



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 03:43 PM UTC

PDB ID : 9ED4 / pdb_00009ed4
EMDB ID : EMD-47932
Title : A composite map of mTORC1-Rag-Ragulator-4EBP1 on membrane
Authors : Cui, Z.; Hurley, J.
Deposited on : 2024-11-15
Resolution : 3.23 Å(reported)

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

We welcome your comments at 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>.

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

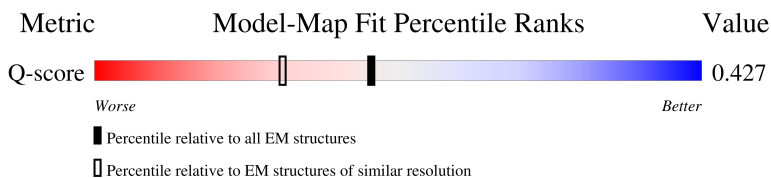
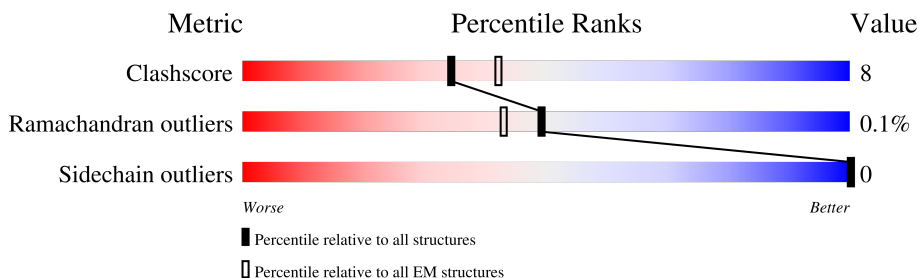
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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 3.23 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.





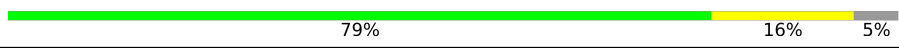



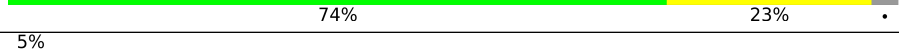
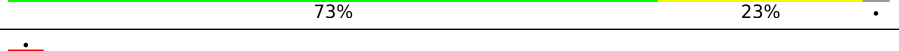
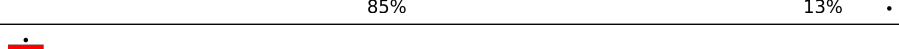
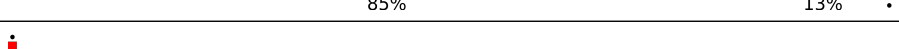
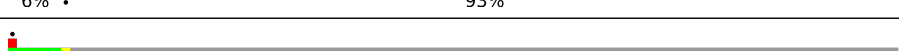
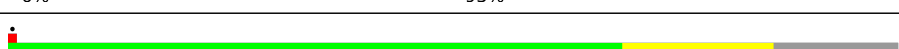


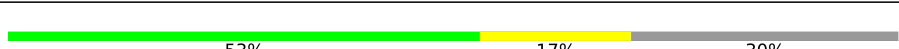





Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	14612 (2.73 - 3.73)

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 ≥ 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	B	326	
1	M	326	
2	L	184	
2	N	184	

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Mol	Chain	Length	Quality of chain
3	A	2549	
3	O	2549	
4	D	313	
4	P	313	
5	G	125	
5	Q	125	
6	H	124	
6	R	124	
7	J	91	
7	S	91	
8	K	118	
8	T	118	
9	C	1335	
9	U	1335	
10	E	399	
10	V	399	
11	F	161	
11	W	161	
12	I	99	
12	X	99	

2 Entry composition

There are 18 unique types of molecules in this entry. The entry contains 161433 atoms, of which 80663 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 Target of rapamycin complex subunit LST8.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	B	317	Total	C	H	N	O	S	0	0
			4797	1526	2341	436	476	18		
1	M	317	Total	C	H	N	O	S	0	0
			4797	1526	2341	436	476	18		

- Molecule 2 is a protein called GTP-binding protein Rheb.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	L	170	Total	C	H	N	O	S	0	0
			2698	860	1355	219	260	4		
2	N	170	Total	C	H	N	O	S	0	0
			2698	860	1355	219	260	4		

- Molecule 3 is a protein called Serine/threonine-protein kinase mTOR.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	A	2305	Total	C	H	N	O	S	0	0
			37222	11782	18711	3247	3357	125		
3	O	2305	Total	C	H	N	O	S	0	0
			37222	11782	18711	3247	3357	125		

- Molecule 4 is a protein called Ras-related GTP-binding protein A.

Mol	Chain	Residues	Atoms						AltConf	Trace
4	D	298	Total	C	H	N	O	S	0	0
			4882	1553	2438	427	447	17		
4	P	298	Total	C	H	N	O	S	0	0
			4882	1553	2438	427	447	17		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	66	LEU	GLN	conflict	UNP Q7L523

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Chain	Residue	Modelled	Actual	Comment	Reference
P	66	LEU	GLN	conflict	UNP Q7L523

- Molecule 5 is a protein called Regulator complex protein LAMTOR2.

Mol	Chain	Residues	Atoms						AltConf	Trace
5	G	124	Total	C	H	N	O	S	0	0
			1888	590	950	161	180	7		
5	Q	124	Total	C	H	N	O	S	0	0
			1888	590	950	161	180	7		

- Molecule 6 is a protein called Regulator complex protein LAMTOR3.

Mol	Chain	Residues	Atoms						AltConf	Trace
6	H	120	Total	C	H	N	O	S	0	0
			1892	601	958	157	175	1		
6	R	120	Total	C	H	N	O	S	0	0
			1892	601	958	157	175	1		

- Molecule 7 is a protein called Regulator complex protein LAMTOR5.

Mol	Chain	Residues	Atoms						AltConf	Trace
7	J	89	Total	C	H	N	O	S	0	0
			1311	400	656	113	135	7		
7	S	89	Total	C	H	N	O	S	0	0
			1311	400	656	113	135	7		

- Molecule 8 is a protein called Eukaryotic translation initiation factor 4E-binding protein 1.

Mol	Chain	Residues	Atoms						AltConf	Trace
8	K	8	Total	C	H	N	O	S	0	0
			126	42	57	9	17	1		
8	T	8	Total	C	H	N	O	S	0	0
			126	42	57	9	17	1		

- Molecule 9 is a protein called Regulatory-associated protein of mTOR.

Mol	Chain	Residues	Atoms						AltConf	Trace
9	C	1142	Total	C	H	N	O	S	0	0
			18164	5804	9067	1581	1651	61		
9	U	1142	Total	C	H	N	O	S	0	0
			18165	5804	9068	1581	1651	61		

- Molecule 10 is a protein called Ras-related GTP-binding protein C.

Mol	Chain	Residues	Atoms						AltConf	Trace
10	E	281	Total	C	H	N	O	S	0	0
			4523	1459	2258	370	424	12		
10	V	281	Total	C	H	N	O	S	0	0
			4523	1459	2258	370	424	12		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	75	ASN	SER	engineered mutation	UNP Q9HB90
V	75	ASN	SER	engineered mutation	UNP Q9HB90

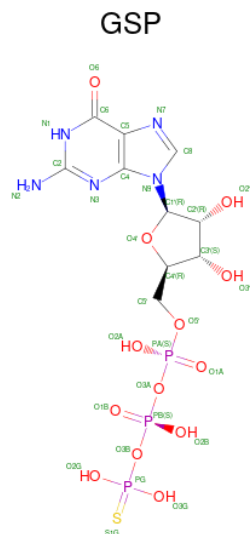
- Molecule 11 is a protein called Ragulator complex protein LAMTOR1.

Mol	Chain	Residues	Atoms						AltConf	Trace
11	F	111	Total	C	H	N	O	S	0	0
			1738	547	870	150	170	1		
11	W	111	Total	C	H	N	O	S	0	0
			1738	547	870	150	170	1		

- Molecule 12 is a protein called Ragulator complex protein LAMTOR4.

Mol	Chain	Residues	Atoms						AltConf	Trace
12	I	84	Total	C	H	N	O	S	0	0
			1294	404	652	115	122	1		
12	X	84	Total	C	H	N	O	S	0	0
			1294	404	652	115	122	1		

- Molecule 13 is 5'-GUANOSINE-DIPHOSPHATE-MONOTHIOPHOSPHATE (CCD ID: GSP) (formula: C₁₀H₁₆N₅O₁₃P₃S).

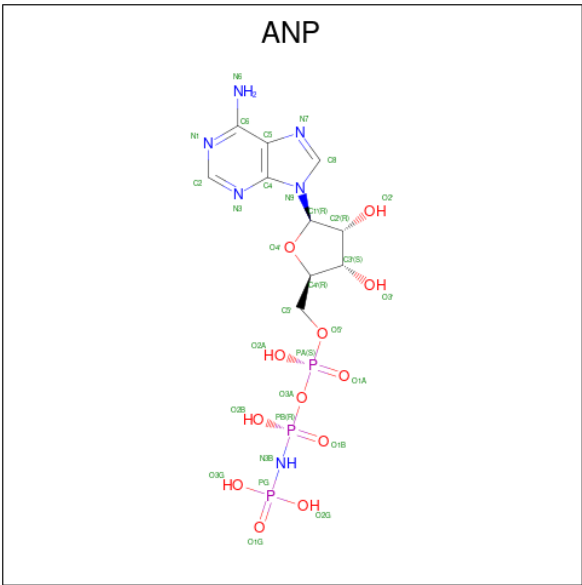


Mol	Chain	Residues	Atoms					AltConf	
13	L	1	Total 32	C 10	N 5	O 13	P 3	S 1	0
13	N	1	Total 32	C 10	N 5	O 13	P 3	S 1	0

- Molecule 14 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

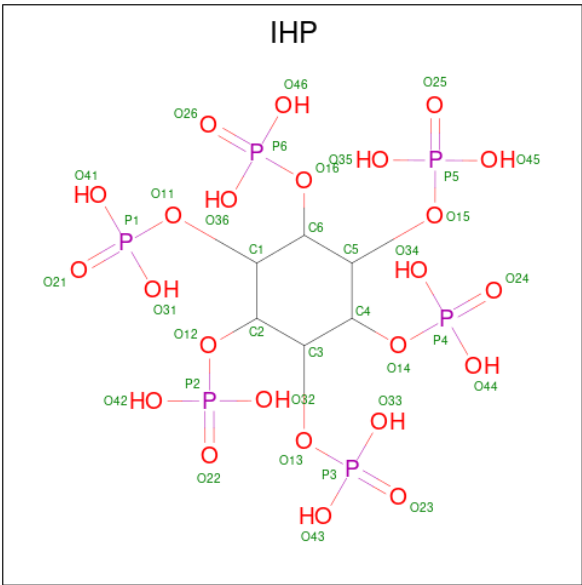
Mol	Chain	Residues	Atoms	AltConf
14	L	1	Total Mg 1 1	0
14	A	2	Total Mg 2 2	0
14	D	1	Total Mg 1 1	0
14	N	1	Total Mg 1 1	0
14	O	2	Total Mg 2 2	0
14	P	1	Total Mg 1 1	0

- Molecule 15 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: $\text{C}_{10}\text{H}_{17}\text{N}_6\text{O}_{12}\text{P}_3$).



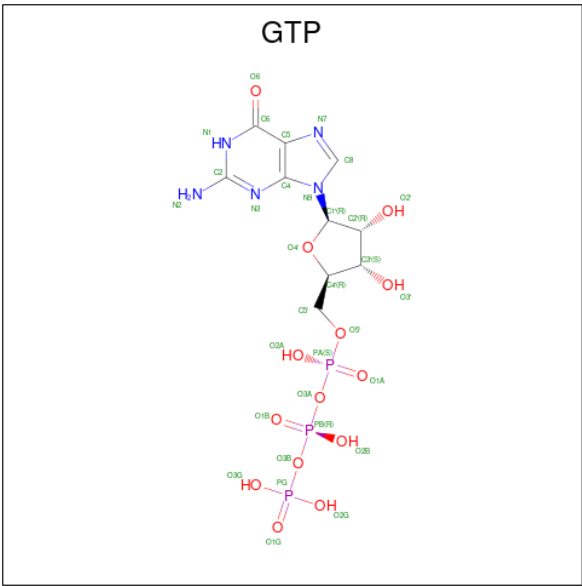
Mol	Chain	Residues	Atoms							AltConf
15	A	1	Total	C	H	N	O	P	0	
			43	10	12	6	12	3		
15	O	1	Total	C	H	N	O	P	0	
			43	10	12	6	12	3		

- Molecule 16 is INOSITOL HEXAKISPHOSPHATE (CCD ID: IHP) (formula: $C_6H_{18}O_{24}P_6$).



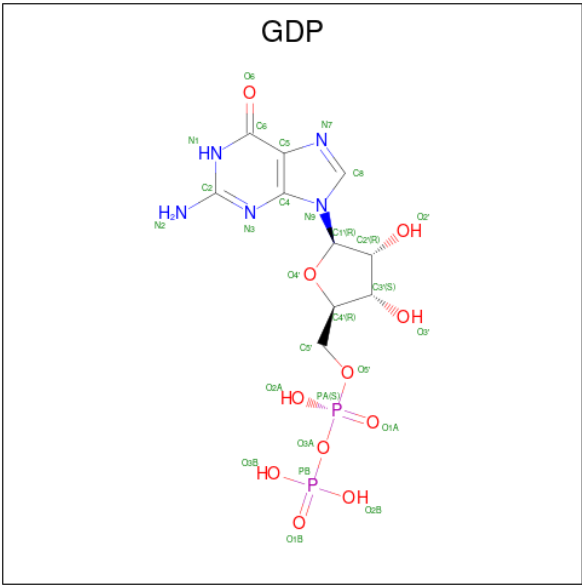
Mol	Chain	Residues	Atoms					AltConf
16	A	1	Total	C	H	O	P	0
			42	6	6	24	6	
16	O	1	Total	C	H	O	P	0
			42	6	6	24	6	

- Molecule 17 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: C₁₀H₁₆N₅O₁₄P₃).



Mol	Chain	Residues	Atoms					AltConf
17	D	1	Total	C	N	O	P	0
			32	10	5	14	3	
17	P	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 18 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C₁₀H₁₅N₅O₁₁P₂).



Mol	Chain	Residues	Atoms					AltConf
18	E	1	Total	C	N	O	P	0
			28	10	5	11	2	

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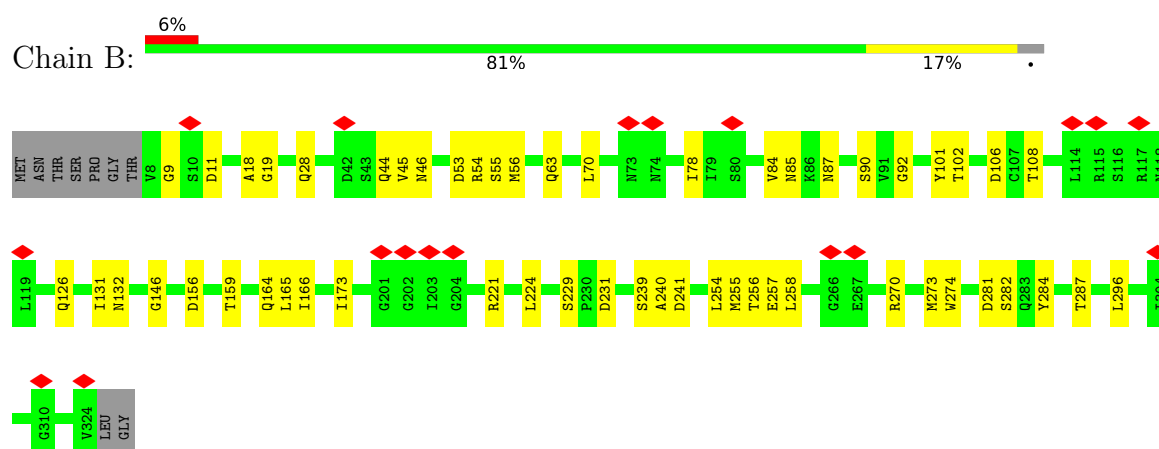
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Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
18	V	1	28	10	5	11	2	0

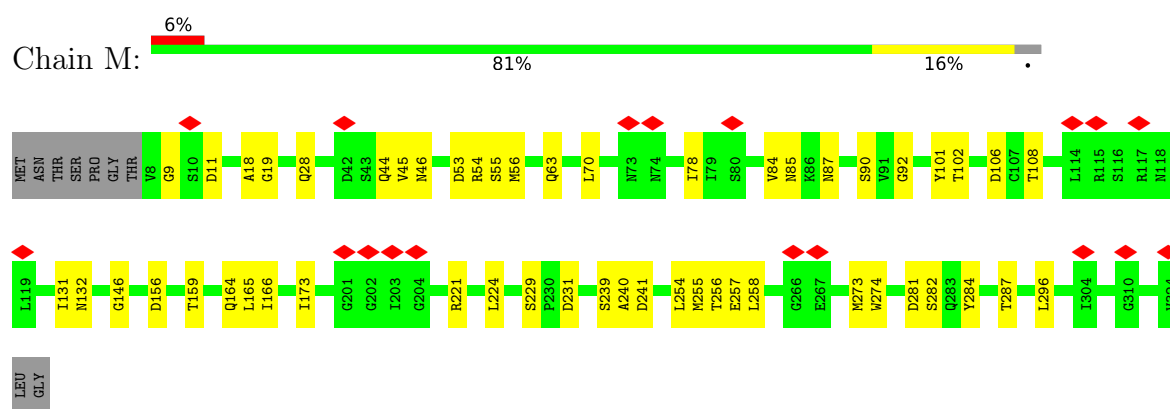
3 Residue-property plots [i](#)

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.

