	0.44
1:BG:419:ALA:HA	1:BG:422:LYS:HG2	1.99	0.44
1:CA:506:LYS:HA	1:CA:509:LYS:HG2	1.99	0.44
1:DG:418:PRO:O	1:DG:421:ARG:HG2	2.17	0.44
2:DH:294:GLU:O	2:DH:298:MET:HG2	2.17	0.44
1:BA:289:TYR:C	1:BA:334:LYS:HD3	2.43	0.44
1:BA:482:PHE:HB2	2:BB:307:HIS:ND1	2.33	0.44
1:BC:361:ARG:NE	1:BC:362:PHE:O	2.32	0.44
2:BD:198:LYS:HE2	2:BD:198:LYS:HB2	1.80	0.44
2:BD:216:THR:HG22	2:BD:217:THR:N	2.32	0.44
2:BF:269:MET:HA	2:BF:269:MET:HE2	2.00	0.44
1:CA:481:THR:HG23	1:CA:484:TYR:H	1.82	0.44
1:CC:431:VAL:HG13	1:CC:440:PRO:HB3	2.00	0.44
2:CD:247:PHE:O	2:CD:251:ARG:N	2.51	0.44
1:CG:371:VAL:O	1:CG:410:GLY:N	2.39	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CH:244:ASN:HD21	2:CH:246:GLN:HB2	1.82	0.44
2:DH:81:LEU:HD22	2:DH:85:ILE:HD13	1.99	0.44
2:DH:228:ASP:OD1	2:DH:228:ASP:N	2.46	0.44
1:AC:369:LEU:HD12	1:AC:445:PRO:HA	2.00	0.44
1:AG:490:TRP:HB3	2:AH:220:ARG:NH1	2.33	0.44
2:BB:245:GLN:CD	2:BB:245:GLN:H	2.26	0.44
2:BD:319:ARG:HH21	1:CC:538:ARG:HD2	1.83	0.44
2:BF:315:ASP:O	2:BF:319:ARG:HG3	2.17	0.44
1:BG:548:LEU:O	1:BG:552:GLU:HG2	2.18	0.44
2:CD:162:GLU:HA	2:CD:165:GLU:HB3	2.00	0.44
1:CE:373:ASN:OD1	1:CE:439:ARG:NH2	2.48	0.44
1:DG:293:CYS:HB2	1:DG:335:LEU:HB2	2.00	0.44
2:DH:151:THR:OG1	2:DH:227:MET:HG2	2.18	0.44
2:DF:152:VAL:HG23	2:DF:155:LEU:HD21	2.00	0.44
2:DF:315:ASP:O	2:DF:319:ARG:HG3	2.18	0.44
1:AG:345:LYS:HE2	1:AG:345:LYS:HB3	1.78	0.43
2:AH:69:THR:HA	2:AH:118:THR:HG22	2.00	0.43
2:AH:334:VAL:O	2:AH:337:ARG:HG2	2.18	0.43
1:BA:442:ILE:HG12	2:BB:275:ILE:HG21	2.00	0.43
1:BC:384:GLU:HB3	1:BC:396:ALA:HB3	2.00	0.43
2:BH:247:PHE:O	2:BH:251:ARG:N	2.46	0.43
2:CB:192:ILE:HG23	2:CB:227:MET:HE1	1.98	0.43
2:CD:101:GLY:N	2:CD:115:ARG:O	2.44	0.43
2:CH:244:ASN:N	2:CH:244:ASN:HD22	2.16	0.43
2:CH:322:GLU:HA	2:CH:325:ARG:HG2	1.99	0.43
1:DA:434:LEU:HA	2:DB:255:PRO:HB3	2.00	0.43
2:DH:259:GLN:O	2:DH:262:SER:OG	2.34	0.43
2:DF:94:PHE:CD2	2:DF:116:LEU:HD21	2.53	0.43
2:DF:265:TYR:O	2:DF:269:MET:HG2	2.18	0.43
1:AA:380:ASN:OD1	1:AA:397:VAL:HA	2.19	0.43
1:AE:483:GLU:OE1	2:AF:219:PRO:HB3	2.18	0.43
2:AF:85:ILE:CG1	2:AF:90:MET:HE3	2.48	0.43
2:BD:320:GLN:HB2	1:CC:535:LEU:HD11	2.00	0.43
1:BE:433:LEU:O	1:BE:434:LEU:HD23	2.18	0.43
1:BE:469:GLU:OE1	2:BF:217:THR:OG1	2.36	0.43
2:BH:151:THR:OG1	2:BH:227:MET:HE3	2.17	0.43
2:BH:254:PRO:O	2:BH:256:ARG:HD2	2.18	0.43
1:CA:308:GLU:O	1:CA:312:LEU:HG	2.18	0.43
1:CA:469:GLU:HG3	2:CB:216:THR:CG2	2.48	0.43
2:CD:151:THR:HB	2:CD:227:MET:SD	2.58	0.43
2:CH:73:ARG:HD3	2:CH:143:PHE:CE1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CH:232:ASP:OD1	2:CH:232:ASP:N	2.51	0.43
2:CH:244:ASN:OD1	2:CH:246:GLN:NE2	2.51	0.43
1:DA:526:HIS:ND1	2:DB:263:PHE:HB2	2.33	0.43
2:DB:101:GLY:HA3	2:DB:115:ARG:HB3	2.00	0.43
2:DD:219:PRO:HD2	2:DD:300:MET:HE3	1.99	0.43
1:AE:292:ARG:HD2	1:AE:395:ARG:HD2	2.00	0.43
1:AG:379:SER:OG	1:AG:380:ASN:N	2.51	0.43
1:BE:300:LEU:HB2	1:BE:329:GLY:C	2.44	0.43
2:BF:133:PRO:HA	2:BF:138:GLN:HA	1.99	0.43
1:BG:532:ARG:HG2	1:BG:532:ARG:HH11	1.82	0.43
2:BH:149:SER:C	2:BH:150:LEU:HD12	2.43	0.43
2:BH:244:ASN:H	2:BH:244:ASN:ND2	2.17	0.43
1:CE:557:LYS:O	1:CE:561:LEU:HD23	2.19	0.43
1:CG:418:PRO:O	1:CG:421:ARG:HG2	2.18	0.43
2:DD:132:MET:HE3	2:DD:139:LEU:HD12	2.00	0.43
1:BA:541:GLU:OE1	1:BA:544:ARG:NH2	2.50	0.43
2:BD:176:ARG:HD3	2:BD:178:VAL:HG13	2.00	0.43
2:BF:330:HIS:O	2:BF:333:GLU:HG3	2.18	0.43
2:CB:301:GLU:OE2	2:CB:304:ARG:NH1	2.51	0.43
1:CE:531:LEU:HB3	1:CE:532:ARG:HH22	1.83	0.43
2:CF:109:LYS:HB3	2:CF:111:PHE:CE2	2.53	0.43
2:CH:167:ALA:HB1	2:CH:213:PHE:CE2	2.53	0.43
1:AA:383:LEU:HD22	1:AA:387:PHE:HE2	1.83	0.43
1:AE:365:HIS:O	1:AE:448:GLN:NE2	2.52	0.43
2:AF:159:VAL:HG21	2:AF:179:VAL:HG11	1.99	0.43
1:AG:570:ARG:HG2	1:AG:574:MET:HE2	2.01	0.43
1:BC:293:CYS:HB3	1:BC:335:LEU:HB2	2.00	0.43
1:BG:457:GLU:HB2	2:BH:162:GLU:OE1	2.18	0.43
2:CD:305:HIS:O	2:CD:309:VAL:HG23	2.18	0.43
2:DB:288:ASN:O	2:DB:291:GLU:HG3	2.18	0.43
1:AA:573:GLU:O	1:AA:576:ILE:HG22	2.19	0.43
2:AB:150:LEU:HB2	2:AB:193:VAL:HB	1.99	0.43
2:AB:324:ARG:HH21	2:DH:327:GLU:HB3	1.81	0.43
1:AC:541:GLU:O	1:AC:544:ARG:HG3	2.19	0.43
1:BA:433:LEU:HD22	2:BB:256:ARG:HH12	1.84	0.43
2:BB:276:GLU:O	2:BB:280:GLN:HG2	2.19	0.43
2:CD:146:HIS:HB3	2:CD:149:SER:HB2	2.01	0.43
2:CF:101:GLY:HA3	2:CF:115:ARG:HB3	2.00	0.43
2:DD:326:MET:O	2:DD:329:LEU:HG	2.18	0.43
1:AA:433:LEU:C	1:AA:434:LEU:HD12	2.44	0.43
1:AE:465:MET:HE1	2:AF:158:TYR:CD1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AE:577:ARG:HG3	1:BC:559:MET:HE1	1.99	0.43
1:BE:434:LEU:HG	1:BE:441:VAL:HG21	2.00	0.43
1:CA:418:PRO:O	1:CA:421:ARG:HG3	2.18	0.43
1:DC:437:THR:HG23	2:DD:250:GLU:OE1	2.19	0.43
1:DC:484:TYR:O	1:DC:488:GLN:HG2	2.19	0.43
2:DD:149:SER:OG	2:DD:227:MET:HE2	2.18	0.43
1:AE:348:LEU:O	1:AE:351:THR:OG1	2.32	0.43
2:AH:89:GLU:OE2	2:AH:135:ARG:NH1	2.49	0.43
1:BA:463:ASN:ND2	1:BA:465:MET:HE3	2.34	0.43
2:BD:198:LYS:N	2:BD:199:PRO:HD2	2.34	0.43
1:BE:288:THR:HA	1:BE:336:GLU:O	2.19	0.43
1:CC:384:GLU:HB2	1:CC:393:ILE:HG21	2.01	0.43
1:CE:417:LYS:HD3	1:CE:417:LYS:C	2.43	0.43
2:CF:215:LEU:HA	2:CF:215:LEU:HD23	1.77	0.43
1:CG:524:HIS:O	1:CG:527:GLN:HG2	2.18	0.43
2:CH:171:PHE:HB2	2:CH:195:PHE:CZ	2.54	0.43
1:DC:457:GLU:OE2	2:DD:160:SER:OG	2.23	0.43
1:AA:563:GLN:OE1	1:CG:574:MET:HB3	2.19	0.43
2:AB:298:MET:HE1	1:BG:579:ARG:HB2	2.01	0.43
1:AC:339:ALA:HB1	2:AD:127:VAL:HG13	2.01	0.43
1:AC:417:LYS:HB3	1:AC:421:ARG:NH2	2.29	0.43
1:AC:455:LEU:HD23	2:AD:159:VAL:O	2.19	0.43
1:AE:345:LYS:HD3	1:AE:362:PHE:HE1	1.83	0.43
1:AE:417:LYS:NZ	1:AE:421:ARG:HB2	2.34	0.43
1:AG:519:MET:HE1	2:AH:267:TYR:CE2	2.54	0.43
1:BA:370:SER:HB2	1:BA:446:LEU:HD13	2.00	0.43
1:BC:375:SER:O	1:BC:378:VAL:HG12	2.19	0.43
2:BD:327:GLU:OE2	1:CC:532:ARG:NH1	2.48	0.43
1:BE:353:MET:N	1:BE:356:ARG:O	2.49	0.43
2:BF:79:GLY:HA2	2:BF:111:PHE:HB3	2.01	0.43
1:BG:457:GLU:HB3	1:BG:458:LYS:NZ	2.34	0.43
2:BH:244:ASN:N	2:BH:244:ASN:ND2	2.66	0.43
2:BH:284:GLN:NE2	2:BH:288:ASN:OD1	2.51	0.43
2:CB:120:THR:O	2:CB:124:ILE:HG12	2.19	0.43
2:CB:125:ALA:O	2:CB:129:LEU:HB3	2.18	0.43
1:CC:496:MET:SD	1:CC:500:GLN:NE2	2.91	0.43
1:CE:508:MET:O	1:CE:509:LYS:C	2.62	0.43
2:CF:237:PRO:HG2	2:CF:240:LEU:HB2	2.00	0.43
1:CG:447:GLU:OE1	1:CG:449:LEU:HG	2.19	0.43
1:DA:470:ARG:HD3	2:DB:163:LEU:HD12	2.00	0.43
2:DD:70:PHE:O	2:DD:115:ARG:NH1	2.43	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:DG:470:ARG:NH1	2:DH:163:LEU:HD13	2.34	0.43
1:AA:310:LYS:HE3	1:AA:322:VAL:HG21	2.00	0.43
1:AC:381:GLU:HA	1:AC:384:GLU:HG2	2.01	0.43
2:AF:126:LYS:HD2	2:AF:143:PHE:CE2	2.54	0.43
1:BA:348:LEU:HB3	1:BA:358:LEU:HD23	2.01	0.43
1:BC:369:LEU:HD23	1:BC:369:LEU:HA	1.84	0.43
2:BD:82:PRO:HG2	2:BD:135:ARG:NH2	2.33	0.43
1:BE:578:GLN:HA	1:CC:559:MET:HE1	2.01	0.43
1:BG:378:VAL:HG23	1:BG:382:LEU:HB2	2.00	0.43
1:CA:308:GLU:OE2	1:CA:312:LEU:HD21	2.18	0.43
1:CA:471:GLU:N	1:CA:471:GLU:OE1	2.51	0.43
2:CB:118:THR:HG22	2:CB:120:THR:H	1.84	0.43
1:CC:295:LEU:O	1:CC:332:PHE:HA	2.18	0.43