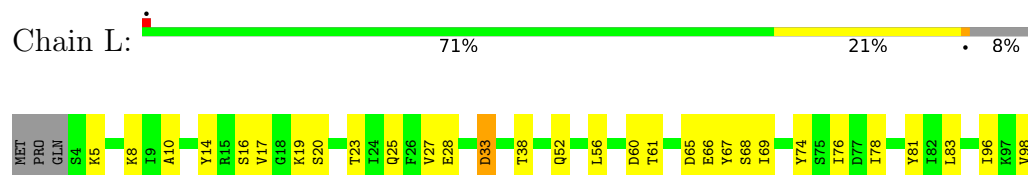
- Molecule 1: Target of rapamycin complex subunit LST8



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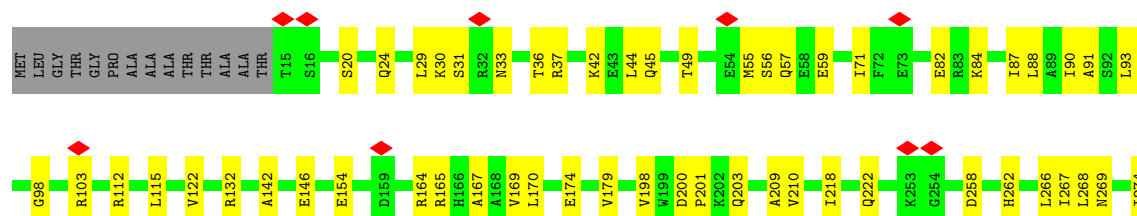


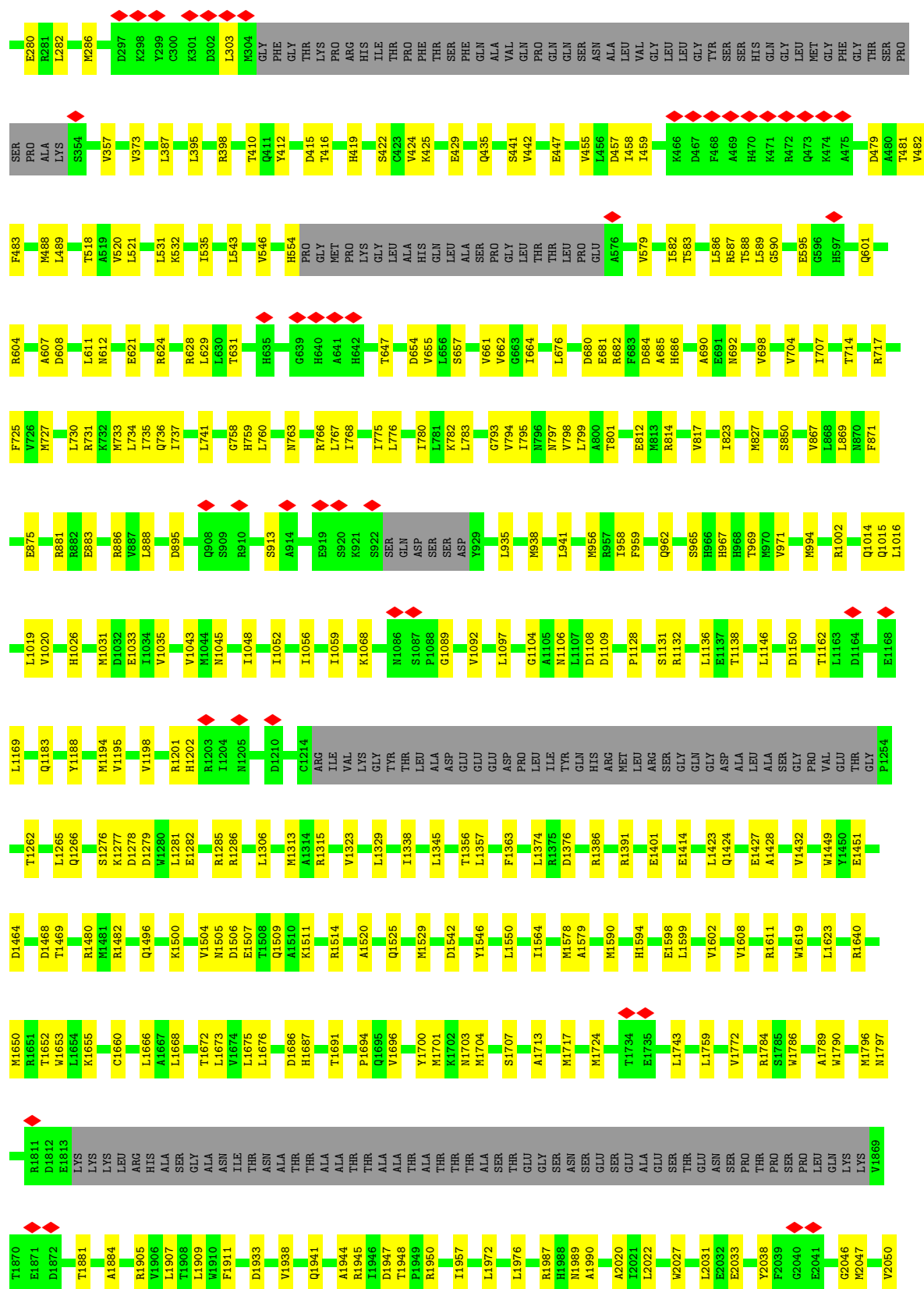
- Molecule 2: GTP-binding protein Rheb

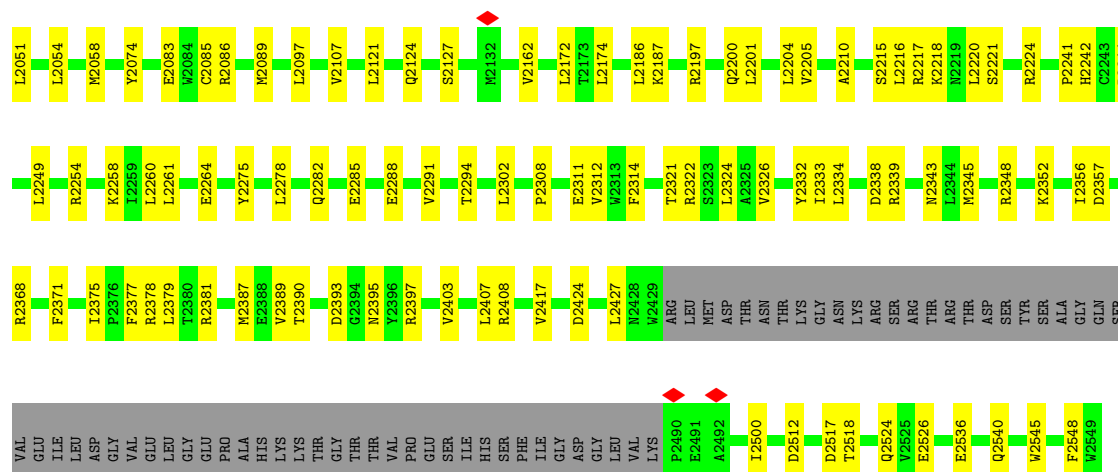




- Molecule 3: Serine/threonine-protein kinase mTOR

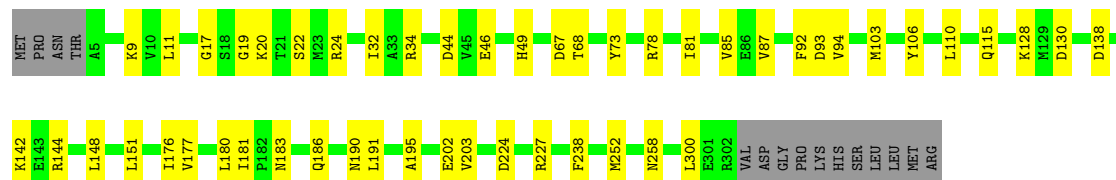






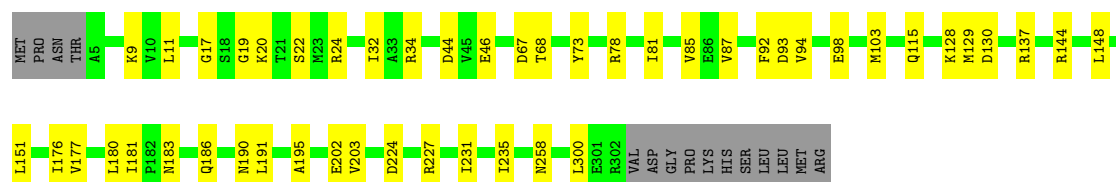
• Molecule 4: Ras-related GTP-binding protein A

Chain D: 79% 16% 5%



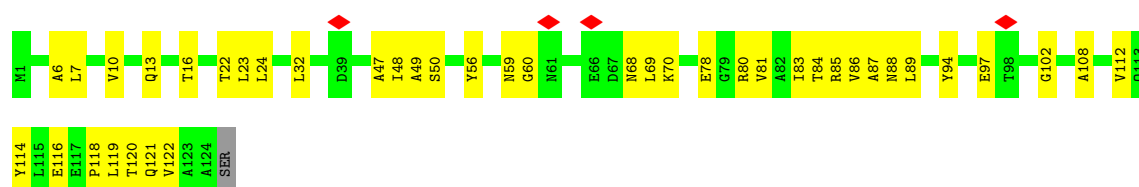
• Molecule 4: Ras-related GTP-binding protein A

Chain P: 80% 15% 5%



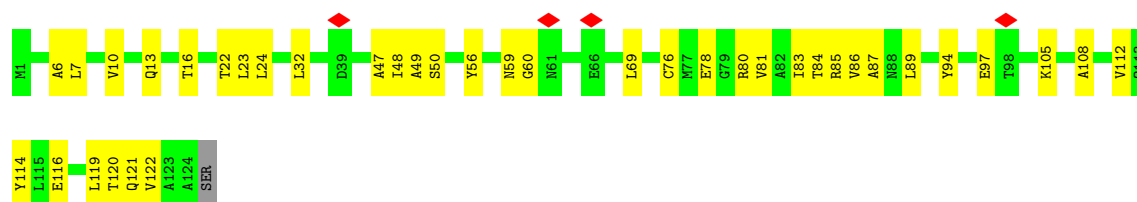
• Molecule 5: Regulator complex protein LAMTOR2

Chain G: 66% 33%

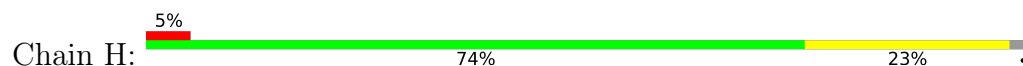


• Molecule 5: Regulator complex protein LAMTOR2

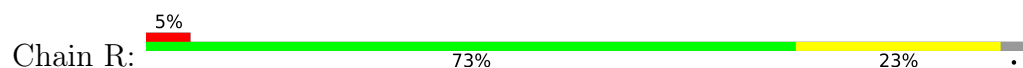
Chain Q: 69% 30%



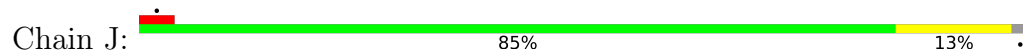
- Molecule 6: Ragulator complex protein LAMTOR3



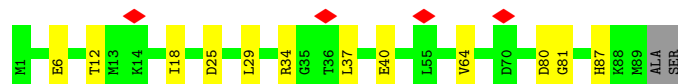
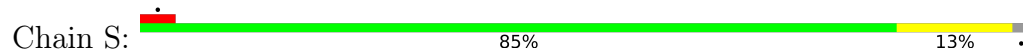
- Molecule 6: Ragulator complex protein LAMTOR3



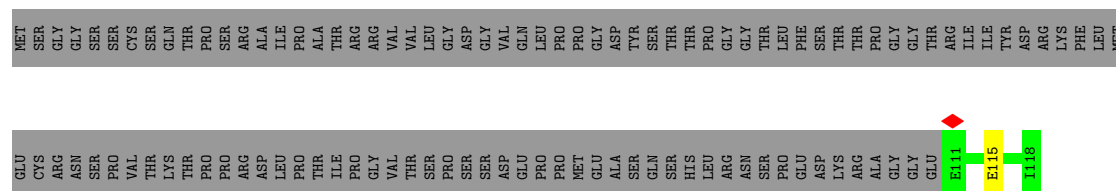
- Molecule 7: Ragulator complex protein LAMTOR5



- Molecule 7: Ragulator complex protein LAMTOR5

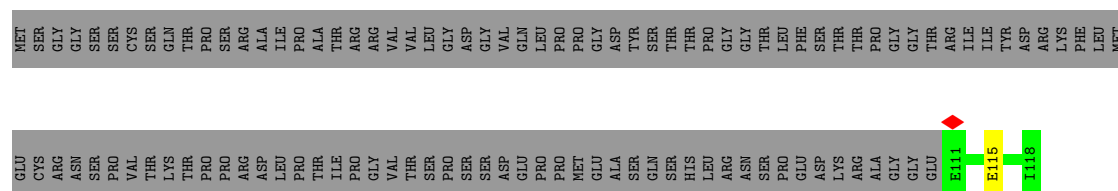


- Molecule 8: Eukaryotic translation initiation factor 4E-binding protein 1



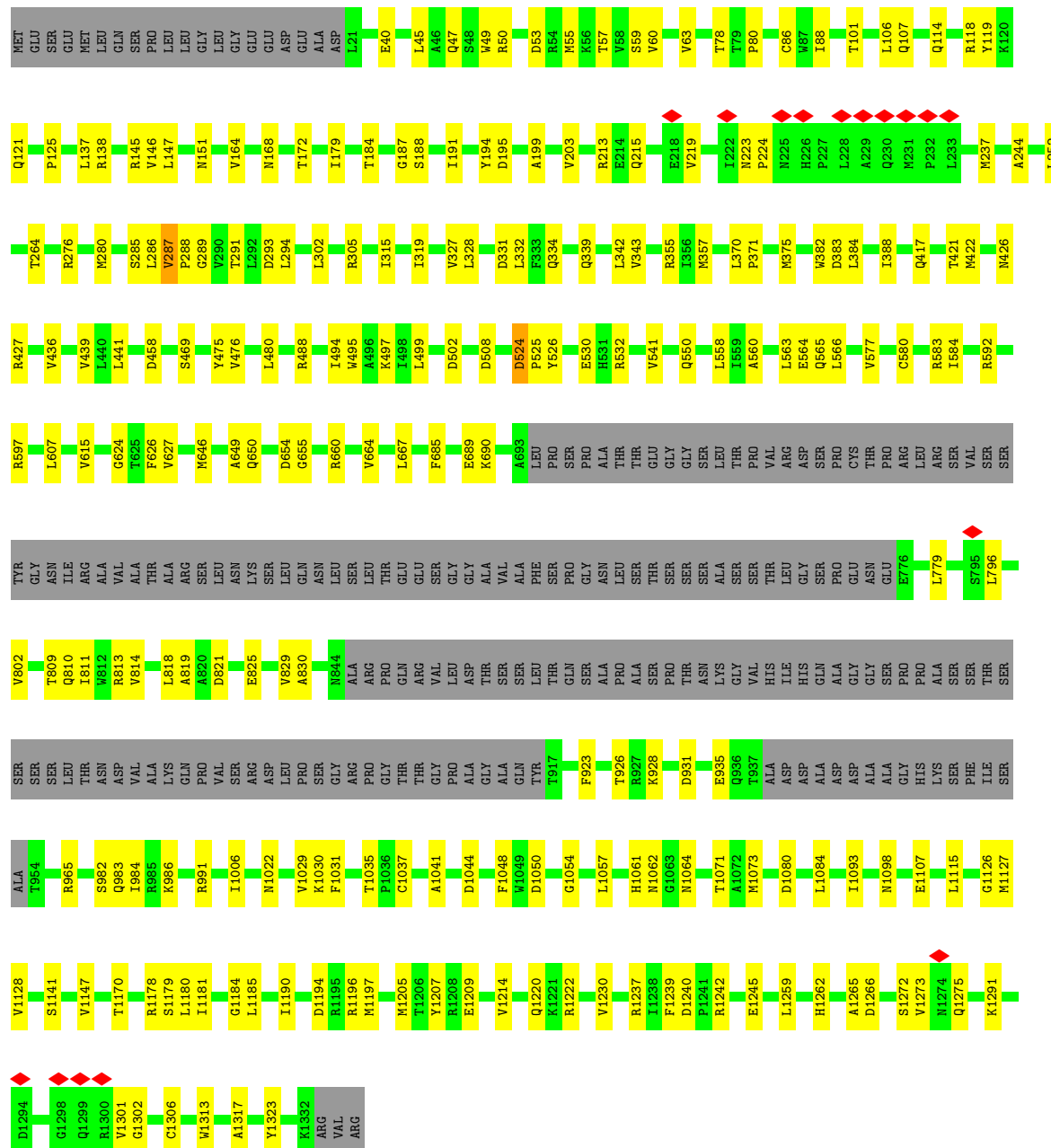
- Molecule 8: Eukaryotic translation initiation factor 4E-binding protein 1





• Molecule 9: Regulatory-associated protein of mTOR

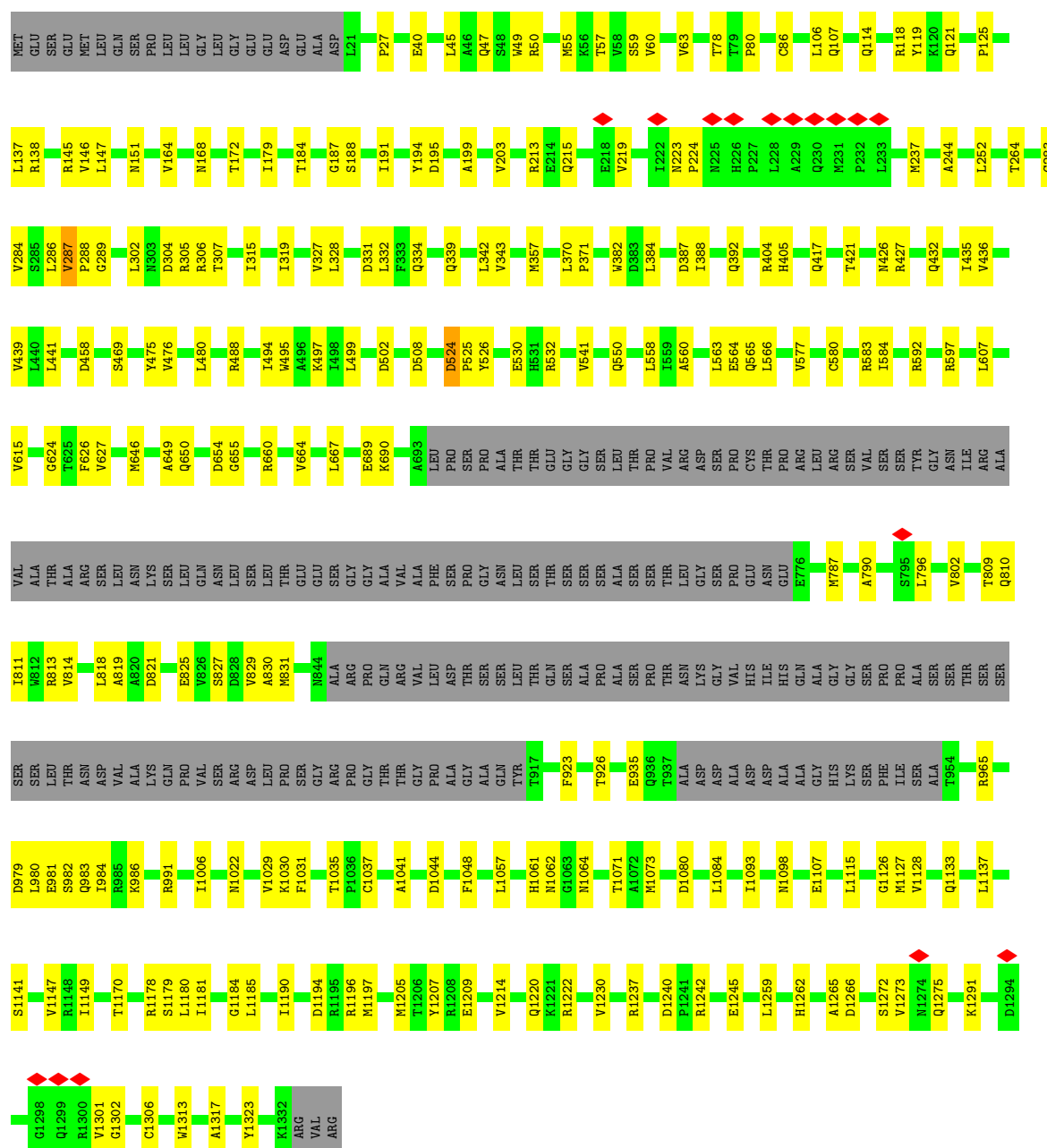
Chain C:



• Molecule 9: Regulatory-associated protein of mTOR

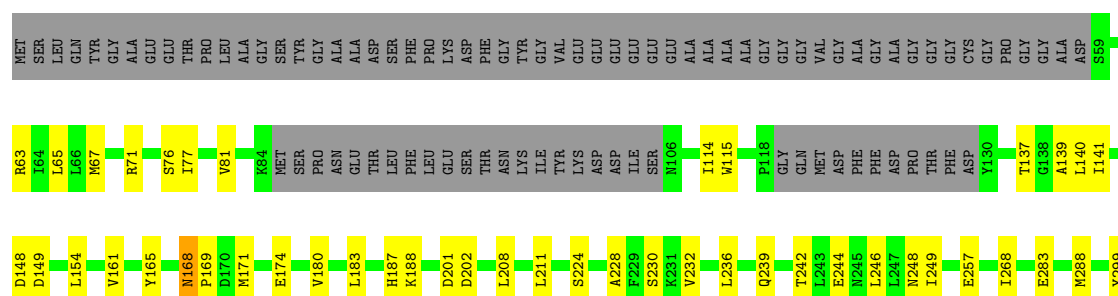
Chain U:



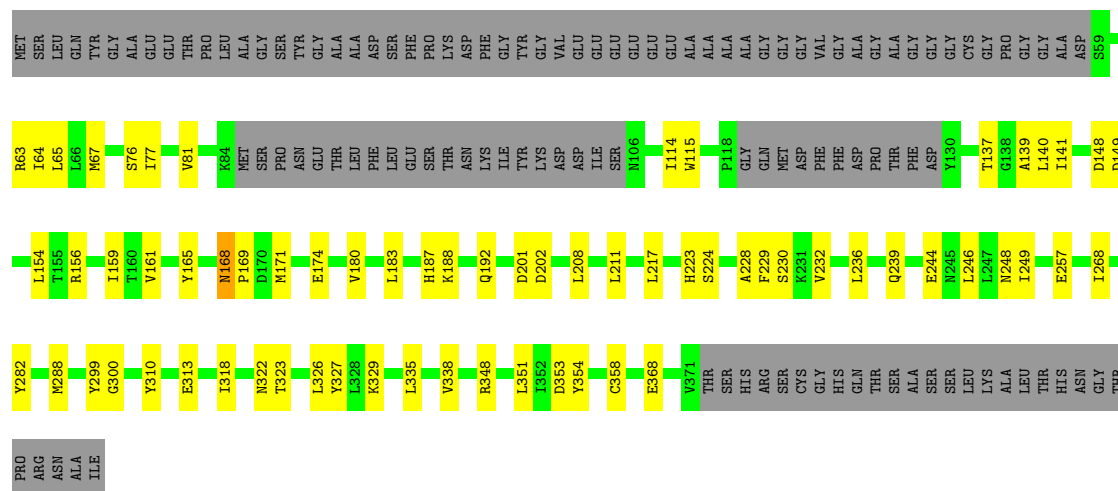


• Molecule 10: Ras-related GTP-binding protein C

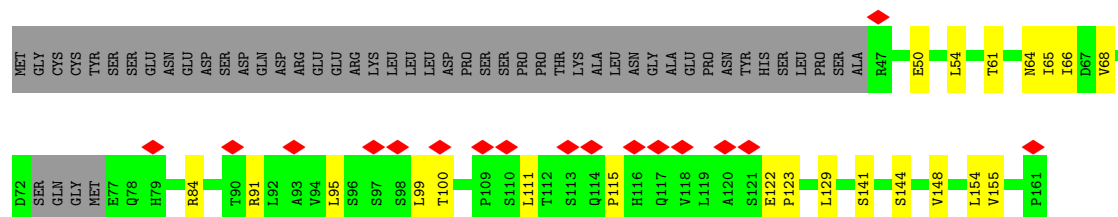
Chain E: 55% 16% 30%



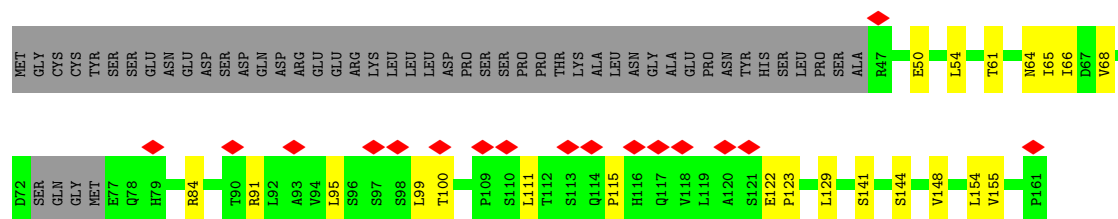
- Molecule 10: Ras-related GTP-binding protein C



- Molecule 11: Ragulator complex protein LAMTOR1

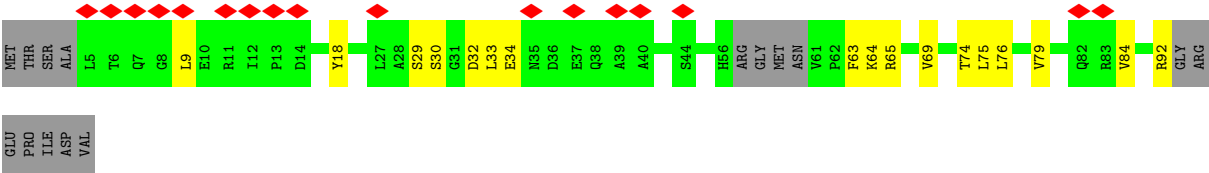


- Molecule 11: Ragulator complex protein LAMTOR1

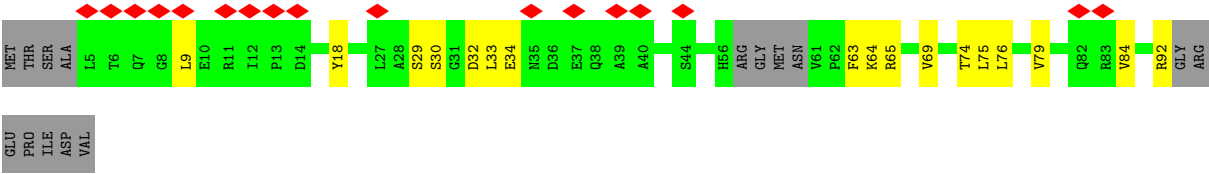


- Molecule 12: Ragulator complex protein LAMTOR4





● Molecule 12: Regulator complex protein LAMTOR4



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	359012	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	900	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	1.123	Depositor
Minimum map value	-0.073	Depositor
Average map value	0.010	Depositor
Map value standard deviation	0.023	Depositor
Recommended contour level	0.06	Depositor
Map size (Å)	465.91998, 465.91998, 465.91998	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.04, 1.04, 1.04	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GDP, IHP, MG, GSP, GTP, ANP

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	B	0.16	0/2514	0.39	0/3426
1	M	0.16	0/2514	0.38	0/3426
2	L	0.22	0/1365	0.42	0/1842
2	N	0.22	0/1365	0.42	0/1842
3	A	0.19	0/18892	0.39	0/25566
3	O	0.19	0/18892	0.39	0/25566
4	D	0.22	0/2489	0.40	0/3350
4	P	0.22	0/2489	0.40	0/3350
5	G	0.18	0/949	0.44	0/1285
5	Q	0.17	0/949	0.43	0/1285
6	H	0.17	0/951	0.38	0/1290
6	R	0.17	0/951	0.39	0/1290
7	J	0.15	0/661	0.38	0/896
7	S	0.14	0/661	0.38	0/896
8	K	0.13	0/69	0.23	0/89
8	T	0.13	0/69	0.22	0/89
9	C	0.21	0/9319	0.40	0/12677
9	U	0.22	0/9319	0.40	0/12677
10	E	0.21	0/2309	0.45	0/3114
10	V	0.22	0/2309	0.45	0/3114
11	F	0.16	0/884	0.37	0/1201
11	W	0.16	0/884	0.37	0/1201
12	I	0.13	0/649	0.34	0/876
12	X	0.13	0/649	0.34	0/876
All	All	0.20	0/82102	0.40	0/111224

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	L	0	1
2	N	0	1
9	C	0	3
9	U	0	3
10	E	0	1
10	V	0	1
All	All	0	10

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (10) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
9	C	223	ASN	Peptide
9	C	287	VAL	Peptide
9	C	524	ASP	Peptide
10	E	168	ASN	Peptide
2	L	33	ASP	Mainchain
2	N	33	ASP	Mainchain
9	U	223	ASN	Peptide
9	U	287	VAL	Peptide
9	U	524	ASP	Peptide
10	V	168	ASN	Peptide

5.2 Too-close contacts [i](#)

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	B	2456	2341	2341	37	0
1	M	2456	2341	2341	35	0
2	L	1343	1355	1355	33	0
2	N	1343	1355	1356	36	0
3	A	18511	18711	18711	294	0
3	O	18511	18711	18711	299	0
4	D	2444	2438	2438	38	0
4	P	2444	2438	2438	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	938	950	950	29	0
5	Q	938	950	950	27	0
6	H	934	958	958	21	0
6	R	934	958	958	24	0
7	J	655	656	656	9	0
7	S	655	656	656	11	0
8	K	69	57	57	1	0
8	T	69	57	57	1	0
9	C	9097	9067	9068	146	0
9	U	9097	9068	9068	143	0
10	E	2265	2258	2258	52	0
10	V	2265	2258	2258	54	0
11	F	868	870	870	18	0
11	W	868	870	870	18	0
12	I	642	652	652	13	0
12	X	642	652	652	14	0
13	L	32	0	12	5	0
13	N	32	0	12	5	0
14	A	2	0	0	0	0
14	D	1	0	0	0	0
14	L	1	0	0	0	0
14	N	1	0	0	0	0
14	O	2	0	0	0	0
14	P	1	0	0	0	0
15	A	31	12	13	1	0
15	O	31	12	13	1	0
16	A	36	6	6	1	0
16	O	36	6	6	1	0
17	D	32	0	12	5	0
17	P	32	0	12	5	0
18	E	28	0	12	3	0
18	V	28	0	12	3	0
All	All	80770	80663	80739	1306	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 8.