1:CE:310:LYS:HG2	1:CE:319:PRO:HG2	2.00	0.43
2:CF:325:ARG:O	2:CF:328:GLU:HG3	2.19	0.43
1:CG:544:ARG:O	1:CG:547:GLU:HG3	2.17	0.43
1:DC:450:ASP:OD1	1:DC:450:ASP:N	2.52	0.43
1:DC:515:LEU:HD23	2:DD:271:TRP:CZ2	2.53	0.43
2:AB:324:ARG:NH1	2:DH:331:ASN:OD1	2.51	0.42
2:AF:173:GLN:N	2:AF:173:GLN:OE1	2.51	0.42
1:AG:482:PHE:O	1:AG:485:GLU:HG3	2.17	0.42
2:BD:72:GLN:NE2	2:BD:195:PHE:O	2.52	0.42
1:CA:469:GLU:O	2:CB:217:THR:HG23	2.19	0.42
1:CC:522:ALA:HB3	2:CD:267:TYR:OH	2.19	0.42
2:CF:69:THR:HG22	2:CF:118:THR:HG22	2.01	0.42
2:DB:129:LEU:HD23	2:DB:129:LEU:HA	1.89	0.42
2:DF:156:PRO:HA	2:DF:220:ARG:NH2	2.34	0.42
1:AC:482:PHE:HB2	2:AD:307:HIS:ND1	2.34	0.42
2:AD:325:ARG:HA	2:AD:328:GLU:HG3	2.01	0.42
1:AE:503:GLN:O	1:AE:507:ASN:OD1	2.37	0.42
1:AG:471:GLU:OE1	1:AG:471:GLU:N	2.52	0.42
1:BA:465:MET:O	1:BA:468:LYS:HG3	2.18	0.42
2:BB:173:GLN:OE1	2:BB:173:GLN:N	2.43	0.42
2:BD:119:ARG:HD2	2:BD:122:ALA:HB3	2.01	0.42
2:BD:253:GLN:HE21	2:BD:253:GLN:HB2	1.70	0.42
1:CA:391:GLY:HA3	1:CA:419:ALA:HB1	2.01	0.42
1:CE:321:GLU:HB3	1:CE:334:LYS:HE2	1.99	0.42
1:CE:504:VAL:O	1:CE:508:MET:HG2	2.19	0.42
2:CF:205:LEU:HD11	2:CF:226:PRO:HD3	2.00	0.42
2:CH:81:LEU:HD22	2:CH:85:ILE:HD13	2.01	0.42
2:DH:322:GLU:HA	2:DH:325:ARG:HG2	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AA:469:GLU:HB3	2:AB:216:THR:CG2	2.49	0.42
2:AD:215:LEU:O	2:AD:216:THR:OG1	2.32	0.42
1:BA:295:LEU:N	1:BA:333:ILE:O	2.52	0.42
1:BA:342:GLU:O	1:BA:345:LYS:HG2	2.18	0.42
2:BB:116:LEU:HD12	2:BB:122:ALA:HA	2.02	0.42
1:BC:345:LYS:NZ	1:BC:362:PHE:HB2	2.34	0.42
1:BC:432:PHE:C	1:BC:433:LEU:HD12	2.44	0.42
2:BF:254:PRO:O	2:BF:256:ARG:HD2	2.19	0.42
1:CG:292:ARG:HH21	1:CG:338:ARG:HD3	1.83	0.42
1:CG:386:ALA:HB1	1:CG:432:PHE:CZ	2.54	0.42
1:DC:476:PHE:CE2	2:DD:213:PHE:HB2	2.54	0.42
1:AA:335:LEU:HD23	1:AA:335:LEU:HA	1.79	0.42
1:AA:470:ARG:HD2	1:AA:470:ARG:HA	1.94	0.42
1:AA:555:LYS:HD3	1:CG:585:MET:SD	2.60	0.42
1:AC:477:ALA:HB1	1:AC:484:TYR:HB2	2.01	0.42
1:AE:572:GLU:OE1	1:AE:572:GLU:HA	2.19	0.42
2:AF:275:ILE:O	2:AF:278:GLU:HB3	2.19	0.42
1:AG:321:GLU:OE1	1:AG:334:LYS:HE3	2.19	0.42
1:AG:548:LEU:O	1:AG:551:GLN:HG2	2.19	0.42
1:BA:586:ARG:NH2	2:CH:301:GLU:HB3	2.34	0.42
1:BC:296:PHE:HD2	1:BC:361:ARG:HB3	1.84	0.42
1:BC:526:HIS:ND1	2:BD:263:PHE:HB2	2.34	0.42
2:BF:179:VAL:O	2:BF:181:VAL:HG23	2.19	0.42
1:CC:569:ARG:O	1:CC:572:GLU:HG3	2.19	0.42
2:CD:176:ARG:HH11	2:CD:178:VAL:HG21	1.83	0.42
1:CE:553:MET:HE3	1:CE:553:MET:HA	2.02	0.42
2:CF:140:ARG:HH21	2:CF:142:ARG:NH2	2.13	0.42
1:AE:402:ASP:OD1	1:AE:402:ASP:N	2.51	0.42
2:AF:153:ARG:HG2	2:AF:190:LYS:HD2	2.02	0.42
1:AG:381:GLU:O	1:AG:384:GLU:HG2	2.19	0.42
1:AG:568:ARG:NH2	2:DB:287:ARG:HD3	2.34	0.42
1:BC:390:PHE:HA	1:BC:422:LYS:NZ	2.35	0.42
1:BG:395:ARG:O	1:BG:413:GLU:HB2	2.19	0.42
1:BG:396:ALA:HB1	1:BG:412:VAL:HG12	2.00	0.42
1:CC:403:ARG:HB2	1:CC:405:ARG:HE	1.84	0.42
1:CE:339:ALA:HB1	2:CF:127:VAL:HG11	2.01	0.42
2:CH:292:ALA:O	2:CH:296:LEU:HD23	2.19	0.42
2:DD:151:THR:N	2:DD:225:GLU:O	2.34	0.42
1:DG:417:LYS:HB3	1:DG:421:ARG:HH21	1.83	0.42
1:AA:508:MET:HB3	1:AA:508:MET:HE2	1.85	0.42
2:AB:168:PHE:HB3	2:AB:195:PHE:HZ	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AC:465:MET:O	1:AC:469:GLU:HB2	2.20	0.42
2:AD:134:LEU:N	2:AD:137:LYS:O	2.52	0.42
1:AE:380:ASN:ND2	1:AE:398:VAL:H	2.17	0.42
1:AE:586:ARG:HH21	1:AE:587:ARG:HD3	1.84	0.42
2:AF:85:ILE:HG12	2:AF:90:MET:HE3	2.00	0.42
1:AG:435:THR:HG23	2:AH:250:GLU:HB3	2.02	0.42
1:BE:310:LYS:HE3	1:BE:322:VAL:HG21	2.00	0.42
2:BF:156:PRO:HA	2:BF:220:ARG:NH2	2.35	0.42
1:BG:563:GLN:HB3	1:DA:574:MET:HE2	2.02	0.42
1:BG:582:GLU:OE1	1:DA:556:ARG:NH2	2.50	0.42
1:CA:436:THR:HG22	2:CB:253:GLN:HG3	2.02	0.42
1:CC:307:ASP:OD2	1:CC:311:ARG:NH1	2.53	0.42
2:CD:105:ILE:HA	2:CD:112:GLY:HA3	2.02	0.42
2:CD:164:LEU:HD22	2:CD:168:PHE:HE2	1.85	0.42
2:DD:93:LEU:HD11	2:DD:132:MET:HE1	2.02	0.42
2:DD:335:GLN:HA	2:DD:338:LYS:HG2	2.02	0.42
2:DH:315:ASP:OD1	2:DH:316:LEU:N	2.51	0.42
1:AG:551:GLN:O	1:AG:555:LYS:HG3	2.20	0.42
1:BG:346:ALA:HB1	2:BH:120:THR:HG23	2.01	0.42
1:CA:486:TYR:CD2	2:CB:219:PRO:HG2	2.55	0.42
2:CB:133:PRO:HA	2:CB:138:GLN:HA	2.01	0.42
2:CH:73:ARG:HH22	2:CH:176:ARG:NH2	2.17	0.42
2:CH:160:SER:OG	2:CH:163:LEU:HG	2.20	0.42
1:DC:437:THR:O	1:DC:439:ARG:N	2.48	0.42
1:DG:391:GLY:HA3	1:DG:419:ALA:HB1	2.01	0.42
1:DE:313:PHE:CZ	1:DE:333:ILE:HG21	2.55	0.42
2:DF:214:LEU:HD11	2:DF:218:PHE:O	2.20	0.42
1:AA:365:HIS:O	1:AA:448:GLN:NE2	2.52	0.42
1:AA:456:PRO:HG2	1:AA:459:LEU:HB2	2.02	0.42
2:AD:121:LEU:HD23	2:AD:121:LEU:HA	1.90	0.42
1:AE:380:ASN:O	1:AE:384:GLU:HG3	2.19	0.42
2:AF:155:LEU:HB3	2:AF:159:VAL:HG11	2.01	0.42
2:BB:238:GLU:H	2:BB:238:GLU:CD	2.27	0.42
2:BF:167:ALA:HB1	2:BF:213:PHE:CE2	2.55	0.42
2:BF:237:PRO:HG2	2:BF:240:LEU:HB2	2.02	0.42
1:BG:553:MET:HE1	1:BG:556:ARG:HH11	1.85	0.42
2:BH:246:GLN:O	2:BH:250:GLU:HG2	2.20	0.42
2:BH:256:ARG:HG2	2:BH:257:PHE:O	2.19	0.42
2:CD:150:LEU:C	2:CD:227:MET:HE2	2.45	0.42
2:CF:84:ASP:OD1	2:CF:84:ASP:N	2.44	0.42
1:CG:483:GLU:HG2	2:CH:219:PRO:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CH:251:ARG:HH22	2:CH:255:PRO:HD3	1.85	0.42
2:DB:263:PHE:O	2:DB:266:GLU:HG3	2.20	0.42
2:DD:259:GLN:O	2:DD:262:SER:OG	2.28	0.42
2:DH:299:GLU:O	2:DH:300:MET:HE2	2.19	0.42
1:AC:457:GLU:HG2	2:AD:162:GLU:OE1	2.20	0.42
2:AD:89:GLU:O	2:AD:93:LEU:HG	2.19	0.42
1:AG:490:TRP:HB3	2:AH:220:ARG:HH11	1.84	0.42
1:BA:298:GLY:HA3	1:BA:359:ARG:NH1	2.35	0.42
2:BB:78:VAL:HG22	2:BB:141:VAL:HG13	2.02	0.42
2:BB:161:ASN:OD1	2:BB:162:GLU:N	2.53	0.42
2:BB:218:PHE:O	2:BB:220:ARG:N	2.49	0.42
1:BC:381:GLU:HB2	2:BD:238:GLU:OE2	2.20	0.42
2:BD:73:ARG:O	2:BD:119:ARG:NH1	2.53	0.42
1:BE:343:ILE:HD12	2:BF:124:ILE:HG12	2.02	0.42
1:CC:482:PHE:HB2	2:CD:307:HIS:CG	2.54	0.42
2:CD:86:THR:HG22	2:CD:88:GLU:H	1.85	0.42
2:CD:89:GLU:O	2:CD:92:LYS:HG3	2.20	0.42
1:CE:292:ARG:HD2	1:CE:413:GLU:OE1	2.20	0.42
1:CG:339:ALA:O	1:CG:343:ILE:HG13	2.20	0.42
2:DB:192:ILE:HA	2:DB:227:MET:CE	2.50	0.42
1:DC:470:ARG:HH12	2:DD:163:LEU:CD2	2.31	0.42
2:DD:329:LEU:O	2:DD:332:GLN:HG2	2.20	0.42
2:DH:237:PRO:HG2	2:DH:240:LEU:HG	2.00	0.42
1:AA:378:VAL:O	2:AB:236:LEU:HD22	2.20	0.42
1:AA:382:LEU:HD11	2:AB:251:ARG:HH22	1.83	0.42
1:AC:552:GLU:O	1:AC:556:ARG:HD3	2.20	0.42
1:AE:343:ILE:HG22	2:AF:124:ILE:HD13	2.02	0.42
1:AG:395:ARG:HH21	1:AG:413:GLU:CD	2.26	0.42
1:AG:559:MET:HA	1:AG:562:ARG:HG2	2.02	0.42
2:BB:200:ALA:O	2:BB:203:LYS:HG2	2.20	0.42
1:BE:436:THR:HA	2:BF:253:GLN:HE21	1.85	0.42
1:CG:378:VAL:HG11	1:CG:434:LEU:HD13	2.02	0.42
1:CG:424:PHE:HA	1:CG:443:VAL:HG21	2.01	0.42
2:DH:167:ALA:HB1	2:DH:213:PHE:CE2	2.55	0.42
1:DE:417:LYS:HZ1	1:DE:421:ARG:HB2	1.85	0.42
2:DF:109:LYS:HB3	2:DF:111:PHE:CE2	2.55	0.42
1:AA:341:ALA:O	1:AA:345:LYS:HG2	2.20	0.41
1:AG:542:LEU:HB2	2:DH:312:MET:HE1	2.01	0.41
2:AH:251:ARG:HA	2:AH:251:ARG:HD3	1.79	0.41
1:BA:544:ARG:O	1:BA:547:GLU:HG3	2.19	0.41