All (1306) 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)
3:O:518:THR:HG21	3:O:588:THR:HG21	1.45	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:518:THR:HG21	3:A:588:THR:HG21	1.45	0.95
9:C:558:LEU:HD23	9:C:584:ILE:HD12	1.54	0.90
9:U:558:LEU:HD23	9:U:584:ILE:HD12	1.54	0.90
2:L:56:LEU:HD21	2:L:164:ILE:HD11	1.52	0.89
2:N:56:LEU:HD21	2:N:164:ILE:HD11	1.56	0.87
10:E:327:TYR:OH	10:E:353:ASP:OD1	1.93	0.85
10:V:327:TYR:OH	10:V:353:ASP:OD2	1.93	0.84
3:O:2339:ARG:NH2	3:O:2357:ASP:O	2.12	0.82
3:A:2339:ARG:NH2	3:A:2357:ASP:O	2.12	0.82
3:A:2022:LEU:HD11	3:A:2121:LEU:HD21	1.62	0.81
7:J:64:VAL:HG11	11:F:129:LEU:HD11	1.62	0.81
3:A:689:GLN:NE2	9:C:422:MET:SD	2.54	0.81
5:Q:49:ALA:HB1	5:Q:83:ILE:HD11	1.63	0.81
10:E:180:VAL:O	10:E:188:LYS:NZ	2.14	0.81
7:S:64:VAL:HG11	11:W:129:LEU:HD11	1.62	0.81
3:A:1414:GLU:OE2	3:A:1449:TRP:NE1	2.15	0.80
2:L:33:ASP:OD1	13:L:201:GSP:O2'	1.99	0.80
4:D:20:LYS:NZ	17:D:401:GTP:O3G	2.13	0.80
2:N:33:ASP:OD1	13:N:201:GSP:O2'	1.99	0.80
5:G:49:ALA:HB1	5:G:83:ILE:HD11	1.63	0.80
3:O:2381:ARG:NH1	3:O:2548:PHE:O	2.15	0.80
4:P:20:LYS:NZ	17:P:401:GTP:O3G	2.14	0.80
3:O:1414:GLU:OE2	3:O:1449:TRP:NE1	2.15	0.79
3:O:2022:LEU:HD11	3:O:2121:LEU:HD21	1.63	0.79
5:Q:84:THR:HG21	5:Q:112:VAL:HG21	1.65	0.79
4:D:24:ARG:NH2	4:D:46:GLU:OE1	2.16	0.79
10:V:180:VAL:O	10:V:188:LYS:NZ	2.15	0.79
3:O:29:LEU:O	3:O:37:ARG:NH1	2.16	0.79
2:L:19:LYS:NZ	13:L:201:GSP:O1B	2.16	0.78
2:N:19:LYS:NZ	13:N:201:GSP:O1B	2.16	0.78
3:A:29:LEU:O	3:A:37:ARG:NH1	2.17	0.78
4:P:24:ARG:NH2	4:P:46:GLU:OE1	2.15	0.78
3:A:895:ASP:OD2	3:A:2217:ARG:NH1	2.17	0.78
3:A:2381:ARG:NH1	3:A:2548:PHE:O	2.16	0.78
3:O:895:ASP:OD2	3:O:2217:ARG:NH1	2.17	0.78
5:G:84:THR:HG21	5:G:112:VAL:HG21	1.64	0.77
4:P:87:VAL:HG21	4:P:180:LEU:HD21	1.67	0.77
4:D:87:VAL:HG21	4:D:180:LEU:HD21	1.67	0.77
9:U:1194:ASP:OD1	9:U:1196:ARG:NH1	2.18	0.77
3:A:30:LYS:NZ	3:A:82:GLU:OE1	2.18	0.76
3:O:1432:VAL:HG22	3:O:2390:THR:HG21	1.66	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:2332:TYR:OH	3:O:2512:ASP:OD2	2.03	0.76
3:A:1432:VAL:HG22	3:A:2390:THR:HG21	1.66	0.76
9:C:1275:GLN:O	9:C:1291:LYS:NZ	2.19	0.76
1:M:239:SER:OG	1:M:241:ASP:OD1	2.02	0.76
9:U:1275:GLN:O	9:U:1291:LYS:NZ	2.19	0.76
1:B:239:SER:OG	1:B:241:ASP:OD1	2.02	0.76
9:C:524:ASP:O	9:C:526:TYR:N	2.19	0.76
9:U:1098:ASN:ND2	9:U:1107:GLU:OE2	2.20	0.75
1:B:11:ASP:OD2	1:B:28:GLN:NE2	2.20	0.75
3:A:1134:ALA:O	3:A:1138:THR:HG23	1.86	0.75
3:O:631:THR:OG1	3:O:682:ARG:NH1	2.20	0.75
10:V:81:VAL:HG11	10:V:229:PHE:HE2	1.52	0.75
9:C:1098:ASN:ND2	9:C:1107:GLU:OE2	2.20	0.75
9:U:991:ARG:NE	9:U:1080:ASP:OD1	2.20	0.75
3:O:686:HIS:O	3:O:692:ASN:ND2	2.20	0.75
9:U:524:ASP:O	9:U:526:TYR:N	2.19	0.75
1:M:11:ASP:OD2	1:M:28:GLN:NE2	2.20	0.75
9:C:660:ARG:NE	9:C:821:ASP:OD2	2.21	0.74
10:V:76:SER:N	18:V:401:GDP:O1A	2.20	0.74
1:B:18:ALA:HB1	1:B:45:VAL:HG11	1.69	0.74
3:A:631:THR:OG1	3:A:682:ARG:NH1	2.21	0.74
3:A:2332:TYR:OH	3:A:2512:ASP:OD2	2.03	0.74
9:U:660:ARG:NE	9:U:821:ASP:OD2	2.21	0.74
3:O:704:VAL:HB	3:O:707:ILE:HD12	1.69	0.74
9:C:991:ARG:NE	9:C:1080:ASP:OD1	2.20	0.74
9:C:1194:ASP:OD1	9:C:1196:ARG:NH1	2.21	0.74
5:Q:80:ARG:NH1	5:Q:97:GLU:O	2.21	0.74
1:M:18:ALA:HB1	1:M:45:VAL:HG11	1.69	0.73
3:A:93:LEU:O	3:A:103:ARG:NH2	2.22	0.73
10:E:67:MET:HG2	10:E:140:LEU:HD11	1.71	0.73
10:E:313:GLU:N	10:E:313:GLU:OE1	2.22	0.72
3:A:554:HIS:O	9:C:986:LYS:NZ	2.20	0.72
4:D:34:ARG:NH2	9:C:926:THR:O	2.22	0.72
3:O:93:LEU:O	3:O:103:ARG:NH2	2.23	0.72
3:O:850:SER:O	3:O:1611:ARG:NH2	2.22	0.72
3:O:958:ILE:HD12	3:O:1313:MET:HE2	1.71	0.72
10:V:368:GLU:N	10:V:368:GLU:OE1	2.23	0.72
3:O:1052:ILE:O	3:O:1056:ILE:HD12	1.90	0.72
4:P:17:GLY:O	4:P:128:LYS:NZ	2.20	0.72
10:V:313:GLU:N	10:V:313:GLU:OE1	2.23	0.72
3:A:958:ILE:HD12	3:A:1313:MET:HE2	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1052:ILE:O	3:A:1056:ILE:HD12	1.90	0.72
9:U:328:LEU:HD21	9:U:370:LEU:HD22	1.71	0.71
2:L:115:MET:HE1	2:L:159:VAL:HG23	1.72	0.71
9:C:40:GLU:O	9:C:965:ARG:NH2	2.23	0.71
9:C:935:GLU:OE1	18:E:401:GDP:O2'	2.09	0.71
2:N:74:TYR:O	2:N:81:TYR:OH	2.09	0.71
3:A:1136:LEU:HD22	3:A:1172:THR:HG23	1.72	0.71
4:P:34:ARG:NH2	9:U:926:THR:O	2.22	0.71
9:U:982:SER:O	9:U:984:ILE:N	2.23	0.71
4:D:17:GLY:O	4:D:128:LYS:NZ	2.19	0.71
10:E:368:GLU:N	10:E:368:GLU:OE1	2.23	0.71
3:O:554:HIS:O	9:U:986:LYS:NZ	2.19	0.71
3:A:686:HIS:O	3:A:692:ASN:ND2	2.23	0.71
13:L:201:GSP:O1B	13:L:201:GSP:O2G	2.09	0.71
9:U:78:THR:OG1	9:U:80:PRO:O	2.09	0.71
3:A:601:GLN:OE1	3:A:604:ARG:NH2	2.24	0.70
4:P:22:SER:OG	17:P:401:GTP:H5'	1.91	0.70
9:U:40:GLU:O	9:U:965:ARG:NH2	2.24	0.70
3:A:1881:THR:HG23	3:A:1909:LEU:HD12	1.73	0.70
3:O:429:GLU:OE1	3:O:429:GLU:N	2.25	0.70
4:D:22:SER:OG	17:D:401:GTP:H5'	1.92	0.70
6:H:108:LYS:NZ	7:J:40:GLU:OE1	2.25	0.70
3:O:1881:THR:HG23	3:O:1909:LEU:HD12	1.72	0.70
2:N:171:ASP:O	3:O:164:ARG:NH2	2.24	0.70
10:V:67:MET:HG2	10:V:140:LEU:HD11	1.74	0.70
3:A:429:GLU:OE1	3:A:429:GLU:N	2.24	0.69
2:L:171:ASP:O	3:A:164:ARG:NH2	2.24	0.69
9:C:291:THR:OG1	9:C:293:ASP:OD1	2.10	0.69
2:N:115:MET:HE1	2:N:159:VAL:HG23	1.73	0.69
3:O:30:LYS:NZ	3:O:82:GLU:OE1	2.25	0.69
3:A:1208:ARG:NH1	3:A:1208:ARG:O	2.26	0.69
10:E:77:ILE:O	10:E:81:VAL:HG12	1.92	0.69
9:C:319:ILE:HD13	9:C:382:TRP:HB2	1.75	0.69
9:C:982:SER:O	9:C:984:ILE:N	2.25	0.69
3:O:1002:ARG:NH2	3:O:1033:GLU:OE2	2.25	0.69
9:U:1030:LYS:NZ	9:U:1073:MET:O	2.24	0.69
10:V:77:ILE:O	10:V:81:VAL:HG12	1.93	0.69
1:B:46:ASN:ND2	1:B:87:ASN:OD1	2.26	0.68
3:A:90:ILE:O	3:A:94:ILE:HD12	1.94	0.68
9:C:458:ASP:OD1	9:C:497:LYS:NZ	2.26	0.68
9:C:1179:SER:OG	9:C:1196:ARG:NH1	2.26	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:198:VAL:HG11	3:O:267:ILE:HD11	1.76	0.68
9:U:1179:SER:OG	9:U:1196:ARG:NH1	2.27	0.68
10:V:168:ASN:ND2	10:V:171:MET:SD	2.67	0.68
6:H:30:VAL:O	11:F:84:ARG:NH2	2.27	0.68
10:E:168:ASN:ND2	10:E:171:MET:SD	2.67	0.68
13:N:201:GSP:O1B	13:N:201:GSP:O2G	2.10	0.68
10:E:71:ARG:NH1	18:E:401:GDP:O5'	2.26	0.68
3:A:1525:GLN:OE1	3:A:1525:GLN:N	2.27	0.68
2:N:20:SER:OG	2:N:60:ASP:OD2	2.10	0.68
3:O:1525:GLN:OE1	3:O:1525:GLN:N	2.27	0.68
9:C:1207:TYR:OH	9:C:1240:ASP:O	2.12	0.67
1:M:46:ASN:ND2	1:M:87:ASN:OD1	2.27	0.67
3:O:2311:GLU:OE2	3:O:2311:GLU:N	2.26	0.67
2:N:14:TYR:O	2:N:17:VAL:HG12	1.95	0.67
3:A:850:SER:O	3:A:1611:ARG:NH2	2.27	0.67
1:M:132:ASN:ND2	1:M:173:ILE:O	2.27	0.67
1:B:132:ASN:ND2	1:B:173:ILE:O	2.27	0.67
10:E:239:GLN:OE1	10:E:239:GLN:N	2.28	0.67
3:A:198:VAL:HG11	3:A:267:ILE:HD11	1.76	0.67
3:A:1151:TYR:OH	3:O:736:GLN:NE2	2.27	0.66
7:J:30:ASN:ND2	7:J:39:ASP:OD1	2.28	0.66
9:U:458:ASP:OD1	9:U:497:LYS:NZ	2.27	0.66
10:V:239:GLN:OE1	10:V:239:GLN:N	2.28	0.66
3:A:647:THR:HG21	9:C:982:SER:HA	1.78	0.66
4:D:20:LYS:NZ	17:D:401:GTP:O2B	2.28	0.66
3:A:1724:MET:SD	3:A:1743:LEU:HD11	2.35	0.66
12:I:69:VAL:HG23	12:I:74:THR:OG1	1.95	0.66
3:O:794:VAL:O	3:O:798:VAL:HG23	1.96	0.66
3:A:282:LEU:HD13	3:A:442:VAL:HG11	1.77	0.66
12:X:69:VAL:HG23	12:X:74:THR:OG1	1.95	0.66
9:U:935:GLU:OE1	18:V:401:GDP:O2'	2.12	0.66
3:A:2324:LEU:HD23	3:A:2387:MET:HE2	1.77	0.66
3:O:731:ARG:NH1	9:U:387:ASP:OD2	2.28	0.66
9:U:558:LEU:HD21	9:U:580:CYS:SG	2.36	0.66
9:U:1207:TYR:OH	9:U:1240:ASP:O	2.15	0.65
3:A:71:ILE:HD11	3:A:93:LEU:HD12	1.79	0.65
9:C:558:LEU:HD21	9:C:580:CYS:SG	2.36	0.65
3:A:793:GLY:O	3:A:797:ASN:ND2	2.29	0.65
6:R:30:VAL:O	11:W:84:ARG:NH2	2.27	0.65
3:A:1097:LEU:HB3	3:A:1138:THR:HG21	1.77	0.65
1:M:229:SER:OG	1:M:231:ASP:OD1	2.15	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:664:ILE:HG23	3:O:698:VAL:HG11	1.78	0.65
2:L:14:TYR:O	2:L:17:VAL:HG12	1.95	0.65
3:O:2536:GLU:O	3:O:2540:GLN:NE2	2.30	0.65
3:A:45:GLN:O	3:A:49:THR:OG1	2.08	0.65
3:O:2333:ILE:HD12	3:O:2407:LEU:HD13	1.78	0.65
3:A:2333:ILE:HD12	3:A:2407:LEU:HD13	1.78	0.65
7:S:25:ASP:OD1	7:S:29:LEU:N	2.30	0.65
3:A:1673:LEU:HD13	3:A:1700:TYR:HA	1.79	0.65
3:A:280:GLU:OE1	3:A:398:ARG:NH1	2.31	0.64
3:O:2324:LEU:HD23	3:O:2387:MET:HE2	1.77	0.64
1:M:281:ASP:O	1:M:282:SER:OG	2.15	0.64
6:H:79:GLN:NE2	6:H:95:SER:O	2.31	0.64
3:O:1031:MET:HE1	3:O:1059:ILE:HG21	1.79	0.64
3:A:2536:GLU:O	3:A:2540:GLN:NE2	2.30	0.64
6:R:108:LYS:NZ	7:S:40:GLU:OE1	2.30	0.64
3:A:962:GLN:O	3:A:965:SER:OG	2.16	0.64
8:K:115:GLU:O	9:C:305:ARG:NH2	2.31	0.64
3:O:91:ALA:O	3:O:132:ARG:NH1	2.30	0.64
6:R:79:GLN:NE2	6:R:95:SER:O	2.31	0.64
3:A:2254:ARG:NH1	3:A:2261:LEU:O	2.31	0.64
9:C:78:THR:OG1	9:C:80:PRO:O	2.09	0.64
11:F:154:LEU:HD12	11:F:155:VAL:HG23	1.80	0.64
3:O:590:GLY:O	3:O:628:ARG:NH1	2.31	0.64
3:O:812:GLU:N	3:O:812:GLU:OE2	2.29	0.64
9:C:138:ARG:NE	9:C:188:SER:OG	2.31	0.63
3:O:735:ILE:HD11	9:U:286:LEU:HD22	1.80	0.63
5:G:80:ARG:NH1	5:G:97:GLU:O	2.31	0.63
9:C:563:LEU:HD23	9:C:566:LEU:HD11	1.80	0.63
3:O:1673:LEU:HD13	3:O:1700:TYR:HA	1.79	0.63
3:O:1594:HIS:NE2	3:O:1598:GLU:OE2	2.31	0.63
1:B:221:ARG:NH2	3:A:2288:GLU:OE1	2.32	0.63
3:A:2124:GLN:N	3:A:2124:GLN:OE1	2.31	0.63
11:W:154:LEU:HD12	11:W:155:VAL:HG23	1.79	0.63
3:O:2197:ARG:NH2	3:O:2424:ASP:OD2	2.32	0.63
5:Q:81:VAL:HG22	5:Q:94:TYR:CD1	2.33	0.63
9:U:187:GLY:HA2	9:U:237:MET:HE1	1.79	0.63
2:L:76:ILE:O	3:A:112:ARG:NH2	2.32	0.63
3:A:590:GLY:O	3:A:628:ARG:NH1	2.31	0.63
7:J:25:ASP:OD1	7:J:29:LEU:N	2.31	0.63
1:M:221:ARG:NH2	3:O:2288:GLU:OE1	2.32	0.63
2:N:76:ILE:O	3:O:112:ARG:NH2	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:1345:LEU:O	3:O:1386:ARG:NH1	2.32	0.63
4:P:129:MET:HE3	4:P:137:ARG:HD2	1.80	0.63
9:U:138:ARG:NE	9:U:188:SER:OG	2.31	0.63
8:T:115:GLU:O	9:U:305:ARG:NH2	2.31	0.63
9:U:319:ILE:HD13	9:U:382:TRP:HB2	1.79	0.63
3:A:2197:ARG:NH2	3:A:2424:ASP:OD2	2.32	0.62
3:O:1104:GLY:O	3:O:1146:LEU:HD21	1.98	0.62
9:C:187:GLY:HA2	9:C:237:MET:HE1	1.80	0.62
3:O:2408:ARG:NH2	3:O:2524:GLN:OE1	2.32	0.62
3:O:1128:PRO:O	3:O:1131:SER:OG	2.16	0.62
3:A:1594:HIS:NE2	3:A:1598:GLU:OE2	2.31	0.62
3:A:2408:ARG:NH2	3:A:2524:GLN:OE1	2.32	0.62
6:H:42:GLU:N	6:H:42:GLU:OE1	2.32	0.62
9:U:563:LEU:HD23	9:U:566:LEU:HD11	1.80	0.62
4:D:78:ARG:NH2	4:D:115:GLN:OE1	2.31	0.62
9:U:1071:THR:HG21	9:U:1126:GLY:HA3	1.81	0.62
3:A:812:GLU:OE2	3:A:812:GLU:N	2.29	0.62
9:C:164:VAL:HG13	9:C:179:ILE:HD11	1.82	0.62
3:A:1345:LEU:O	3:A:1386:ARG:NH1	2.33	0.62
6:R:22:ILE:HG23	6:R:92:PHE:HE1	1.64	0.62
3:A:1026:HIS:CD2	9:U:78:THR:HG22	2.34	0.62
5:G:81:VAL:HG22	5:G:94:TYR:CD1	2.35	0.62
3:O:2254:ARG:NH1	3:O:2261:LEU:O	2.32	0.62
4:P:20:LYS:NZ	17:P:401:GTP:O2B	2.31	0.62
1:M:273:MET:HE1	1:M:287:THR:HG21	1.81	0.61
6:R:21:ALA:HB3	6:R:93:ILE:HB	1.81	0.61
6:R:92:PHE:CD2	6:R:103:ILE:HD12	2.35	0.61
1:M:132:ASN:N	1:M:146:GLY:O	2.33	0.61
6:R:42:GLU:N	6:R:42:GLU:OE1	2.32	0.61
3:A:286:MET:SD	3:A:435:GLN:NE2	2.72	0.61
3:O:869:LEU:HD12	3:O:1579:ALA:CB	2.30	0.61
3:O:1650:MET:HG3	3:O:1676:LEU:HD21	1.82	0.61
4:P:78:ARG:NH2	4:P:115:GLN:OE1	2.32	0.61
3:A:1650:MET:HG3	3:A:1676:LEU:HD21	1.82	0.61
9:U:164:VAL:HG13	9:U:179:ILE:HD11	1.82	0.61
11:W:122:GLU:OE1	12:X:65:ARG:NH1	2.34	0.61
9:C:488:ARG:NH2	9:C:524:ASP:OD2	2.33	0.61
12:X:18:TYR:N	12:X:30:SER:OG	2.33	0.61
1:B:132:ASN:N	1:B:146:GLY:O	2.33	0.61
12:I:18:TYR:N	12:I:30:SER:OG	2.33	0.61
1:B:281:ASP:O	1:B:282:SER:OG	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:733:MET:O	3:A:737:ILE:HD12	2.01	0.60
3:A:1031:MET:HE1	3:A:1059:ILE:HG21	1.84	0.60
9:C:1071:THR:HG21	9:C:1126:GLY:HA3	1.81	0.60
10:E:348:ARG:HE	10:E:351:LEU:HD11	1.64	0.60
3:A:1101:GLN:NE2	3:A:1138:THR:HG22	2.16	0.60
3:O:2345:MET:SD	3:O:2356:ILE:HG21	2.41	0.60
10:V:348:ARG:HE	10:V:351:LEU:HD11	1.65	0.60
3:O:286:MET:SD	3:O:435:GLN:NE2	2.75	0.60
3:O:1947:ASP:OD2	3:O:1987:ARG:NH1	2.34	0.60
9:C:566:LEU:HD22	9:C:607:LEU:HD11	1.84	0.60
10:E:183:LEU:HD12	10:E:187:HIS:HB3	1.83	0.60
11:F:122:GLU:OE1	12:I:65:ARG:NH1	2.34	0.60
9:U:1006:ILE:HD12	9:U:1265:ALA:HB2	1.83	0.60
3:O:90:ILE:O	3:O:94:ILE:HD12	2.01	0.60
9:C:1006:ILE:HD12	9:C:1265:ALA:HB2	1.83	0.60
9:U:566:LEU:HD22	9:U:607:LEU:HD11	1.84	0.60
3:A:759:HIS:O	3:A:763:ASN:ND2	2.33	0.60
1:B:53:ASP:OD2	1:B:55:SER:OG	2.15	0.60
3:O:71:ILE:HD11	3:O:93:LEU:HD12	1.83	0.60
3:A:2345:MET:SD	3:A:2356:ILE:HG21	2.41	0.59
2:L:74:TYR:O	2:L:81:TYR:OH	2.09	0.59
3:A:1947:ASP:OD2	3:A:1987:ARG:NH1	2.35	0.59
1:M:274:TRP:NE1	3:O:2285:GLU:OE1	2.35	0.59
10:V:322:ASN:O	10:V:323:THR:OG1	2.17	0.59
2:L:27:VAL:HG23	2:L:28:GLU:HG3	1.84	0.59
3:A:579:VAL:O	3:A:583:THR:OG1	2.17	0.59
3:A:1108:ASP:OD1	3:A:1109:ASP:N	2.36	0.59
9:C:331:ASP:OD1	9:C:332:LEU:N	2.35	0.59
3:O:1655:LYS:NZ	16:O:3003:IHP:O26	2.34	0.59
9:U:488:ARG:NH2	9:U:524:ASP:OD2	2.35	0.59
1:B:274:TRP:NE1	3:A:2285:GLU:OE1	2.35	0.59
9:C:1184:GLY:HA2	9:C:1190:ILE:HD13	1.84	0.59
6:R:22:ILE:HG23	6:R:92:PHE:CE1	2.37	0.59
9:C:60:VAL:HG22	9:C:147:LEU:HB3	1.85	0.59
3:O:607:ALA:HA	3:O:611:LEU:HD12	1.83	0.59
3:A:1655:LYS:NZ	16:A:3003:IHP:O26	2.35	0.58
3:O:1108:ASP:OD1	3:O:1109:ASP:N	2.37	0.58
9:U:331:ASP:OD1	9:U:332:LEU:N	2.35	0.58
3:A:1276:SER:OG	3:A:1278:ASP:OD1	2.13	0.58
3:O:2326:VAL:HG22	3:O:2403:VAL:HG21	1.84	0.58
3:A:883:GLU:OE2	3:A:886:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:417:GLN:O	9:C:421:THR:HG23	2.02	0.58
10:E:322:ASN:O	10:E:323:THR:OG1	2.17	0.58
2:N:25:GLN:NE2	2:N:150:ALA:O	2.36	0.58
4:P:177:VAL:O	4:P:181:ILE:HD12	2.03	0.58
3:A:956:MET:HE2	3:A:956:MET:HA	1.85	0.58
3:A:1650:MET:CG	3:A:1676:LEU:HD21	2.33	0.58
3:A:2326:VAL:HG22	3:A:2403:VAL:HG21	1.84	0.58
9:U:1184:GLY:HA2	9:U:1190:ILE:HD13	1.84	0.58
10:V:81:VAL:HG11	10:V:229:PHE:CE2	2.37	0.58
9:C:168:ASN:ND2	9:C:172:THR:OG1	2.34	0.58
3:O:1701:MET:HE3	3:O:1717:MET:HE2	1.86	0.58
1:M:53:ASP:OD2	1:M:55:SER:OG	2.15	0.58
3:O:1169:LEU:O	3:O:1169:LEU:HD23	2.04	0.58
3:O:1650:MET:CG	3:O:1676:LEU:HD21	2.33	0.58
9:U:60:VAL:HG22	9:U:147:LEU:HB3	1.84	0.58
10:V:183:LEU:HD12	10:V:187:HIS:HB3	1.84	0.58
6:H:21:ALA:HB3	6:H:93:ILE:HB	1.85	0.58
3:O:280:GLU:OE1	3:O:398:ARG:NH1	2.36	0.58
3:A:1278:ASP:OD1	3:A:1279:ASP:N	2.37	0.58
9:C:86:CYS:SG	9:C:106:LEU:HD13	2.44	0.58
3:O:1278:ASP:OD1	3:O:1279:ASP:N	2.37	0.58
4:D:177:VAL:O	4:D:181:ILE:HD12	2.04	0.57
3:O:1089:GLY:O	3:O:1092:VAL:HG12	2.04	0.57
9:C:328:LEU:HD21	9:C:370:LEU:HD22	1.85	0.57
10:E:174:GLU:OE1	10:E:232:VAL:HG22	2.04	0.57
3:O:42:LYS:NZ	3:O:45:GLN:OE1	2.29	0.57
3:O:579:VAL:O	3:O:583:THR:OG1	2.19	0.57
3:O:2368:ARG:NH1	3:O:2371:PHE:O	2.37	0.57
5:G:32:LEU:O	5:G:32:LEU:HD23	2.05	0.57
3:O:956:MET:HE2	3:O:956:MET:HA	1.85	0.57
3:O:1500:LYS:O	3:O:1504:VAL:HG23	2.04	0.57
9:U:57:THR:HG21	9:U:342:LEU:HD23	1.86	0.57
9:U:287:VAL:O	9:U:289:GLY:N	2.36	0.57
3:A:1701:MET:HE3	3:A:1717:MET:HE2	1.85	0.57
3:A:2393:ASP:OD1	3:A:2397:ARG:NH1	2.38	0.57
1:M:63:GLN:NE2	1:M:85:ASN:O	2.37	0.57
1:B:63:GLN:NE2	1:B:85:ASN:O	2.37	0.57
3:A:1128:PRO:O	3:A:1131:SER:OG	2.17	0.57
9:C:293:ASP:OD1	9:C:294:LEU:N	2.36	0.57
2:N:26:PHE:O	2:N:45:LYS:NZ	2.26	0.57
3:O:45:GLN:O	3:O:49:THR:OG1	2.07	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:647:THR:HG21	9:U:982:SER:HA	1.86	0.57
11:W:141:SER:O	11:W:144:SER:OG	2.18	0.57
1:B:156:ASP:OD2	1:B:159:THR:N	2.38	0.57
9:C:57:THR:HG21	9:C:342:LEU:HD23	1.87	0.57
3:O:1941:GLN:OE1	3:O:2200:GLN:NE2	2.38	0.57
9:U:334:GLN:NE2	9:U:469:SER:O	2.36	0.57
3:A:2187:LYS:NZ	15:A:3000:ANP:O1A	2.23	0.57
3:A:2536:GLU:OE1	3:A:2536:GLU:N	2.34	0.57
3:O:733:MET:O	3:O:737:ILE:HD12	2.05	0.57
9:U:417:GLN:O	9:U:421:THR:HG23	2.05	0.57
9:U:1062:ASN:ND2	9:U:1064:ASN:OD1	2.38	0.57
10:V:174:GLU:OE1	10:V:232:VAL:HG22	2.05	0.57
10:V:288:MET:HE3	10:V:338:VAL:HG13	1.87	0.57
3:A:1500:LYS:O	3:A:1504:VAL:HG23	2.05	0.56
10:E:148:ASP:OD1	10:E:149:ASP:N	2.37	0.56
10:E:288:MET:HE3	10:E:338:VAL:HG13	1.86	0.56
9:U:86:CYS:SG	9:U:106:LEU:HD13	2.45	0.56
2:L:5:LYS:NZ	2:L:52:GLN:OE1	2.37	0.56
3:A:961:ASP:OD2	3:A:963:SER:OG	2.23	0.56
1:B:90:SER:O	1:B:102:THR:OG1	2.12	0.56
3:A:268:LEU:HD13	3:A:373:VAL:HG23	1.87	0.56
9:C:334:GLN:NE2	9:C:469:SER:O	2.37	0.56
2:N:27:VAL:HG23	2:N:28:GLU:HG3	1.85	0.56
3:O:1911:PHE:HE2	3:O:1957:ILE:HD11	1.71	0.56
10:E:288:MET:CE	10:E:338:VAL:HG13	2.35	0.56
3:O:883:GLU:OE2	3:O:886:ARG:NH1	2.38	0.56
10:V:288:MET:CE	10:V:338:VAL:HG13	2.36	0.56
12:X:79:VAL:HG22	12:X:84:VAL:HG12	1.87	0.56
9:C:107:GLN:OE1	9:C:121:GLN:NE2	2.38	0.56
3:A:867:VAL:HG12	3:A:871:PHE:CZ	2.41	0.56
9:C:1115:LEU:HD12	9:C:1127:MET:HG3	1.87	0.56
1:M:156:ASP:OD2	1:M:159:THR:N	2.38	0.56
3:O:2393:ASP:OD1	3:O:2397:ARG:NH1	2.39	0.56
9:U:50:ARG:NH2	9:U:508:ASP:OD2	2.39	0.56
3:A:869:LEU:HD12	3:A:1579:ALA:CB	2.36	0.56
3:A:913:SER:O	3:A:2224:ARG:NH1	2.39	0.56
5:G:47:ALA:O	5:G:50:SER:OG	2.22	0.56
5:Q:32:LEU:O	5:Q:32:LEU:HD23	2.04	0.56
9:U:304:ASP:OD2	9:U:307:THR:HG23	2.05	0.56
5:G:13:GLN:O	5:G:16:THR:HG22	2.06	0.56
6:H:19:LEU:HG	6:H:103:ILE:HD11	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:65:LEU:O	10:E:140:LEU:HD12	2.05	0.56
3:O:608:ASP:O	3:O:612:ASN:ND2	2.36	0.56
3:O:1306:LEU:HD23	3:O:1313:MET:HE3	1.88	0.56
3:O:1686:ASP:OD1	3:O:1687:HIS:N	2.38	0.56
3:A:1089:GLY:O	3:A:1092:VAL:HG12	2.06	0.56
3:A:1911:PHE:HE2	3:A:1957:ILE:HD11	1.71	0.56
12:I:79:VAL:HG22	12:I:84:VAL:HG12	1.87	0.56
9:U:107:GLN:OE1	9:U:121:GLN:NE2	2.39	0.56
9:U:1115:LEU:HD12	9:U:1127:MET:HG3	1.87	0.56
5:G:89:LEU:HD12	5:G:119:LEU:HD13	1.86	0.55
9:U:45:LEU:O	9:U:47:GLN:NE2	2.38	0.55
9:U:106:LEU:HD11	9:U:264:THR:HG21	1.88	0.55
1:B:18:ALA:CB	1:B:45:VAL:HG11	2.36	0.55
3:A:2368:ARG:NH1	3:A:2371:PHE:O	2.39	0.55
9:C:1185:LEU:O	9:C:1214:VAL:HG12	2.06	0.55
3:O:2124:GLN:OE1	3:O:2124:GLN:N	2.35	0.55
5:Q:13:GLN:O	5:Q:16:THR:HG22	2.06	0.55
9:U:1185:LEU:O	9:U:1214:VAL:HG12	2.06	0.55
10:V:161:VAL:HG22	10:V:211:LEU:HD21	1.89	0.55
3:A:958:ILE:CD1	3:A:1313:MET:HE2	2.36	0.55
9:C:1141:SER:OG	9:C:1147:VAL:HG22	2.05	0.55
3:O:867:VAL:HG12	3:O:871:PHE:CZ	2.41	0.55
3:O:2258:LYS:HE3	3:O:2258:LYS:HA	1.88	0.55
9:C:375:MET:SD	3:O:1183:GLN:NE2	2.78	0.55
9:U:1141:SER:OG	9:U:1147:VAL:HG22	2.06	0.55
3:O:2249:LEU:HD22	3:O:2302:LEU:HD21	1.89	0.55
4:P:224:ASP:O	4:P:227:ARG:NH1	2.39	0.55
3:A:1014:GLN:OE1	3:A:1015:GLN:NE2	2.40	0.55