2:BD:251:ARG:HH12	2:BD:255:PRO:HD3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:BG:582:GLU:CD	1:DA:556:ARG:HH21	2.28	0.41
1:CC:526:HIS:ND1	2:CD:263:PHE:HB2	2.34	0.41
1:DC:431:VAL:HG22	2:DD:272:LYS:HE3	2.01	0.41
2:DD:152:VAL:HG11	2:DD:168:PHE:CZ	2.55	0.41
1:DE:292:ARG:O	1:DE:338:ARG:NH1	2.53	0.41
1:DE:482:PHE:HB2	2:DF:307:HIS:CG	2.55	0.41
1:AE:365:HIS:ND1	1:AE:413:GLU:HB2	2.35	0.41
2:AH:323:LEU:HD22	1:BG:532:ARG:NH2	2.34	0.41
2:BF:239:LYS:HG3	2:BF:240:LEU:HD22	2.02	0.41
2:BF:246:GLN:O	2:BF:250:GLU:HG2	2.20	0.41
1:CC:341:ALA:O	1:CC:345:LYS:HG2	2.19	0.41
1:CC:431:VAL:HG11	2:CD:268:ALA:CB	2.49	0.41
1:CE:475:ARG:HH22	2:CF:217:THR:HA	1.86	0.41
1:CG:401:ASP:OD1	1:CG:405:ARG:N	2.52	0.41
1:DG:464:PRO:HG2	1:DG:465:MET:SD	2.60	0.41
2:DF:305:HIS:O	2:DF:309:VAL:HG23	2.20	0.41
1:AA:432:PHE:C	1:AA:433:LEU:HD12	2.44	0.41
1:AC:425:GLU:O	1:AC:428:SER:N	2.48	0.41
1:BA:452:GLU:HA	2:BB:176:ARG:NH2	2.35	0.41
1:BC:296:PHE:N	1:BC:361:ARG:O	2.43	0.41
1:BC:369:LEU:O	1:BC:411:ILE:HD12	2.19	0.41
1:BG:345:LYS:HE2	1:BG:345:LYS:HB3	1.81	0.41
2:BH:119:ARG:HH22	2:BH:143:PHE:HB3	1.85	0.41
1:CC:296:PHE:HD2	1:CC:361:ARG:HB3	1.84	0.41
1:CC:482:PHE:HB2	2:CD:307:HIS:ND1	2.36	0.41
2:CF:70:PHE:O	2:CF:115:ARG:NH1	2.53	0.41
2:CF:167:ALA:HB1	2:CF:213:PHE:HZ	1.85	0.41
1:DA:427:CYS:HB3	1:DA:443:VAL:HG21	2.02	0.41
2:DB:109:LYS:HE3	2:DB:111:PHE:CZ	2.55	0.41
1:DC:548:LEU:O	1:DC:552:GLU:HG2	2.20	0.41
2:DH:150:LEU:O	2:DH:227:MET:HE3	2.20	0.41
2:DH:246:GLN:O	2:DH:250:GLU:HG2	2.21	0.41
1:DE:292:ARG:HD2	1:DE:395:ARG:HD3	2.02	0.41
1:AA:474:PRO:O	1:AA:475:ARG:HD2	2.20	0.41
1:AA:496:MET:O	1:AA:499:GLN:HG2	2.20	0.41
2:AB:220:ARG:O	2:AB:220:ARG:HG3	2.19	0.41
1:AE:516:GLU:HA	1:AE:519:MET:HE3	2.02	0.41
1:AE:534:ASP:OD2	1:AE:538:ARG:NH1	2.53	0.41
2:AF:183:ASP:OD1	2:AF:184:ARG:N	2.53	0.41
1:AG:378:VAL:HG21	1:AG:434:LEU:HD13	2.02	0.41
2:AH:154:ASN:CG	2:AH:220:ARG:HH21	2.29	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BD:256:ARG:HG2	2:BD:257:PHE:O	2.20	0.41
2:BD:319:ARG:NH2	1:CC:538:ARG:HD2	2.35	0.41
2:BF:300:MET:HE3	2:BF:300:MET:HB2	1.85	0.41
1:BG:548:LEU:O	1:BG:551:GLN:HG2	2.20	0.41
1:BG:583:GLU:OE2	1:BG:583:GLU:HA	2.21	0.41
1:CA:375:SER:HB3	1:CA:378:VAL:HG23	2.01	0.41
1:CA:475:ARG:HG2	1:CA:477:ALA:H	1.84	0.41
2:CB:118:THR:HB	2:CB:121:LEU:HD13	2.02	0.41
2:CF:79:GLY:HA2	2:CF:111:PHE:HB3	2.02	0.41
2:DD:117:GLU:CD	2:DD:118:THR:HG23	2.45	0.41
2:DD:154:ASN:HB3	2:DD:220:ARG:CZ	2.49	0.41
1:AA:474:PRO:HB3	2:AB:215:LEU:HA	2.02	0.41
1:AC:315:LYS:HG3	1:AC:316:TYR:HD1	1.84	0.41
1:AC:519:MET:HE1	2:AD:267:TYR:HE2	1.86	0.41
1:AE:519:MET:HE1	2:AF:267:TYR:OH	2.20	0.41
1:BC:417:LYS:N	1:BC:418:PRO:HD2	2.35	0.41
1:BE:294:ARG:HA	1:BE:333:ILE:O	2.20	0.41
2:BF:287:ARG:NH1	2:BF:290:LYS:HD3	2.35	0.41
1:CC:530:LEU:HD23	1:CC:530:LEU:HA	1.92	0.41
2:CF:218:PHE:CE1	2:CF:300:MET:HE1	2.56	0.41
1:DA:375:SER:HB3	1:DA:378:VAL:HG23	2.02	0.41
1:DA:391:GLY:HA3	1:DA:419:ALA:HB1	2.02	0.41
1:DC:297:VAL:HA	1:DC:360:VAL:HA	2.03	0.41
2:DF:164:LEU:HB3	2:DF:177:ALA:HB1	2.03	0.41
2:DF:206:ASP:OD1	2:DF:207:ARG:N	2.53	0.41
1:AA:395:ARG:HB3	1:AA:413:GLU:OE1	2.20	0.41
2:AH:302:ALA:HB2	1:BG:556:ARG:NH1	2.35	0.41
1:BA:406:SER:OG	2:BB:236:LEU:HD11	2.20	0.41
1:BC:473:PRO:O	1:BC:475:ARG:HD2	2.21	0.41
1:BE:319:PRO:HB3	1:BE:333:ILE:HD11	2.03	0.41
1:CE:541:GLU:O	1:CE:545:MET:HG3	2.21	0.41
1:DE:409:LYS:HE3	1:DE:409:LYS:HB3	1.80	0.41
1:DE:424:PHE:HA	1:DE:443:VAL:HG21	2.02	0.41
2:DF:192:ILE:HG13	2:DF:227:MET:HE3	2.01	0.41
1:AC:562:ARG:O	1:AC:566:GLU:HG2	2.20	0.41
2:BB:169:SER:HA	2:BB:172:GLY:O	2.20	0.41
2:BD:72:GLN:HE22	2:BD:148:ALA:HB3	1.85	0.41
2:BD:215:LEU:HD23	2:BD:215:LEU:H	1.86	0.41
1:CC:568:ARG:NH2	2:CF:287:ARG:HG3	2.35	0.41
1:CE:509:LYS:HE3	1:CE:509:LYS:HB3	1.92	0.41
2:CF:73:ARG:HH22	2:CF:194:GLU:HG2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:CF:156:PRO:HA	2:CF:220:ARG:NH2	2.36	0.41
1:CG:371:VAL:HG13	1:CG:441:VAL:HG13	2.03	0.41
1:CG:448:GLN:O	1:CG:449:LEU:HD23	2.20	0.41
2:CH:78:VAL:HG22	2:CH:141:VAL:HG13	2.02	0.41
1:AA:321:GLU:O	1:AA:333:ILE:HA	2.21	0.41
1:AE:417:LYS:N	1:AE:418:PRO:HD2	2.36	0.41
1:AG:555:LYS:O	1:AG:558:GLU:HG2	2.21	0.41
2:BB:77:PHE:HB2	2:BB:144:ALA:HB2	2.01	0.41
1:BE:361:ARG:HH21	1:BE:453:ASP:HB3	1.85	0.41
2:BF:165:GLU:O	2:BF:169:SER:HB2	2.21	0.41
1:BG:305:THR:HG23	1:BG:308:GLU:H	1.85	0.41
1:BG:448:GLN:OE1	1:BG:448:GLN:N	2.53	0.41
2:BH:183:ASP:OD1	2:BH:184:ARG:N	2.54	0.41
2:CD:126:LYS:O	2:CD:130:ASP:HB2	2.21	0.41
2:CH:82:PRO:HG2	2:CH:135:ARG:HH21	1.86	0.41
2:DH:126:LYS:O	2:DH:130:ASP:HB2	2.21	0.41
1:AA:478:GLN:O	1:AA:481:THR:HG22	2.21	0.41
2:AB:183:ASP:OD1	2:AB:184:ARG:N	2.54	0.41
2:AB:230:LEU:H	2:AB:230:LEU:HD23	1.86	0.41
1:AE:475:ARG:HH22	2:AF:217:THR:HA	1.84	0.41
1:AE:543:ARG:NH1	1:AE:544:ARG:HH12	2.19	0.41
1:AG:382:LEU:HD21	2:AH:251:ARG:HH22	1.86	0.41
1:AG:402:ASP:OD1	1:AG:403:ARG:HG2	2.21	0.41
2:AH:133:PRO:HA	2:AH:138:GLN:HA	2.03	0.41
2:AH:134:LEU:N	2:AH:137:LYS:O	2.51	0.41
1:BA:429:GLU:HG2	1:BA:430:GLY:N	2.35	0.41
1:BA:519:MET:HE1	2:BB:267:TYR:CE2	2.56	0.41
2:BB:166:GLU:O	2:BB:169:SER:OG	2.36	0.41
1:BC:312:LEU:HD23	1:BC:312:LEU:HA	1.97	0.41
1:BC:474:PRO:HB3	2:BD:215:LEU:HA	2.02	0.41
2:BD:152:VAL:HG11	2:BD:168:PHE:CZ	2.56	0.41
1:BE:372:ARG:HB3	1:BE:409:LYS:HG2	2.02	0.41
1:BE:381:GLU:OE1	1:BE:381:GLU:N	2.46	0.41
2:BF:329:LEU:HA	2:BF:332:GLN:HG2	2.03	0.41
2:BH:90:MET:HE3	2:BH:90:MET:HB2	1.96	0.41
2:CB:70:PHE:CE2	2:CB:117:GLU:HA	2.56	0.41
2:CB:237:PRO:HG2	2:CB:240:LEU:HB2	2.03	0.41
1:CC:381:GLU:O	1:CC:384:GLU:HG2	2.21	0.41
1:CE:353:MET:N	1:CE:356:ARG:O	2.52	0.41
1:CE:381:GLU:CD	2:CF:238:GLU:HG3	2.46	0.41
1:CE:470:ARG:CZ	2:CF:163:LEU:HB2	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:560:GLN:NE2	1:CE:561:LEU:HD22	2.35	0.41
2:CF:171:PHE:HA	2:CF:203:LYS:HE3	2.02	0.41
2:CH:68:LYS:HA	2:CH:68:LYS:HD3	1.83	0.41
1:DA:379:SER:OG	1:DA:380:ASN:N	2.52	0.41
2:DB:183:ASP:OD1	2:DB:184:ARG:N	2.53	0.41
1:DC:384:GLU:HB3	1:DC:396:ALA:HB3	2.03	0.41
1:DC:487:SER:HB3	2:DD:212:SER:OG	2.20	0.41
1:DC:490:TRP:HH2	2:DD:293:ARG:HG3	1.86	0.41
2:DD:86:THR:HG23	2:DD:89:GLU:H	1.85	0.41
1:DG:520:GLU:HB3	1:DG:524:HIS:CE1	2.56	0.41
2:DH:70:PHE:O	2:DH:115:ARG:NH1	2.54	0.41
1:DE:418:PRO:O	1:DE:422:LYS:HG2	2.21	0.41
1:AA:382:LEU:HD21	2:AB:251:ARG:NH1	2.36	0.41
1:AC:418:PRO:O	1:AC:422:LYS:HG2	2.21	0.41
1:AC:557:LYS:O	1:AC:561:LEU:HD23	2.21	0.41
2:AD:202:ARG:NH2	2:AD:206:ASP:OD1	2.54	0.41
2:AF:152:VAL:HG11	2:AF:168:PHE:CZ	2.56	0.41
2:AF:206:ASP:OD1	2:AF:207:ARG:N	2.54	0.41
2:AF:232:ASP:OD1	2:AF:232:ASP:N	2.54	0.41
2:AH:132:MET:HE3	2:AH:132:MET:HA	2.03	0.41
2:AH:198:LYS:N	2:AH:199:PRO:HD2	2.36	0.41
2:AH:332:GLN:HG2	2:AH:336:LYS:HE3	2.03	0.41
1:BA:310:LYS:HE3	1:BA:322:VAL:HG21	2.02	0.41
2:BB:212:SER:O	2:BB:212:SER:OG	2.38	0.41
1:BE:384:GLU:HA	1:BE:393:ILE:HD13	2.02	0.41
1:BE:401:ASP:OD1	1:BE:403:ARG:N	2.49	0.41
1:CE:483:GLU:HG2	2:CF:219:PRO:HB3	2.03	0.41
1:CG:514:LYS:HD2	1:CG:514:LYS:O	2.21	0.41