3:A:2249:LEU:HD22	3:A:2302:LEU:HD21	1.89	0.55
9:C:45:LEU:O	9:C:47:GLN:NE2	2.39	0.55
10:E:161:VAL:HG22	10:E:211:LEU:HD21	1.88	0.55
1:M:90:SER:O	1:M:102:THR:OG1	2.13	0.55
3:O:759:HIS:O	3:O:763:ASN:ND2	2.34	0.55
3:O:913:SER:O	3:O:2224:ARG:NH1	2.39	0.55
4:P:186:GLN:OE1	4:P:186:GLN:N	2.38	0.55
9:U:194:TYR:HB2	9:U:199:ALA:HB1	1.89	0.55
3:A:1598:GLU:O	3:A:1602:VAL:HG23	2.07	0.55
3:A:1686:ASP:OD1	3:A:1687:HIS:N	2.39	0.55
2:N:130:SER:OG	2:N:133:GLU:OE1	2.19	0.55
4:P:258:ASN:ND2	10:V:300:GLY:O	2.38	0.55
3:A:1466:LYS:HG3	3:A:1476:LEU:HD21	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:958:ILE:CD1	3:O:1313:MET:HE2	2.36	0.55
9:U:1205:MET:HE1	9:U:1207:TYR:CE2	2.41	0.55
3:A:772:MET:HE1	3:A:816:TRP:CZ3	2.42	0.55
6:H:27:ARG:NH1	6:H:86:LEU:O	2.40	0.55
3:O:84:LYS:O	3:O:88:LEU:HD23	2.07	0.55
7:S:37:LEU:HD11	7:S:87:HIS:HB2	1.88	0.55
1:B:229:SER:OG	1:B:231:ASP:OD1	2.15	0.54
4:D:92:PHE:CZ	4:D:148:LEU:HD21	2.42	0.54
12:I:74:THR:C	12:I:75:LEU:HD12	2.32	0.54
9:C:287:VAL:O	9:C:289:GLY:N	2.37	0.54
3:O:2047:MET:O	3:O:2051:LEU:HD23	2.07	0.54
11:W:99:LEU:O	11:W:100:THR:OG1	2.24	0.54
2:L:25:GLN:NE2	2:L:150:ALA:O	2.37	0.54
9:C:106:LEU:HD11	9:C:264:THR:HG21	1.89	0.54
3:O:1772:VAL:HG11	3:O:1796:MET:HE3	1.89	0.54
4:P:44:ASP:O	4:P:73:TYR:OH	2.15	0.54
4:P:191:LEU:HD11	4:P:203:VAL:HG11	1.89	0.54
3:A:1772:VAL:HG11	3:A:1796:MET:HE3	1.89	0.54
9:C:1062:ASN:ND2	9:C:1064:ASN:OD1	2.39	0.54
1:M:19:GLY:O	1:M:45:VAL:HG12	2.08	0.54
3:O:1451:GLU:OE2	3:O:1482:ARG:NE	2.40	0.54
3:A:1306:LEU:HD23	3:A:1313:MET:HE3	1.88	0.54
3:A:2038:TYR:CE2	3:A:2097:LEU:HD21	2.42	0.54
3:O:2038:TYR:CE1	3:O:2097:LEU:HD21	2.42	0.54
2:L:20:SER:OG	2:L:60:ASP:OD2	2.19	0.54
3:A:2020:ALA:HB2	3:A:2186:LEU:HD21	1.90	0.54
3:O:1480:ARG:NH1	3:O:1496:GLN:OE1	2.39	0.54
10:V:148:ASP:OD1	10:V:149:ASP:N	2.37	0.54
12:X:74:THR:C	12:X:75:LEU:HD12	2.32	0.54
3:A:1265:LEU:HD21	3:A:1329:LEU:HD11	1.90	0.54
9:C:1022:ASN:N	9:C:1323:TYR:O	2.41	0.54
5:Q:56:TYR:HB3	5:Q:69:LEU:HD11	1.88	0.54
9:U:151:ASN:ND2	9:U:195:ASP:OD2	2.41	0.54
9:C:50:ARG:NH2	9:C:508:ASP:OD2	2.39	0.54
9:C:426:ASN:OD1	9:C:427:ARG:N	2.41	0.54
3:A:2311:GLU:N	3:A:2311:GLU:OE1	2.36	0.54
5:Q:116:GLU:O	5:Q:120:THR:OG1	2.23	0.54
1:M:18:ALA:CB	1:M:45:VAL:HG11	2.36	0.54
2:N:5:LYS:NZ	2:N:52:GLN:OE1	2.37	0.54
6:R:117:LEU:O	6:R:121:VAL:HG22	2.08	0.54
9:U:1022:ASN:N	9:U:1323:TYR:O	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:LEU:HD11	1:B:256:THR:O	2.08	0.53
4:D:44:ASP:O	4:D:73:TYR:OH	2.15	0.53
5:G:56:TYR:HB3	5:G:69:LEU:HD11	1.88	0.53
3:O:1014:GLN:OE1	3:O:1015:GLN:NE2	2.39	0.53
4:D:186:GLN:OE1	4:D:186:GLN:N	2.38	0.53
5:G:22:THR:C	5:G:23:LEU:HD12	2.33	0.53
5:G:86:VAL:HG22	5:G:112:VAL:HG22	1.88	0.53
7:J:37:LEU:HD11	7:J:87:HIS:HB2	1.89	0.53
9:C:530:GLU:N	9:C:530:GLU:OE1	2.41	0.53
3:O:601:GLN:OE1	3:O:604:ARG:NH2	2.39	0.53
4:P:98:GLU:N	4:P:98:GLU:OE2	2.40	0.53
9:U:436:VAL:HA	9:U:439:VAL:HG12	1.89	0.53
3:A:888:LEU:HD13	3:A:1590:MET:HE2	1.89	0.53
4:P:92:PHE:CZ	4:P:148:LEU:HD21	2.43	0.53
5:Q:22:THR:C	5:Q:23:LEU:HD12	2.33	0.53
5:Q:86:VAL:HG22	5:Q:112:VAL:HG22	1.89	0.53
1:B:19:GLY:O	1:B:45:VAL:HG12	2.08	0.53
9:C:436:VAL:HA	9:C:439:VAL:HG12	1.89	0.53
3:A:1468:ASP:OD1	3:A:1469:THR:HG23	2.08	0.53
3:A:1480:ARG:NH1	3:A:1496:GLN:OE1	2.39	0.53
6:H:117:LEU:O	6:H:121:VAL:HG22	2.09	0.53
9:C:194:TYR:HB2	9:C:199:ALA:HB1	1.89	0.53
2:N:23:THR:O	2:N:27:VAL:HG22	2.09	0.53
3:O:888:LEU:HD13	3:O:1590:MET:HE2	1.89	0.53
3:O:1507:GLU:OE2	3:O:1511:LYS:NZ	2.41	0.53
6:R:27:ARG:NH1	6:R:86:LEU:O	2.40	0.53
9:U:530:GLU:OE1	9:U:530:GLU:N	2.41	0.53
3:A:84:LYS:O	3:A:88:LEU:HD23	2.08	0.53
5:Q:56:TYR:CB	5:Q:69:LEU:HD11	2.39	0.53
3:A:1421:ASN:ND2	3:A:1452:LYS:O	2.41	0.53
3:A:1451:GLU:OE2	3:A:1482:ARG:NE	2.42	0.53
9:C:1230:VAL:HG11	9:C:1259:LEU:HD13	1.91	0.53
11:F:141:SER:O	11:F:144:SER:OG	2.18	0.53
9:U:168:ASN:ND2	9:U:172:THR:OG1	2.34	0.53
10:V:201:ASP:OD1	10:V:202:ASP:N	2.42	0.53
3:A:2517:ASP:OD1	3:A:2518:THR:N	2.42	0.53
3:O:793:GLY:O	3:O:797:ASN:ND2	2.41	0.53
9:U:426:ASN:OD1	9:U:427:ARG:N	2.41	0.53
3:A:2258:LYS:HA	3:A:2258:LYS:HE3	1.91	0.53
4:D:258:ASN:ND2	10:E:300:GLY:O	2.38	0.53
3:O:1724:MET:SD	3:O:1743:LEU:HD11	2.49	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:2020:ALA:HB2	3:O:2186:LEU:HD21	1.90	0.53
3:O:2517:ASP:OD1	3:O:2518:THR:N	2.42	0.53
4:D:191:LEU:HD11	4:D:203:VAL:HG11	1.90	0.52
3:O:758:GLY:HA2	3:O:801:THR:HG23	1.91	0.52
3:A:535:ILE:HD12	3:A:535:ILE:H	1.74	0.52
3:A:888:LEU:HD13	3:A:1590:MET:CE	2.40	0.52
3:O:727:MET:HE2	3:O:766:ARG:HE	1.73	0.52
3:O:888:LEU:HD13	3:O:1590:MET:CE	2.39	0.52
3:O:1198:VAL:HG12	3:O:1201:ARG:NH2	2.25	0.52
3:O:2397:ARG:NH2	3:O:2526:GLU:OE1	2.42	0.52
4:P:191:LEU:HD11	4:P:203:VAL:CG1	2.39	0.52
1:B:273:MET:HE1	1:B:287:THR:HG21	1.90	0.52
11:F:50:GLU:O	11:F:54:LEU:HD13	2.10	0.52
2:L:69:ILE:HD13	3:A:969:THR:HG21	1.92	0.52
10:E:201:ASP:OD1	10:E:202:ASP:N	2.42	0.52
3:O:684:ASP:OD1	3:O:685:ALA:N	2.43	0.52
3:O:714:THR:HG23	3:O:717:ARG:NH2	2.24	0.52
1:M:254:LEU:HD11	1:M:256:THR:O	2.08	0.52
3:O:1265:LEU:HD21	3:O:1329:LEU:HD11	1.91	0.52
9:U:1209:GLU:OE1	9:U:1237:ARG:NH1	2.42	0.52
5:G:56:TYR:CB	5:G:69:LEU:HD11	2.40	0.52
3:O:1468:ASP:OD1	3:O:1469:THR:HG23	2.08	0.52
2:L:23:THR:O	2:L:27:VAL:HG22	2.09	0.52
3:A:210:VAL:HG21	3:A:266:LEU:HB3	1.91	0.52
5:G:108:ALA:O	5:G:112:VAL:HG23	2.10	0.52
3:O:535:ILE:HD12	3:O:535:ILE:H	1.74	0.52
3:O:676:LEU:HD12	3:O:707:ILE:HG23	1.91	0.52
5:Q:121:GLN:NE2	5:Q:122:VAL:HG23	2.25	0.52
3:A:617:GLU:OE1	3:A:617:GLU:N	2.30	0.52
9:C:285:SER:O	9:C:286:LEU:HD22	2.10	0.52
1:M:11:ASP:O	1:M:54:ARG:NH2	2.41	0.52
2:N:69:ILE:HD13	3:O:969:THR:HG21	1.92	0.52
3:A:727:MET:HE2	3:A:766:ARG:HE	1.74	0.52
3:A:2397:ARG:NH2	3:A:2526:GLU:OE1	2.42	0.52
9:U:1230:VAL:HG11	9:U:1259:LEU:HD13	1.92	0.52
3:A:1759:LEU:CD2	3:A:1772:VAL:HG21	2.40	0.51
9:C:1128:VAL:HG11	9:C:1170:THR:O	2.10	0.51
3:O:1598:GLU:O	3:O:1602:VAL:HG23	2.10	0.51
3:O:1989:ASN:OD1	3:O:1990:ALA:N	2.42	0.51
9:U:1128:VAL:HG11	9:U:1170:THR:O	2.10	0.51
11:W:50:GLU:O	11:W:54:LEU:HD13	2.10	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:419:HIS:O	3:A:422:SER:OG	2.22	0.51
3:A:1507:GLU:OE2	3:A:1511:LYS:NZ	2.43	0.51
9:C:191:ILE:HD11	9:C:343:VAL:HG22	1.92	0.51
9:C:532:ARG:NH1	9:C:565:GLN:OE1	2.40	0.51
1:B:11:ASP:O	1:B:54:ARG:NH2	2.41	0.51
3:A:1464:ASP:OD1	3:A:1480:ARG:NE	2.44	0.51
9:C:49:TRP:NE1	9:C:502:ASP:OD2	2.43	0.51
4:D:103:MET:SD	4:D:151:LEU:HD21	2.50	0.51
10:E:154:LEU:HD23	10:E:154:LEU:O	2.11	0.51
9:U:532:ARG:NH1	9:U:565:GLN:OE1	2.40	0.51
3:O:412:TYR:O	3:O:416:THR:HG22	2.11	0.51
4:P:231:ILE:HG22	4:P:235:ILE:HD12	1.91	0.51
10:V:65:LEU:O	10:V:140:LEU:HD12	2.09	0.51
4:D:191:LEU:HD11	4:D:203:VAL:CG1	2.40	0.51
5:G:88:ASN:O	5:G:89:LEU:HD23	2.10	0.51
12:I:29:SER:OG	12:I:34:GLU:OE1	2.26	0.51
3:O:87:ILE:CD1	3:O:122:VAL:HG23	2.40	0.51
3:O:455:VAL:O	3:O:458:ILE:HG22	2.10	0.51
12:X:29:SER:OG	12:X:34:GLU:OE1	2.26	0.51
3:A:87:ILE:CD1	3:A:122:VAL:HG23	2.41	0.51
3:A:684:ASP:OD1	3:A:685:ALA:N	2.44	0.51
2:N:61:THR:HG22	2:N:74:TYR:CE2	2.45	0.51
3:O:2218:LYS:O	3:O:2322:ARG:NH1	2.43	0.51
3:O:2278:LEU:HD23	3:O:2282:GLN:HB3	1.92	0.51
9:U:191:ILE:HD11	9:U:343:VAL:HG22	1.91	0.51
9:U:1041:ALA:HB2	9:U:1073:MET:SD	2.51	0.51
3:A:714:THR:HG23	3:A:717:ARG:NH2	2.25	0.51
3:O:2536:GLU:OE1	3:O:2536:GLU:N	2.35	0.51
9:U:1240:ASP:OD2	9:U:1242:ARG:NH2	2.44	0.51
3:A:412:TYR:O	3:A:416:THR:HG22	2.10	0.51
3:A:1989:ASN:OD1	3:A:1990:ALA:N	2.44	0.51
3:O:479:ASP:OD1	3:O:482:VAL:HG23	2.11	0.51
5:Q:7:LEU:HD21	5:Q:24:LEU:HD12	1.92	0.51
9:U:145:ARG:NH2	9:U:339:GLN:OE1	2.44	0.51
9:U:1190:ILE:HD11	9:U:1214:VAL:HG21	1.93	0.51
3:A:447:GLU:OE1	3:A:447:GLU:N	2.44	0.51
3:A:2378:ARG:NH2	3:A:2545:TRP:O	2.44	0.51
3:O:1759:LEU:CD2	3:O:1772:VAL:HG21	2.41	0.51
3:A:435:GLN:OE1	3:A:481:THR:HG23	2.11	0.50
9:U:802:VAL:HG21	10:V:257:GLU:OE1	2.11	0.50
1:B:131:ILE:HG22	1:B:132:ASN:O	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1122:PHE:HZ	3:A:1139:VAL:HG11	1.77	0.50
3:A:2278:LEU:HD23	3:A:2282:GLN:HB3	1.92	0.50
9:C:114:GLN:O	9:C:119:TYR:OH	2.19	0.50
9:C:802:VAL:HG21	10:E:257:GLU:OE1	2.11	0.50
9:C:1262:HIS:NE2	9:C:1313:TRP:O	2.42	0.50
3:A:42:LYS:NZ	3:A:45:GLN:OE1	2.28	0.50
3:A:457:ASP:OD1	3:A:458:ILE:N	2.44	0.50
3:A:2074:TYR:CD2	3:A:2107:VAL:HG23	2.47	0.50
5:G:7:LEU:HD21	5:G:24:LEU:HD12	1.93	0.50
5:G:48:ILE:HD11	10:E:354:TYR:CD2	2.46	0.50
3:O:531:LEU:O	3:O:535:ILE:HD12	2.12	0.50
5:Q:48:ILE:HD11	10:V:354:TYR:CD2	2.46	0.50
3:A:2218:LYS:O	3:A:2322:ARG:NH1	2.44	0.50
9:C:145:ARG:NH2	9:C:339:GLN:OE1	2.45	0.50
11:F:111:LEU:HD23	12:I:64:LYS:C	2.37	0.50
5:Q:48:ILE:HD11	10:V:354:TYR:CE2	2.47	0.50
10:V:154:LEU:HD23	10:V:154:LEU:O	2.11	0.50
2:L:61:THR:HG22	2:L:74:TYR:CE2	2.47	0.50
3:A:1136:LEU:HD23	3:A:1173:ALA:HA	1.93	0.50
9:C:825:GLU:O	9:C:829:VAL:HG23	2.12	0.50
9:C:1044:ASP:O	9:C:1061:HIS:ND1	2.43	0.50
10:E:288:MET:CG	10:E:318:ILE:HD12	2.41	0.50
3:O:1619:TRP:O	3:O:1640:ARG:NH2	2.45	0.50