2:DH:334:VAL:O	2:DH:337:ARG:HG2	2.21	0.41
2:DF:307:HIS:HA	2:DF:310:MET:HG3	2.03	0.41
2:AB:73:ARG:HH12	2:AB:176:ARG:NH1	2.19	0.40
1:AC:310:LYS:HE3	1:AC:322:VAL:HG21	2.03	0.40
2:AD:320:GLN:CG	1:BC:535:LEU:HD11	2.51	0.40
2:AF:330:HIS:O	2:AF:333:GLU:HG3	2.20	0.40
1:AG:573:GLU:OE2	1:AG:577:ARG:NH2	2.54	0.40
2:AH:109:LYS:HE3	2:AH:111:PHE:CZ	2.55	0.40
1:BA:424:PHE:HA	1:BA:443:VAL:HG11	2.02	0.40
1:BC:418:PRO:O	1:BC:421:ARG:HG2	2.21	0.40
2:BD:302:ALA:HB2	1:CC:556:ARG:HH12	1.86	0.40
1:BG:369:LEU:HD12	1:BG:369:LEU:HA	1.92	0.40
1:CC:486:TYR:HE1	1:CC:489:ARG:HH11	1.69	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:CE:540:GLU:HA	1:CE:543:ARG:NH1	2.36	0.40
1:CG:310:LYS:HE3	1:CG:322:VAL:HG21	2.03	0.40
2:DB:200:ALA:HA	2:DB:203:LYS:HG2	2.03	0.40
2:DB:253:GLN:HA	2:DB:254:PRO:HD3	1.96	0.40
1:DC:533:GLN:O	1:DC:536:MET:HG3	2.21	0.40
1:DG:429:GLU:HG2	1:DG:430:GLY:N	2.36	0.40
1:AC:418:PRO:HA	1:AC:421:ARG:HG2	2.04	0.40
1:AE:319:PRO:HB3	1:AE:333:ILE:HD11	2.03	0.40
2:BD:325:ARG:O	2:BD:328:GLU:HG3	2.20	0.40
1:BE:291:GLN:H	1:BE:394:GLU:CD	2.29	0.40
1:BE:333:ILE:HD12	1:BE:333:ILE:HA	1.92	0.40
2:DB:161:ASN:OD1	2:DB:162:GLU:N	2.54	0.40
1:DC:288:THR:HG22	1:DC:289:TYR:CD2	2.56	0.40
1:DC:293:CYS:HB3	1:DC:335:LEU:N	2.33	0.40
1:DE:437:THR:OG1	2:DF:250:GLU:OE1	2.32	0.40
1:DE:475:ARG:NH1	2:DF:214:LEU:HB3	2.36	0.40
1:AC:418:PRO:O	1:AC:421:ARG:HG2	2.21	0.40
1:AE:390:PHE:CE1	1:AE:426:ARG:HG2	2.56	0.40
1:AG:296:PHE:HD2	1:AG:361:ARG:HB3	1.86	0.40
1:AG:545:MET:HE1	2:DH:309:VAL:CG2	2.51	0.40
2:AH:79:GLY:HA2	2:AH:111:PHE:HB3	2.03	0.40
2:AH:184:ARG:NH1	2:AH:186:ARG:HE	2.19	0.40
2:AH:218:PHE:CE1	2:AH:300:MET:HE1	2.57	0.40
2:BB:203:LYS:HB2	2:BB:207:ARG:NH2	2.36	0.40
2:BF:311:LEU:HD23	2:BF:311:LEU:HA	1.86	0.40
1:BG:526:HIS:ND1	2:BH:263:PHE:HB2	2.36	0.40
2:BH:148:ALA:HB1	2:BH:201:ALA:HB2	2.03	0.40
2:CD:150:LEU:O	2:CD:227:MET:HE2	2.22	0.40
2:CH:171:PHE:HB2	2:CH:195:PHE:HZ	1.86	0.40
2:CH:237:PRO:HG2	2:CH:240:LEU:HG	2.04	0.40
1:DA:509:LYS:HB2	1:DA:509:LYS:HE3	1.91	0.40
1:DC:295:LEU:HD13	1:DC:360:VAL:HG11	2.02	0.40
1:DC:463:ASN:O	1:DC:467:GLN:NE2	2.55	0.40
1:DE:348:LEU:O	1:DE:351:THR:OG1	2.35	0.40
1:AA:384:GLU:OE1	1:AA:393:ILE:HB	2.21	0.40
1:AC:421:ARG:O	1:AC:425:GLU:HG2	2.21	0.40
2:AD:177:ALA:HB1	2:AD:193:VAL:HG12	2.03	0.40
1:AG:513:ASP:OD1	1:AG:513:ASP:C	2.64	0.40
1:AG:545:MET:HA	1:AG:548:LEU:HG	2.03	0.40
1:BA:463:ASN:OD1	1:BA:465:MET:HG2	2.21	0.40
2:BD:74:SER:HA	2:BD:119:ARG:HH11	1.86	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:BD:140:ARG:HB3	2:BD:140:ARG:CZ	2.52	0.40
2:BD:246:GLN:O	2:BD:250:GLU:HG2	2.22	0.40
1:BE:380:ASN:O	1:BE:384:GLU:HG3	2.20	0.40
2:BF:177:ALA:HB1	2:BF:193:VAL:HG22	2.03	0.40
1:BG:448:GLN:O	1:BG:449:LEU:HD23	2.21	0.40
2:BH:178:VAL:HG12	2:BH:192:ILE:HB	2.03	0.40
1:CC:381:GLU:OE1	1:CC:381:GLU:N	2.55	0.40
1:CE:538:ARG:HG2	2:DF:316:LEU:HD21	2.02	0.40
2:CF:212:SER:O	2:CF:212:SER:OG	2.38	0.40
2:CF:334:VAL:HG23	2:CF:335:GLN:HE21	1.85	0.40
2:DD:81:LEU:O	2:DD:137:LYS:NZ	2.37	0.40
2:DF:310:MET:SD	2:DF:311:LEU:N	2.95	0.40
1:AA:345:LYS:HE3	1:AA:360:VAL:C	2.46	0.40
2:AD:294:GLU:O	2:AD:298:MET:HG2	2.20	0.40
1:BA:454:GLY:HA2	2:BB:178:VAL:HG13	2.03	0.40
2:BB:73:ARG:HG3	2:BB:146:HIS:NE2	2.37	0.40
1:BC:470:ARG:CZ	1:BC:470:ARG:HB3	2.51	0.40
2:BD:275:ILE:HD13	2:BD:275:ILE:HA	1.92	0.40
2:BH:244:ASN:HD21	2:BH:246:GLN:HB2	1.86	0.40
2:CD:192:ILE:HA	2:CD:227:MET:HE1	2.04	0.40
2:CD:230:LEU:H	2:CD:230:LEU:HD23	1.85	0.40
1:CE:439:ARG:HE	1:CE:439:ARG:HB3	1.76	0.40
1:CE:476:PHE:CE1	2:CF:213:PHE:HD1	2.39	0.40
1:CG:532:ARG:O	1:CG:536:MET:HG2	2.21	0.40
2:CH:244:ASN:ND2	2:CH:246:GLN:HB2	2.36	0.40
1:DA:291:GLN:HA	1:DA:334:LYS:HE2	2.04	0.40
2:DD:183:ASP:OD1	2:DD:184:ARG:N	2.54	0.40
2:DF:334:VAL:HA	2:DF:337:ARG:HG3	2.03	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	AA	306/703 (44%)	300 (98%)	6 (2%)	0	100	100
1	AC	302/703 (43%)	295 (98%)	7 (2%)	0	100	100
1	AE	306/703 (44%)	300 (98%)	6 (2%)	0	100	100
1	AG	306/703 (44%)	297 (97%)	9 (3%)	0	100	100
1	BA	306/703 (44%)	300 (98%)	6 (2%)	0	100	100
1	BC	306/703 (44%)	297 (97%)	9 (3%)	0	100	100
1	BE	306/703 (44%)	298 (97%)	8 (3%)	0	100	100
1	BG	306/703 (44%)	294 (96%)	12 (4%)	0	100	100
1	CA	273/703 (39%)	268 (98%)	5 (2%)	0	100	100
1	CC	306/703 (44%)	302 (99%)	4 (1%)	0	100	100
1	CE	306/703 (44%)	296 (97%)	10 (3%)	0	100	100
1	CG	306/703 (44%)	301 (98%)	5 (2%)	0	100	100
1	DA	306/703 (44%)	300 (98%)	6 (2%)	0	100	100
1	DC	274/703 (39%)	270 (98%)	4 (2%)	0	100	100
1	DE	234/703 (33%)	229 (98%)	5 (2%)	0	100	100
1	DG	237/703 (34%)	231 (98%)	6 (2%)	0	100	100
2	AB	271/472 (57%)	264 (97%)	7 (3%)	0	100	100
2	AD	271/472 (57%)	266 (98%)	5 (2%)	0	100	100
2	AF	271/472 (57%)	265 (98%)	6 (2%)	0	100	100
2	AH	271/472 (57%)	268 (99%)	3 (1%)	0	100	100
2	BB	271/472 (57%)	263 (97%)	8 (3%)	0	100	100
2	BD	271/472 (57%)	265 (98%)	6 (2%)	0	100	100
2	BF	271/472 (57%)	260 (96%)	11 (4%)	0	100	100
2	BH	271/472 (57%)	267 (98%)	4 (2%)	0	100	100
2	CB	271/472 (57%)	266 (98%)	5 (2%)	0	100	100
2	CD	241/472 (51%)	236 (98%)	5 (2%)	0	100	100
2	CF	271/472 (57%)	267 (98%)	4 (2%)	0	100	100
2	CH	271/472 (57%)	260 (96%)	11 (4%)	0	100	100
2	DB	242/472 (51%)	237 (98%)	5 (2%)	0	100	100
2	DD	271/472 (57%)	268 (99%)	3 (1%)	0	100	100
2	DF	271/472 (57%)	266 (98%)	5 (2%)	0	100	100
2	DH	271/472 (57%)	266 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	8963/18800 (48%)	8762 (98%)	201 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	AA	273/557 (49%)	273 (100%)	0	100	100
1	AC	269/557 (48%)	269 (100%)	0	100	100
1	AE	273/557 (49%)	273 (100%)	0	100	100
1	AG	273/557 (49%)	273 (100%)	0	100	100
1	BA	273/557 (49%)	273 (100%)	0	100	100
1	BC	273/557 (49%)	273 (100%)	0	100	100
1	BE	273/557 (49%)	273 (100%)	0	100	100
1	BG	273/557 (49%)	273 (100%)	0	100	100
1	CA	240/557 (43%)	240 (100%)	0	100	100
1	CC	273/557 (49%)	273 (100%)	0	100	100
1	CE	273/557 (49%)	273 (100%)	0	100	100
1	CG	273/557 (49%)	273 (100%)	0	100	100
1	DA	273/557 (49%)	273 (100%)	0	100	100
1	DC	241/557 (43%)	241 (100%)	0	100	100
1	DE	202/557 (36%)	202 (100%)	0	100	100
1	DG	205/557 (37%)	205 (100%)	0	100	100
2	AB	243/406 (60%)	243 (100%)	0	100	100
2	AD	243/406 (60%)	243 (100%)	0	100	100
2	AF	243/406 (60%)	243 (100%)	0	100	100
2	AH	243/406 (60%)	243 (100%)	0	100	100
2	BB	243/406 (60%)	243 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	BD	243/406 (60%)	242 (100%)	1 (0%)	84	83
2	BF	243/406 (60%)	243 (100%)	0	100	100
2	BH	243/406 (60%)	242 (100%)	1 (0%)	84	83
2	CB	243/406 (60%)	243 (100%)	0	100	100
2	CD	213/406 (52%)	213 (100%)	0	100	100
2	CF	243/406 (60%)	243 (100%)	0	100	100
2	CH	243/406 (60%)	242 (100%)	1 (0%)	84	83
2	DB	214/406 (53%)	214 (100%)	0	100	100
2	DD	243/406 (60%)	243 (100%)	0	100	100
2	DF	243/406 (60%)	243 (100%)	0	100	100
2	DH	243/406 (60%)	242 (100%)	1 (0%)	84	83
All	All	7989/15408 (52%)	7985 (100%)	4 (0%)	87	89

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	BD	253	GLN
2	BH	244	ASN
2	CH	244	ASN
2	DH	244	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	AC	533	GLN
2	AD	339	GLN
1	AE	524	HIS
2	AF	332	GLN
2	BD	253	GLN
2	CB	131	ASN
2	CB	320	GLN
2	DB	307	HIS
1	DC	365	HIS
1	DE	463	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

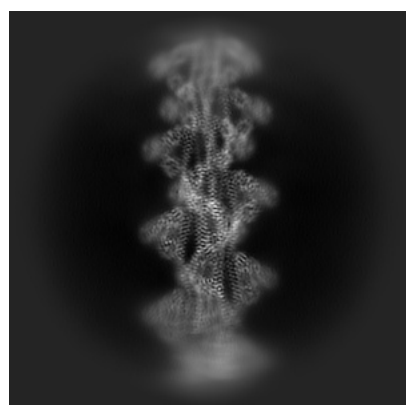
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51471. These allow visual inspection of the internal detail of the map and identification of artifacts.

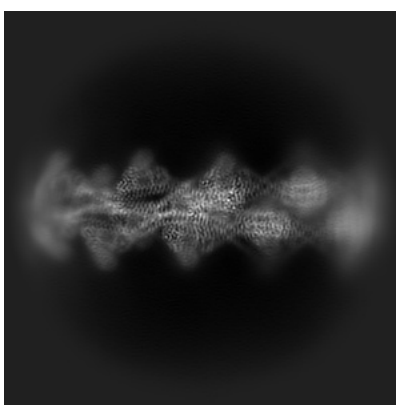
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