4:D:224:ASP:O	4:D:227:ARG:NH1	2.40	0.50
9:C:480:LEU:HD21	9:C:495:TRP:CD1	2.46	0.50
3:O:447:GLU:N	3:O:447:GLU:OE1	2.44	0.50
3:O:1464:ASP:OD1	3:O:1480:ARG:NE	2.44	0.50
5:Q:108:ALA:O	5:Q:112:VAL:HG23	2.11	0.50
9:U:106:LEU:HD11	9:U:264:THR:CG2	2.41	0.50
2:L:38:THR:N	13:L:201:GSP:O3G	2.45	0.50
3:A:531:LEU:O	3:A:535:ILE:HD12	2.12	0.50
9:C:106:LEU:HD11	9:C:264:THR:CG2	2.42	0.50
1:M:131:ILE:HG22	1:M:132:ASN:O	2.12	0.50
9:U:480:LEU:HD21	9:U:495:TRP:CD1	2.46	0.50
2:L:130:SER:OG	2:L:133:GLU:OE1	2.18	0.50
3:O:664:ILE:CG2	3:O:698:VAL:HG11	2.42	0.50
9:U:55:MET:O	9:U:339:GLN:NE2	2.44	0.50
9:U:1044:ASP:O	9:U:1061:HIS:ND1	2.43	0.50
3:A:1666:LEU:HD21	3:A:1707:SER:HB3	1.94	0.49
3:O:179:VAL:O	3:O:179:VAL:HG13	2.11	0.49
3:O:959:PHE:HB2	3:O:971:VAL:HG11	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:103:MET:SD	4:P:151:LEU:HD21	2.51	0.49
11:W:123:PRO:O	12:X:92:ARG:NH1	2.44	0.49
1:B:56:MET:HE2	1:B:78:ILE:HD11	1.94	0.49
3:A:1423:LEU:HD23	3:A:2314:PHE:CE2	2.47	0.49
10:E:230:SER:HA	10:E:268:ILE:HG23	1.94	0.49
11:W:111:LEU:HD23	12:X:64:LYS:C	2.37	0.49
9:C:654:ASP:OD1	9:C:655:GLY:N	2.46	0.49
9:C:1041:ALA:HB2	9:C:1073:MET:SD	2.51	0.49
10:E:310:TYR:OH	10:E:335:LEU:O	2.30	0.49
3:O:268:LEU:HD13	3:O:373:VAL:HG23	1.94	0.49
3:O:657:SER:O	3:O:661:VAL:HG23	2.12	0.49
3:O:875:GLU:O	3:O:881:ARG:NH1	2.46	0.49
3:O:1423:LEU:HD23	3:O:2314:PHE:CE2	2.47	0.49
9:U:49:TRP:NE1	9:U:502:ASP:OD2	2.42	0.49
2:L:19:LYS:O	2:L:23:THR:HG23	2.13	0.49
4:D:183:ASN:ND2	4:D:300:LEU:O	2.46	0.49
3:O:1162:THR:CG2	3:O:1169:LEU:HD22	2.43	0.49
3:O:2264:GLU:HG3	3:O:2294:THR:HG21	1.95	0.49
3:A:1068:LYS:NZ	3:A:1106:ASN:O	2.36	0.49
3:A:1153:SER:OG	3:O:698:VAL:HG13	2.13	0.49
9:C:55:MET:O	9:C:339:GLN:NE2	2.44	0.49
9:C:1240:ASP:OD2	9:C:1242:ARG:NH2	2.46	0.49
3:O:1666:LEU:HD21	3:O:1707:SER:HB3	1.94	0.49
3:O:1701:MET:HE3	3:O:1717:MET:CE	2.43	0.49
9:U:1048:PHE:O	9:U:1057:LEU:N	2.46	0.49
9:C:151:ASN:ND2	9:C:195:ASP:OD2	2.46	0.49
9:C:1190:ILE:HD11	9:C:1214:VAL:HG21	1.94	0.49
3:O:419:HIS:O	3:O:422:SER:OG	2.23	0.49
3:O:2074:TYR:CD2	3:O:2107:VAL:HG23	2.47	0.49
3:O:2378:ARG:NH2	3:O:2545:TRP:O	2.44	0.49
3:A:959:PHE:HB2	3:A:971:VAL:HG11	1.94	0.49
3:A:1119:VAL:HG22	3:A:1155:ILE:HG22	1.94	0.49
9:C:1209:GLU:OE1	9:C:1237:ARG:NH1	2.45	0.49
10:V:288:MET:CG	10:V:318:ILE:HD12	2.43	0.49
3:A:1401:GLU:HB3	3:A:2389:VAL:HG11	1.95	0.49
4:D:202:GLU:OE1	10:E:299:TYR:OH	2.20	0.49
5:G:48:ILE:HD11	10:E:354:TYR:CE2	2.47	0.49
7:J:80:ASP:OD1	7:J:81:GLY:N	2.46	0.49
10:E:246:LEU:HD23	10:E:249:ILE:HD11	1.94	0.49
3:O:2083:GLU:OE2	3:O:2086:ARG:NH1	2.46	0.49
3:A:741:LEU:O	3:A:782:LYS:NZ	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2083:GLU:OE2	3:A:2086:ARG:NH1	2.46	0.49
6:H:44:ALA:O	6:H:45:LEU:HD22	2.13	0.49
9:C:78:THR:HG22	3:O:1026:HIS:ND1	2.28	0.49
10:E:63:ARG:NH2	10:E:137:THR:OG1	2.46	0.49
3:A:799:LEU:HD11	3:A:827:MET:SD	2.53	0.48
1:M:56:MET:HE2	1:M:78:ILE:HD11	1.94	0.48
3:O:1097:LEU:HB3	3:O:1138:THR:HG21	1.95	0.48
3:O:1401:GLU:HB3	3:O:2389:VAL:HG11	1.95	0.48
5:Q:47:ALA:O	5:Q:50:SER:OG	2.23	0.48
9:U:114:GLN:O	9:U:119:TYR:OH	2.17	0.48
9:U:825:GLU:O	9:U:829:VAL:HG23	2.13	0.48
10:V:76:SER:OG	18:V:401:GDP:O1A	2.22	0.48
10:V:228:ALA:O	10:V:232:VAL:HG23	2.13	0.48
11:W:115:PRO:HG2	12:X:9:LEU:HD21	1.95	0.48
3:A:179:VAL:O	3:A:179:VAL:HG13	2.12	0.48
11:F:111:LEU:HD21	12:I:63:PHE:CD1	2.49	0.48
9:U:1222:ARG:NH1	9:U:1266:ASP:OD1	2.46	0.48
3:A:218:ILE:HD13	3:A:274:ILE:HD13	1.95	0.48
3:A:1701:MET:HE3	3:A:1717:MET:CE	2.43	0.48
6:H:26:ASP:OD1	6:H:26:ASP:N	2.47	0.48
9:C:923:PHE:HD1	10:E:224:SER:HB3	1.77	0.48
3:O:435:GLN:OE1	3:O:481:THR:HG23	2.13	0.48
3:A:758:GLY:HA2	3:A:801:THR:HG23	1.93	0.48
3:A:2264:GLU:HG3	3:A:2294:THR:HG21	1.95	0.48
11:F:115:PRO:HG2	12:I:9:LEU:HD21	1.95	0.48
9:U:649:ALA:HB1	9:U:814:VAL:HG21	1.95	0.48
10:V:165:TYR:CD2	10:V:208:LEU:HD22	2.49	0.48
3:A:875:GLU:O	3:A:881:ARG:NH1	2.46	0.48
9:C:1048:PHE:O	9:C:1057:LEU:N	2.46	0.48
3:O:31:SER:O	3:O:37:ARG:NE	2.46	0.48
7:S:6:GLU:OE1	7:S:34:ARG:NH2	2.46	0.48
11:W:111:LEU:HD21	12:X:63:PHE:CD1	2.49	0.48
4:D:181:ILE:HD12	4:D:181:ILE:H	1.78	0.48
4:D:252:MET:HG3	10:E:318:ILE:HG12	1.95	0.48
1:M:106:ASP:OD1	1:M:108:THR:OG1	2.27	0.48
3:O:2201:LEU:HD23	3:O:2334:LEU:HD13	1.95	0.48
6:R:26:ASP:OD1	6:R:26:ASP:N	2.46	0.48
9:U:654:ASP:OD1	9:U:655:GLY:N	2.46	0.48
10:V:230:SER:HA	10:V:268:ILE:HG23	1.94	0.48
3:A:657:SER:O	3:A:661:VAL:HG23	2.13	0.48
9:C:1205:MET:HE1	9:C:1207:TYR:CZ	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:141:ILE:HD11	10:E:232:VAL:HG21	1.96	0.48
2:N:19:LYS:O	2:N:23:THR:HG23	2.13	0.48
3:O:1428:ALA:O	3:O:1432:VAL:HG23	2.14	0.48
7:S:80:ASP:OD1	7:S:81:GLY:N	2.46	0.48
9:U:252:LEU:HD13	9:U:357:MET:HE1	1.94	0.48
3:A:1016:LEU:O	3:A:1020:VAL:HG23	2.14	0.48
3:A:1619:TRP:O	3:A:1640:ARG:NH2	2.45	0.48
3:O:218:ILE:HD13	3:O:274:ILE:HD13	1.94	0.48
3:O:457:ASP:OD1	3:O:458:ILE:N	2.47	0.48
7:S:64:VAL:HG13	12:X:69:VAL:CG1	2.44	0.48
3:A:31:SER:O	3:A:37:ARG:NE	2.47	0.48
3:A:415:ASP:OD1	3:A:416:THR:N	2.47	0.48
3:A:2201:LEU:HD23	3:A:2334:LEU:HD13	1.95	0.48
9:C:285:SER:C	9:C:286:LEU:HD22	2.39	0.48
3:O:2051:LEU:HD13	3:O:2054:LEU:HD12	1.96	0.48
6:R:44:ALA:O	6:R:45:LEU:HD22	2.13	0.48
10:V:63:ARG:NH2	10:V:137:THR:OG1	2.47	0.48
10:V:246:LEU:HD23	10:V:249:ILE:HD11	1.96	0.48
1:B:44:GLN:NE2	1:B:46:ASN:OD1	2.43	0.48
3:A:656:LEU:HD13	3:A:683:PHE:CD1	2.48	0.48
7:J:64:VAL:HG13	12:I:69:VAL:CG1	2.44	0.48
9:C:1222:ARG:NH1	9:C:1266:ASP:OD1	2.46	0.48
3:O:1505:ASN:O	3:O:1509:GLN:N	2.42	0.48
9:U:1071:THR:OG1	9:U:1127:MET:O	2.28	0.48
1:M:166:ILE:HG23	1:M:166:ILE:O	2.13	0.47
3:O:1043:VAL:HG23	3:O:1045:ASN:OD1	2.15	0.47
3:O:2322:ARG:O	3:O:2326:VAL:HG23	2.14	0.47
4:P:183:ASN:ND2	4:P:300:LEU:O	2.46	0.47
1:B:166:ILE:HG23	1:B:166:ILE:O	2.14	0.47
3:A:967:HIS:O	3:A:971:VAL:HG23	2.14	0.47
9:C:649:ALA:HB1	9:C:814:VAL:HG21	1.96	0.47
11:F:123:PRO:O	12:I:92:ARG:NH1	2.44	0.47
1:M:44:GLN:NE2	1:M:46:ASN:OD1	2.43	0.47
3:O:1016:LEU:O	3:O:1020:VAL:HG23	2.14	0.47
3:O:1673:LEU:HD12	3:O:1703:ASN:HD22	1.80	0.47
9:U:1205:MET:HE1	9:U:1207:TYR:CZ	2.48	0.47
3:A:1282:GLU:OE2	3:A:1285:ARG:NH1	2.47	0.47
4:P:93:ASP:OD1	4:P:94:VAL:N	2.47	0.47
3:A:1428:ALA:O	3:A:1432:VAL:HG23	2.14	0.47
2:N:65:ASP:OD1	2:N:68:SER:N	2.48	0.47
3:O:799:LEU:HD11	3:O:827:MET:SD	2.54	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1153:SER:OG	3:O:698:VAL:HG22	2.14	0.47
9:C:59:SER:OG	9:C:146:VAL:HG23	2.14	0.47
9:C:566:LEU:HD23	9:C:577:VAL:HG23	1.97	0.47
3:O:222:GLN:NE2	3:O:357:VAL:HG11	2.29	0.47
3:A:582:ILE:O	3:A:586:LEU:HD23	2.15	0.47
9:C:1071:THR:OG1	9:C:1127:MET:O	2.29	0.47
10:E:76:SER:OG	18:E:401:GDP:H5''	2.15	0.47
4:P:181:ILE:HD12	4:P:181:ILE:H	1.79	0.47
2:L:152:GLU:O	2:L:155:THR:N	2.39	0.47
3:A:1552:LEU:HD12	3:A:1560:ALA:HB1	1.97	0.47
3:A:1673:LEU:HD12	3:A:1703:ASN:HD22	1.79	0.47
3:A:2338:ASP:OD2	3:A:2343:ASN:ND2	2.47	0.47
4:D:176:ILE:O	4:D:180:LEU:HD23	2.15	0.47
5:G:116:GLU:O	5:G:120:THR:OG1	2.23	0.47
2:N:83:LEU:C	2:N:96:ILE:HD11	2.39	0.47
3:O:582:ILE:O	3:O:586:LEU:HD23	2.15	0.47
3:O:2291:VAL:HG13	3:O:2381:ARG:HD2	1.96	0.47
9:U:1178:ARG:NH2	9:U:1220:GLN:O	2.48	0.47
10:V:64:ILE:HG23	10:V:141:ILE:CD1	2.45	0.47
3:A:2322:ARG:O	3:A:2326:VAL:HG23	2.14	0.47
6:H:16:VAL:HG12	6:H:19:LEU:HD23	1.97	0.47
3:O:1660:CYS:SG	3:O:1668:LEU:HD22	2.55	0.47
7:S:12:THR:HG22	7:S:18:ILE:HG21	1.97	0.47
10:V:288:MET:HG2	10:V:318:ILE:HD12	1.95	0.47
1:M:255:MET:O	1:M:256:THR:OG1	2.31	0.47
2:N:76:ILE:O	3:O:112:ARG:NH1	2.48	0.47
4:P:93:ASP:O	4:P:144:ARG:NH2	2.47	0.47
9:U:1262:HIS:NE2	9:U:1313:TRP:O	2.40	0.47
3:A:479:ASP:OD1	3:A:482:VAL:HG23	2.14	0.47
3:A:608:ASP:O	3:A:612:ASN:ND2	2.44	0.47
3:A:664:ILE:CD1	3:A:699:ALA:HB2	2.45	0.47
3:A:2291:VAL:HG13	3:A:2381:ARG:HD2	1.96	0.47
12:I:32:ASP:OD1	12:I:33:LEU:N	2.47	0.47
3:O:146:GLU:OE2	3:O:1286:ARG:NH2	2.48	0.47
3:O:258:ASP:OD2	3:O:258:ASP:N	2.48	0.47
6:R:16:VAL:HG12	6:R:19:LEU:HD23	1.97	0.47
9:U:59:SER:OG	9:U:146:VAL:HG23	2.15	0.47
10:V:310:TYR:OH	10:V:335:LEU:O	2.30	0.47
10:E:288:MET:HE2	10:E:326:LEU:HB3	1.97	0.46
3:O:210:VAL:HG21	3:O:266:LEU:HB3	1.96	0.46
3:O:2512:ASP:OD1	3:O:2512:ASP:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:V:288:MET:HE2	10:V:326:LEU:HB3	1.96	0.46
3:A:532:LYS:NZ	3:A:595:GLU:OE2	2.48	0.46
3:A:1660:CYS:SG	3:A:1668:LEU:HD22	2.55	0.46
9:C:215:GLN:O	9:C:219:VAL:HG23	2.15	0.46
2:N:17:VAL:HG13	2:N:19:LYS:HG3	1.96	0.46
2:N:152:GLU:O	2:N:155:THR:N	2.40	0.46
3:O:776:LEU:O	3:O:780:ILE:HG13	2.15	0.46
3:O:967:HIS:O	3:O:971:VAL:HG23	2.15	0.46
4:P:87:VAL:HG21	4:P:180:LEU:CD2	2.43	0.46
9:U:566:LEU:HD23	9:U:577:VAL:HG23	1.97	0.46
2:L:65:ASP:OD1	2:L:68:SER:N	2.48	0.46
3:A:772:MET:HG2	3:A:805:LEU:HD11	1.98	0.46
2:N:38:THR:N	13:N:201:GSP:O3G	2.49	0.46
3:O:823:ILE:HG22	3:O:827:MET:HE3	1.98	0.46
3:O:1132:ARG:O	3:O:1136:LEU:HD23	2.16	0.46
3:A:20:SER:O	3:A:24:GLN:OE1	2.33	0.46
3:A:222:GLN:NE2	3:A:357:VAL:HG11	2.31	0.46