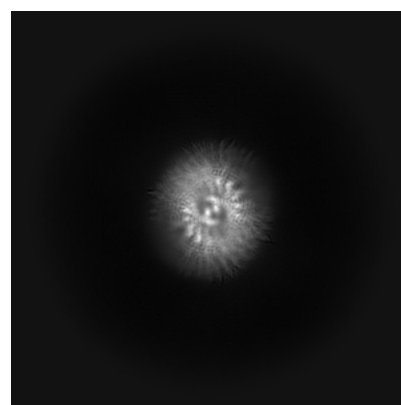
#### 6.1.1 Primary map



X



Y

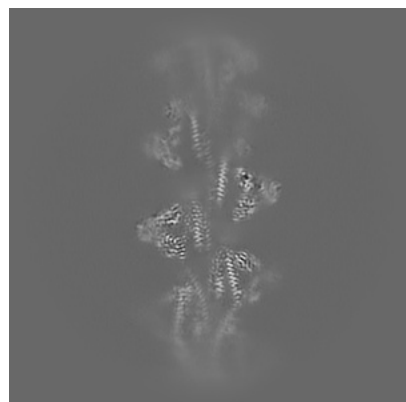


Z

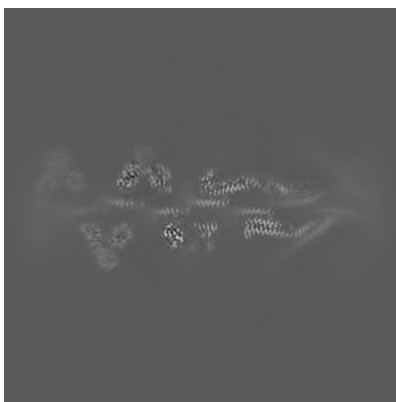
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

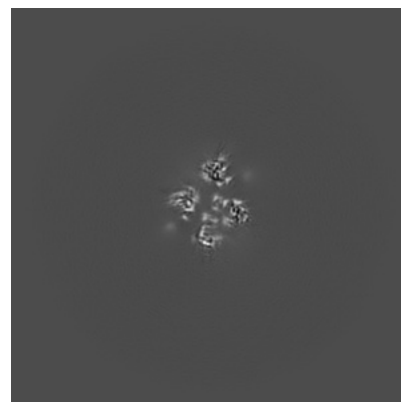
#### 6.2.1 Primary map



X Index: 256



Y Index: 256

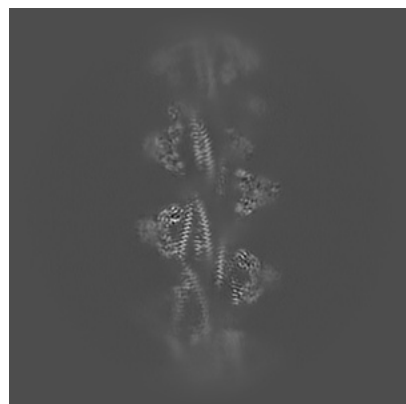


Z Index: 256

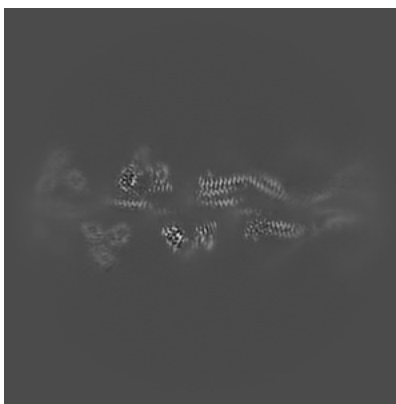
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

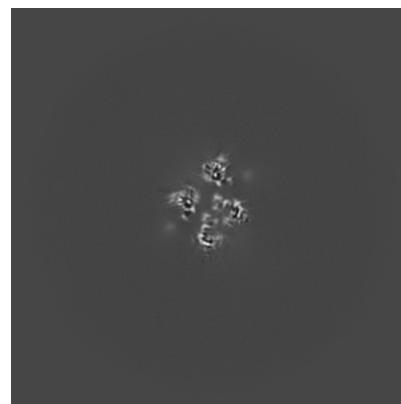
### 6.3.1 Primary map



X Index: 251



Y Index: 260

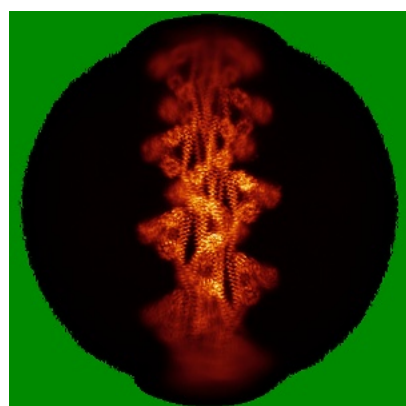


Z Index: 255

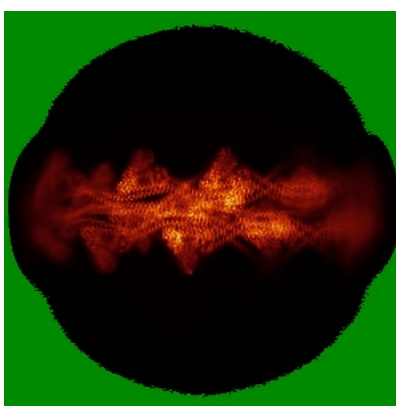
The images above show the largest variance slices of the map in three orthogonal directions.

## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

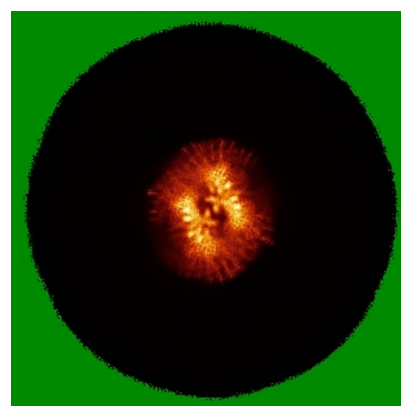
### 6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

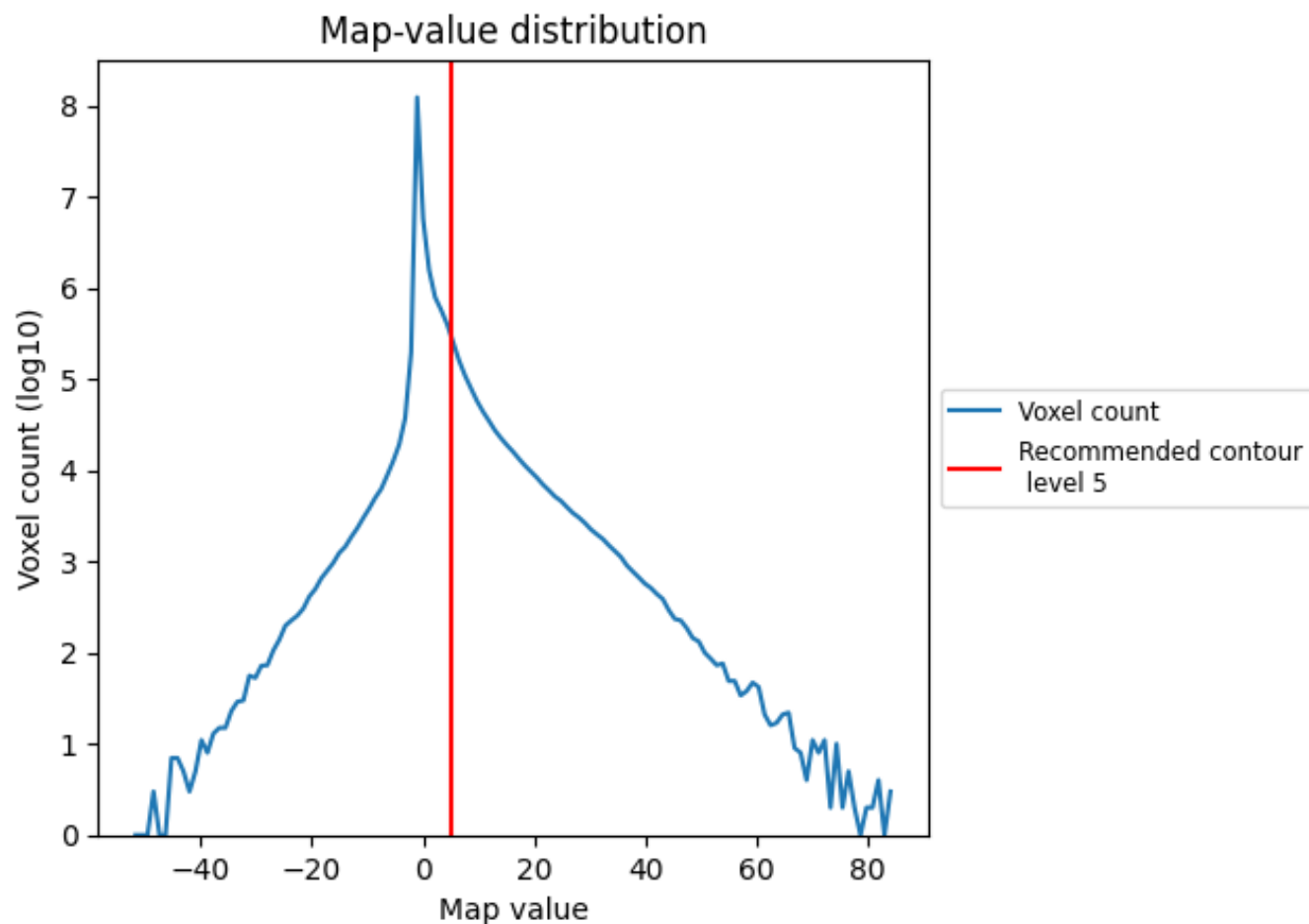
## 6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

## 7 Map analysis [i](#)

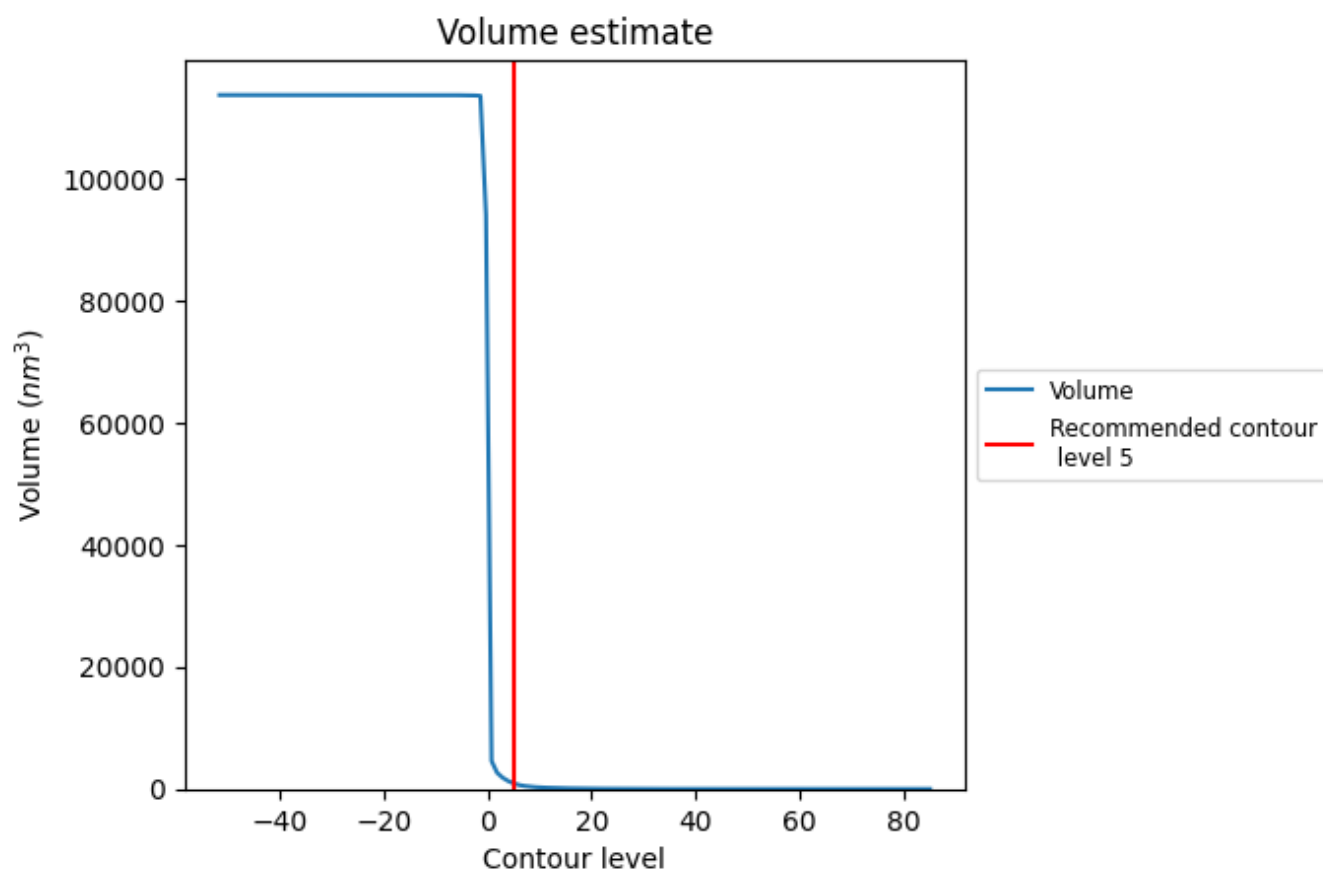
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

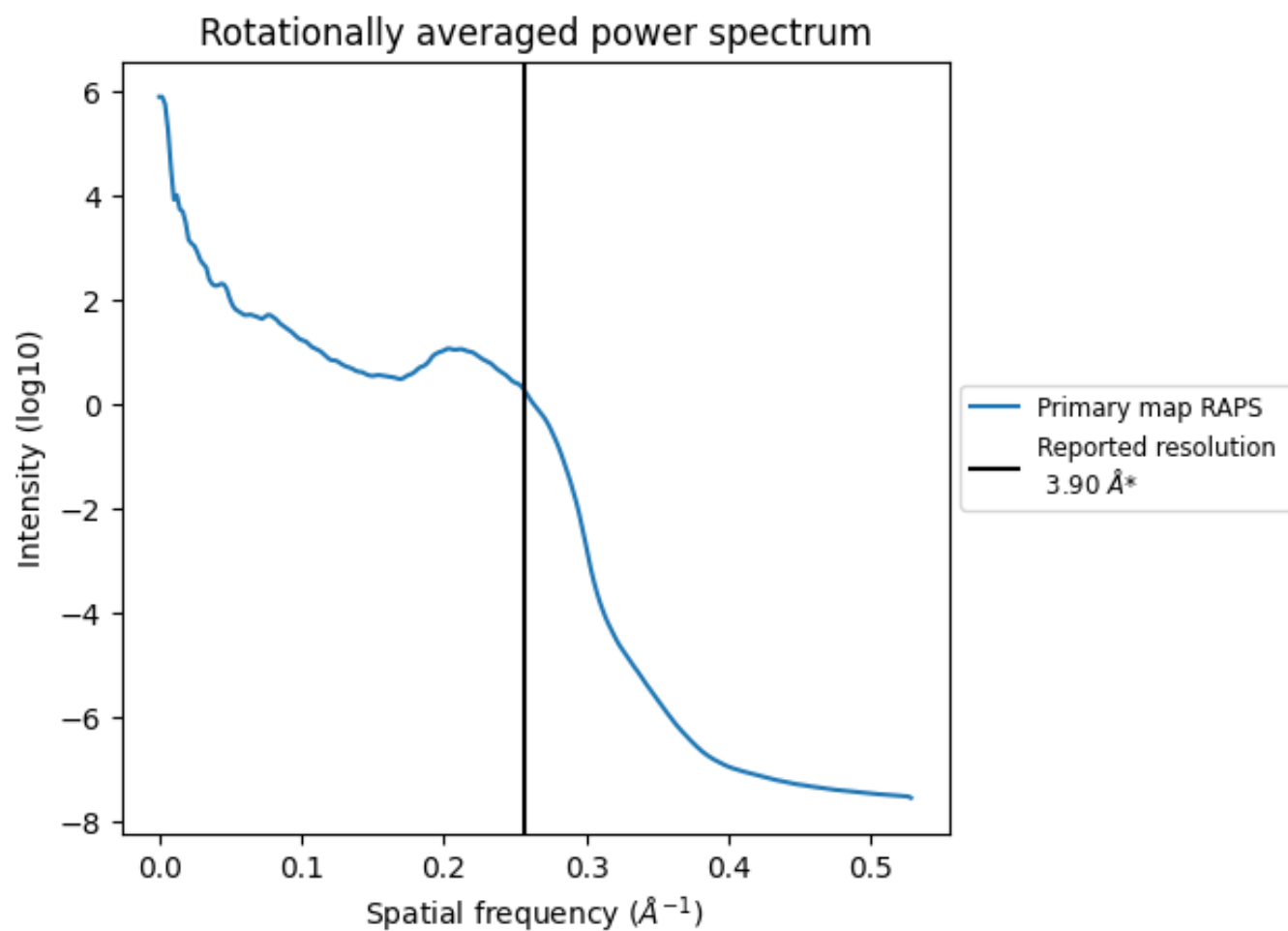
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 899 nm<sup>3</sup>; this corresponds to an approximate mass of 812 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

### 7.3 Rotationally averaged power spectrum ⓘ



\*Reported resolution corresponds to spatial frequency of 0.256 Å<sup>-1</sup>



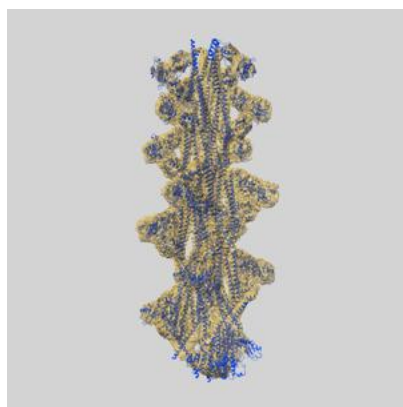
## 8 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

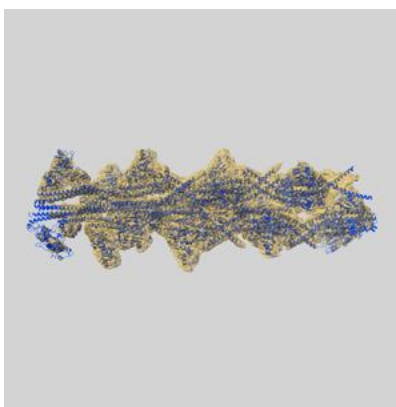
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51471 and PDB model 9GNI. Per-residue inclusion information can be found in section [3](#) on page [7](#).

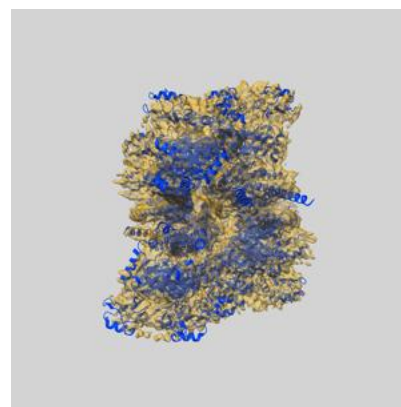
### 9.1 Map-model overlay [i](#)



X



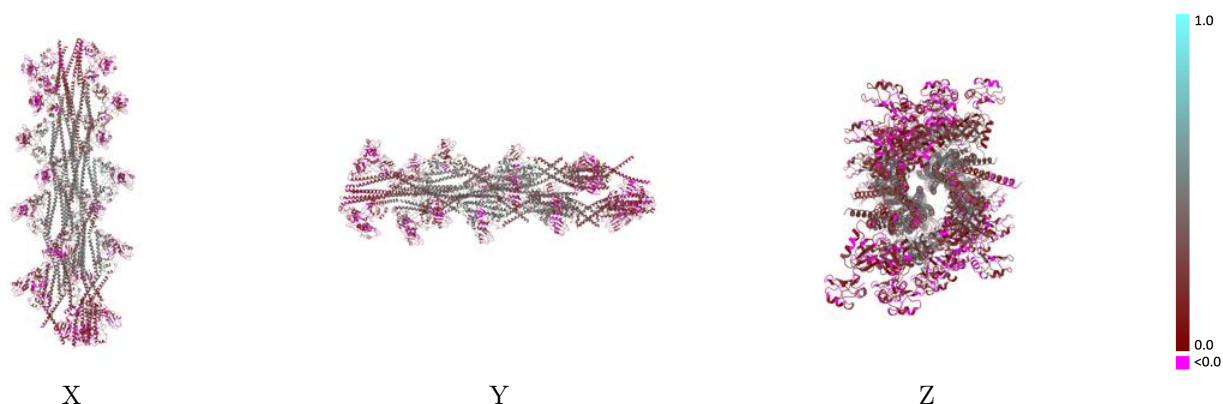
Y



Z

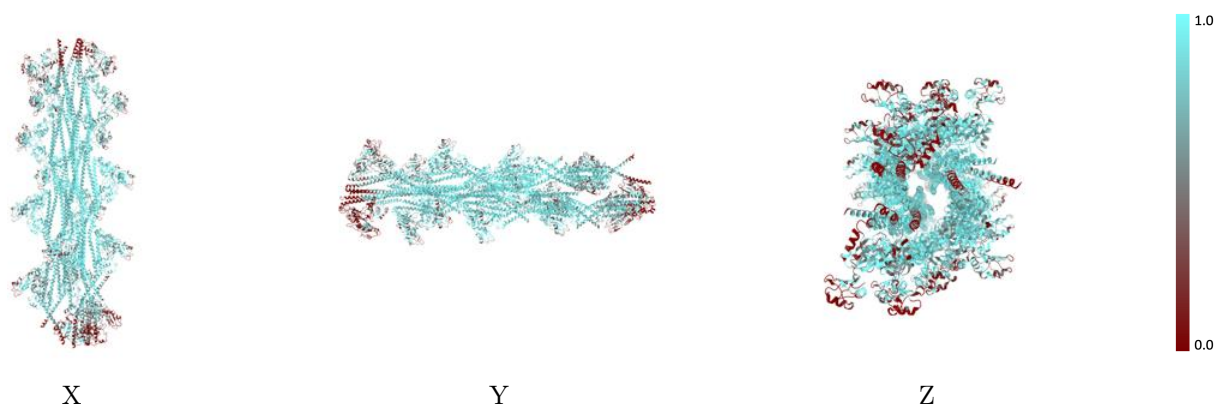
The images above show the 3D surface view of the map at the recommended contour level 5.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

## 9.2 Q-score mapped to coordinate model [i](#)



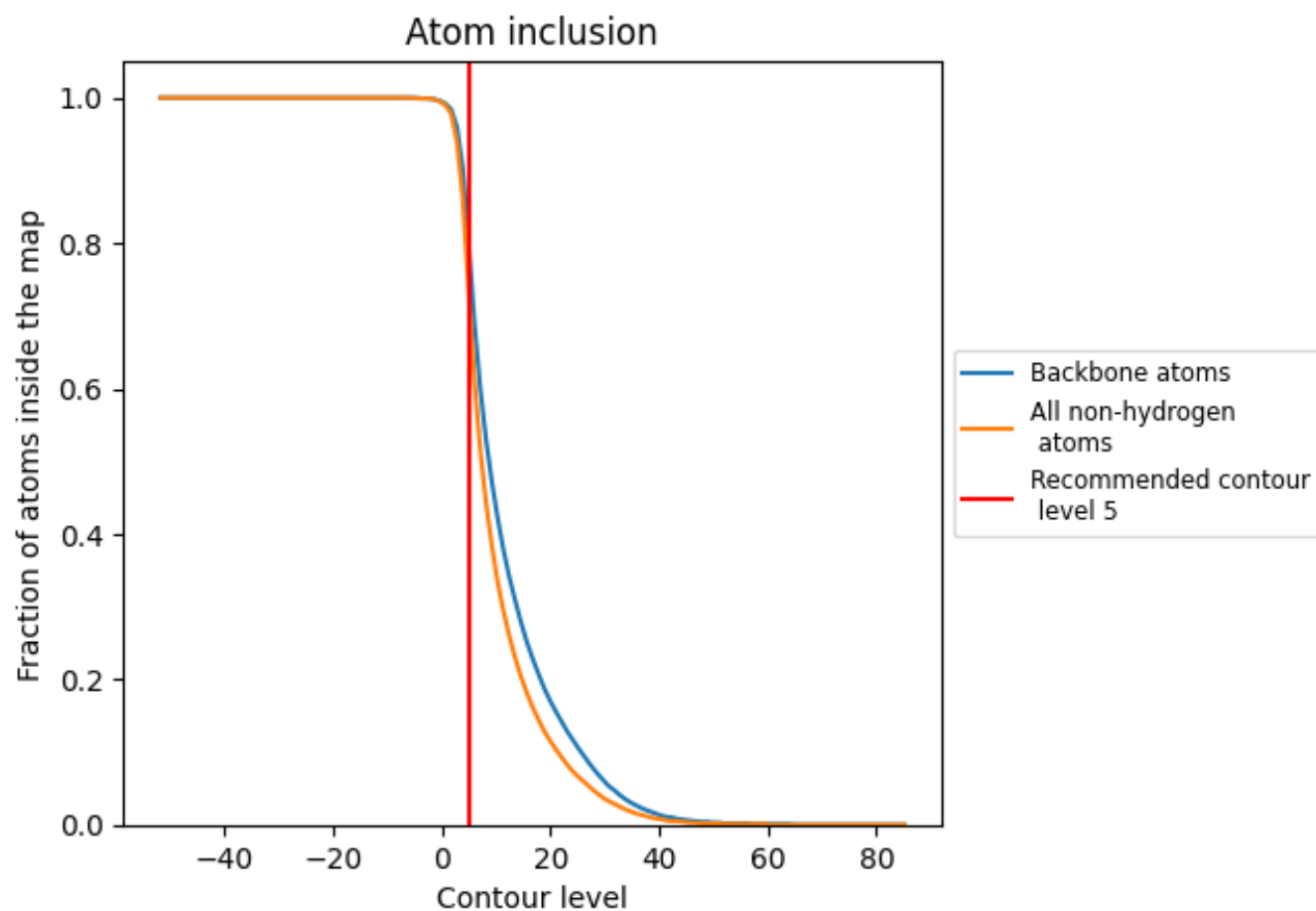
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

## 9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (5).



































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 80% of all backbone atoms, 73% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary

The table lists the average atom inclusion at the recommended contour level (5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7330	 0.2560
AA	 0.8540	 0.3370
AB	 0.8020	 0.3120
AC	 0.8610	 0.3170
AD	 0.8920	 0.3490
AE	 0.7600	 0.2560
AF	 0.6970	 0.2230
AG	 0.7340	 0.2710
AH	 0.8550	 0.3320
BA	 0.8620	 0.3240
BB	 0.8870	 0.3340
BC	 0.8490	 0.3390
BD	 0.8270	 0.3380
BE	 0.8890	 0.3660
BF	 0.8860	 0.3630
BG	 0.8840	 0.3350
BH	 0.9210	 0.3860
CA	 0.6580	 0.1700
CB	 0.7230	 0.2190
CC	 0.6340	 0.1850
CD	 0.5030	 0.1360
CE	 0.7270	 0.2620
CF	 0.8450	 0.3280
CG	 0.8080	 0.2670
CH	 0.7570	 0.2360
DA	 0.5990	 0.1850
DB	 0.4670	 0.1260
DC	 0.6580	 0.1500
DD	 0.7500	 0.2100
DE	 0.2690	 0.1010
DF	 0.3480	 0.0940
DG	 0.4390	 0.0860
DH	 0.5500	 0.1230