3:A:258:ASP:OD2	3:A:258:ASP:N	2.48	0.46
3:A:1505:ASN:O	3:A:1509:GLN:N	2.43	0.46
4:D:130:ASP:CG	17:D:401:GTP:HN1	2.24	0.46
10:E:244:GLU:O	10:E:248:ASN:ND2	2.48	0.46
11:F:99:LEU:O	11:F:100:THR:OG1	2.24	0.46
3:O:2338:ASP:OD2	3:O:2343:ASN:ND2	2.48	0.46
9:U:215:GLN:O	9:U:219:VAL:HG23	2.15	0.46
3:A:55:MET:HE2	3:A:59:GLU:HG2	1.97	0.46
3:A:531:LEU:H	3:A:531:LEU:HD23	1.81	0.46
3:A:2121:LEU:HD13	3:A:2162:VAL:HG21	1.97	0.46
5:G:121:GLN:NE2	5:G:122:VAL:HG23	2.30	0.46
7:J:12:THR:HG22	7:J:18:ILE:HG21	1.96	0.46
3:O:1068:LYS:NZ	3:O:1106:ASN:O	2.32	0.46
9:U:819:ALA:HA	9:U:830:ALA:HB3	1.97	0.46
2:L:76:ILE:O	3:A:112:ARG:NH1	2.48	0.46
3:O:415:ASP:OD1	3:O:416:THR:N	2.48	0.46
3:O:734:LEU:HD11	3:O:775:ILE:HD11	1.96	0.46
3:O:760:LEU:HG	3:O:768:ILE:HD11	1.97	0.46
3:O:2205:VAL:HG22	3:O:2407:LEU:HD21	1.97	0.46
9:U:476:VAL:HG23	9:U:495:TRP:CZ2	2.51	0.46
2:L:83:LEU:C	2:L:96:ILE:HD11	2.40	0.46
2:L:115:MET:CE	2:L:159:VAL:HG23	2.45	0.46
3:A:823:ILE:HG22	3:A:827:MET:HE3	1.98	0.46
6:H:80:VAL:HG22	6:H:93:ILE:HG12	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:E:288:MET:HG2	10:E:318:ILE:HD12	1.96	0.46
3:O:55:MET:HE2	3:O:59:GLU:HG2	1.96	0.46
3:O:1282:GLU:OE2	3:O:1285:ARG:NH1	2.49	0.46
4:P:9:LYS:NZ	4:P:81:ILE:O	2.45	0.46
9:U:923:PHE:HD1	10:V:224:SER:HB3	1.80	0.46
3:A:1676:LEU:HD22	3:A:1696:VAL:HG21	1.97	0.46
3:A:1786:TRP:CE3	3:A:1789:ALA:HB2	2.51	0.46
4:D:9:LYS:NZ	4:D:81:ILE:O	2.46	0.46
4:D:93:ASP:OD1	4:D:94:VAL:N	2.47	0.46
4:D:93:ASP:O	4:D:144:ARG:NH2	2.48	0.46
4:D:106:TYR:CE1	4:D:110:LEU:HD21	2.51	0.46
10:E:165:TYR:CD2	10:E:208:LEU:HD22	2.50	0.46
3:O:87:ILE:HD13	3:O:122:VAL:HG23	1.98	0.46
9:U:809:THR:HG22	9:U:813:ARG:NH1	2.31	0.46
10:V:244:GLU:O	10:V:248:ASN:ND2	2.49	0.46
3:A:1704:MET:SD	3:A:1713:ALA:HB2	2.56	0.46
9:C:624:GLY:O	9:C:627:VAL:HG22	2.16	0.46
10:E:165:TYR:CE2	10:E:208:LEU:HD22	2.51	0.46
3:O:2204:LEU:HD22	3:O:2417:VAL:HG21	1.98	0.46
1:M:231:ASP:OD2	1:M:282:SER:OG	2.34	0.46
2:N:10:ALA:HB2	2:N:78:ILE:HD12	1.98	0.46
3:O:1704:MET:SD	3:O:1713:ALA:HB2	2.56	0.46
3:O:2058:MET:SD	3:O:2058:MET:N	2.89	0.46
9:U:1031:PHE:CE2	9:U:1317:ALA:HB2	2.51	0.46
3:A:1031:MET:HE3	3:A:1035:VAL:CG1	2.46	0.45
9:C:476:VAL:HG23	9:C:495:TRP:CZ2	2.51	0.45
9:C:1030:LYS:NZ	9:C:1073:MET:O	2.42	0.45
3:O:1338:ILE:HG23	3:O:1374:LEU:HA	1.98	0.45
3:O:2121:LEU:HD13	3:O:2162:VAL:HG21	1.97	0.45
4:P:176:ILE:O	4:P:180:LEU:HD23	2.15	0.45
12:X:32:ASP:OD1	12:X:33:LEU:N	2.47	0.45
2:L:23:THR:HG21	2:L:60:ASP:HB2	1.98	0.45
3:A:98:GLY:O	3:A:103:ARG:NH1	2.48	0.45
3:A:286:MET:HG3	3:A:488:MET:HE1	1.98	0.45
3:A:2205:VAL:HG22	3:A:2407:LEU:HD21	1.97	0.45
3:O:532:LYS:NZ	3:O:595:GLU:OE2	2.48	0.45
3:O:2427:LEU:HD13	3:O:2500:ILE:HD13	1.98	0.45
9:U:1180:LEU:C	9:U:1181:ILE:HD13	2.41	0.45
9:C:276:ARG:HG2	9:C:280:MET:HE1	1.97	0.45
9:C:441:LEU:HD21	9:C:475:TYR:CE2	2.51	0.45
9:C:685:PHE:HE1	9:C:779:LEU:HD21	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
9:C:1050:ASP:O	9:C:1054:GLY:N	2.46	0.45
9:U:441:LEU:HD21	9:U:475:TYR:CE2	2.52	0.45
9:U:796:LEU:O	9:U:796:LEU:HD12	2.17	0.45
2:L:17:VAL:HG13	2:L:19:LYS:HG3	1.97	0.45
3:A:87:ILE:HD13	3:A:122:VAL:HG23	1.99	0.45
3:A:654:ASP:OD1	3:A:655:VAL:N	2.49	0.45
3:A:1608:VAL:O	3:A:1608:VAL:HG23	2.17	0.45
9:C:809:THR:HG22	9:C:813:ARG:NH1	2.30	0.45
9:C:1178:ARG:NH2	9:C:1220:GLN:O	2.48	0.45
10:E:139:ALA:CB	10:E:236:LEU:HD11	2.47	0.45
3:O:611:LEU:HD22	3:O:662:VAL:HG21	1.98	0.45
3:O:2275:TYR:HA	3:O:2278:LEU:CD1	2.47	0.45
6:R:80:VAL:HG22	6:R:93:ILE:HG12	1.97	0.45
9:U:1048:PHE:HZ	9:U:1084:LEU:HD22	1.82	0.45
3:A:737:ILE:HG21	3:A:757:LEU:HB2	1.99	0.45
3:A:1424:GLN:OE1	3:A:1424:GLN:N	2.50	0.45
10:E:228:ALA:O	10:E:232:VAL:HG23	2.16	0.45
1:B:270:ARG:HA	1:B:270:ARG:NE	2.32	0.45
3:A:2204:LEU:HD22	3:A:2417:VAL:HG21	1.99	0.45
4:D:87:VAL:HG21	4:D:180:LEU:CD2	2.43	0.45
9:C:384:LEU:O	9:C:388:ILE:HG13	2.16	0.45
9:C:422:MET:SD	9:C:422:MET:N	2.89	0.45
9:C:1180:LEU:C	9:C:1181:ILE:HD13	2.41	0.45
3:O:814:ARG:O	3:O:817:VAL:HG12	2.16	0.45
3:O:2260:LEU:HD23	3:O:2260:LEU:H	1.81	0.45
3:A:998:LEU:HD12	3:A:1033:GLU:OE1	2.17	0.45
3:A:1043:VAL:HG23	3:A:1045:ASN:OD1	2.16	0.45
9:C:45:LEU:HD23	9:C:45:LEU:H	1.82	0.45
2:N:23:THR:HG21	2:N:60:ASP:HB2	1.98	0.45
3:O:20:SER:O	3:O:24:GLN:OE1	2.33	0.45
3:O:286:MET:HG3	3:O:488:MET:HE1	1.98	0.45
3:O:1315:ARG:NH2	3:O:1356:THR:OG1	2.50	0.45
3:O:1423:LEU:HD23	3:O:2314:PHE:CZ	2.52	0.45
9:U:45:LEU:H	9:U:45:LEU:HD23	1.82	0.45
9:U:203:VAL:HG23	9:U:244:ALA:HB2	1.99	0.45
11:W:91:ARG:O	11:W:95:LEU:HD23	2.17	0.45
3:A:776:LEU:O	3:A:780:ILE:HG13	2.16	0.45
5:Q:105:LYS:CG	7:S:29:LEU:HD22	2.47	0.45
1:B:63:GLN:HA	1:B:84:VAL:HG13	1.99	0.45
4:D:238:PHE:CZ	10:E:318:ILE:HD13	2.51	0.45
9:C:1031:PHE:CE2	9:C:1317:ALA:HB2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:20:SER:OG	2:N:38:THR:HG21	2.16	0.45
3:O:33:ASN:OD1	3:O:36:THR:N	2.46	0.45
3:O:1676:LEU:HD22	3:O:1696:VAL:HG21	1.98	0.45
3:O:2046:GLY:O	3:O:2050:VAL:HG12	2.16	0.45
3:O:2244:ASP:OD2	3:O:2348:ARG:NE	2.50	0.45
3:A:1315:ARG:NH2	3:A:1356:THR:OG1	2.50	0.45
3:O:1972:LEU:HG	3:O:1976:LEU:HD12	1.99	0.45
3:O:2377:PHE:HE1	3:O:2379:LEU:HD22	1.82	0.45
9:U:592:ARG:NE	9:U:626:PHE:O	2.49	0.45
3:A:732:LYS:NZ	3:O:1150:ASP:OD2	2.47	0.44
3:A:938:MET:HE3	3:A:941:LEU:HB2	1.99	0.44
3:A:2377:PHE:HE1	3:A:2379:LEU:HD22	1.82	0.44
1:B:231:ASP:OD2	1:B:282:SER:OG	2.34	0.44
2:L:10:ALA:HB2	2:L:78:ILE:HD12	1.99	0.44
3:A:1905:ARG:O	3:A:1909:LEU:HD23	2.18	0.44
3:A:2244:ASP:OD2	3:A:2348:ARG:NE	2.50	0.44
3:A:2275:TYR:HA	3:A:2278:LEU:CD1	2.47	0.44
9:C:592:ARG:NE	9:C:626:PHE:O	2.50	0.44
6:R:19:LEU:HG	6:R:103:ILE:HD11	1.99	0.44
9:U:63:VAL:HG13	9:U:125:PRO:HG3	2.00	0.44
3:A:138:ASP:OD1	3:A:138:ASP:N	2.48	0.44
3:A:1323:VAL:HG21	3:A:1363:PHE:HE2	1.82	0.44
3:A:2427:LEU:HD13	3:A:2500:ILE:HD13	1.98	0.44
6:H:19:LEU:HD22	6:H:94:ALA:HB2	2.00	0.44
9:C:819:ALA:HA	9:C:830:ALA:HB3	2.00	0.44
3:O:1424:GLN:N	3:O:1424:GLN:OE1	2.50	0.44
3:A:2204:LEU:HD22	3:A:2417:VAL:CG2	2.48	0.44
3:O:282:LEU:HD13	3:O:442:VAL:HG11	2.00	0.44
3:O:1786:TRP:CE3	3:O:1789:ALA:HB2	2.52	0.44
10:V:165:TYR:CE2	10:V:208:LEU:HD22	2.52	0.44
3:A:971:VAL:HG22	3:A:1306:LEU:CD2	2.47	0.44
3:O:971:VAL:HG22	3:O:1306:LEU:CD2	2.47	0.44
9:C:63:VAL:HG13	9:C:125:PRO:HG3	1.99	0.44
3:O:303:LEU:HD22	3:O:579:VAL:HG12	1.98	0.44
5:Q:105:LYS:HG3	7:S:29:LEU:HD22	1.99	0.44
9:U:60:VAL:HB	9:U:119:TYR:HD1	1.83	0.44
1:B:106:ASP:OD1	1:B:108:THR:OG1	2.32	0.44
1:B:255:MET:O	1:B:256:THR:OG1	2.31	0.44
4:D:195:ALA:HB2	4:D:203:VAL:HG21	2.00	0.44
2:N:135:LYS:O	2:N:138:ALA:N	2.50	0.44
3:O:654:ASP:OD1	3:O:655:VAL:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:1198:VAL:O	3:O:1202:HIS:ND1	2.42	0.44
6:R:19:LEU:HD22	6:R:94:ALA:HB2	1.99	0.44
9:U:327:VAL:HG12	9:U:371:PRO:HG2	1.99	0.44
1:B:164:GLN:C	1:B:165:LEU:HD22	2.43	0.44
9:C:252:LEU:HD13	9:C:357:MET:HE1	2.00	0.44
9:C:1048:PHE:HZ	9:C:1084:LEU:HD22	1.82	0.44
1:M:9:GLY:N	1:M:70:LEU:O	2.51	0.44
1:M:92:GLY:N	1:M:101:TYR:O	2.51	0.44
1:M:257:GLU:C	1:M:258:LEU:HD22	2.43	0.44
3:O:690:ALA:HB2	3:O:725:PHE:HE2	1.82	0.44
3:O:1323:VAL:HG21	3:O:1363:PHE:HE2	1.82	0.44
9:U:328:LEU:HD23	9:U:371:PRO:HD2	1.99	0.44
10:V:67:MET:CG	10:V:140:LEU:HD11	2.44	0.44
10:V:183:LEU:O	10:V:188:LYS:NZ	2.45	0.44
11:W:61:THR:O	11:W:64:ASN:N	2.50	0.44
3:A:55:MET:HE2	3:A:59:GLU:CG	2.47	0.44
3:A:1338:ILE:HG23	3:A:1374:LEU:HA	1.99	0.44
3:A:1972:LEU:HG	3:A:1976:LEU:HD12	1.99	0.44
3:A:2260:LEU:HD23	3:A:2260:LEU:H	1.82	0.44
3:A:2512:ASP:OD1	3:A:2512:ASP:N	2.48	0.44
4:D:138:ASP:O	4:D:142:LYS:HD3	2.18	0.44
3:O:2221:SER:OG	3:O:2352:LYS:NZ	2.51	0.44
9:U:1197:MET:HG3	9:U:1197:MET:O	2.18	0.44
11:F:91:ARG:O	11:F:95:LEU:HD23	2.17	0.43
3:O:1608:VAL:O	3:O:1608:VAL:HG23	2.17	0.43
3:O:2172:LEU:HD21	3:O:2174:LEU:CD1	2.49	0.43
4:P:202:GLU:OE1	10:V:299:TYR:OH	2.21	0.43
9:U:827:SER:O	9:U:831:MET:HG2	2.18	0.43
3:A:543:LEU:HA	3:A:546:VAL:HG12	2.00	0.43
9:C:203:VAL:HG23	9:C:244:ALA:HB2	1.99	0.43
1:M:63:GLN:HA	1:M:84:VAL:HG13	1.99	0.43
3:O:55:MET:HE2	3:O:59:GLU:CG	2.47	0.43
3:O:2127:SER:O	3:O:2127:SER:OG	2.33	0.43
9:U:384:LEU:O	9:U:388:ILE:HG13	2.18	0.43
9:U:787:MET:HE3	9:U:790:ALA:HB3	1.99	0.43
3:A:282:LEU:CD1	3:A:442:VAL:HG11	2.45	0.43
3:A:1691:THR:HG22	3:A:1691:THR:O	2.19	0.43
5:G:102:GLY:N	7:J:30:ASN:O	2.49	0.43
6:H:68:ASN:OD1	6:H:69:LYS:N	2.51	0.43
3:O:543:LEU:HA	3:O:546:VAL:HG12	2.00	0.43
3:O:2204:LEU:HD22	3:O:2417:VAL:CG2	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:46:GLU:OE2	9:U:597:ARG:NH1	2.51	0.43
3:A:794:VAL:O	3:A:798:VAL:HG23	2.18	0.43
3:A:1933:ASP:OD1	3:A:1933:ASP:N	2.52	0.43
3:A:2221:SER:OG	3:A:2352:LYS:NZ	2.51	0.43
1:M:284:TYR:HB3	1:M:296:LEU:HD11	2.00	0.43
3:O:98:GLY:O	3:O:103:ARG:NH1	2.52	0.43
3:O:115:LEU:HD12	3:O:167:ALA:HB1	2.00	0.43
3:O:1376:ASP:OD1	3:O:1376:ASP:N	2.51	0.43
9:U:499:LEU:HB3	9:U:541:VAL:HG11	2.01	0.43
9:U:810:GLN:O	9:U:814:VAL:HG23	2.18	0.43
1:B:9:GLY:N	1:B:70:LEU:O	2.52	0.43
1:B:284:TYR:HB3	1:B:296:LEU:HD11	2.00	0.43
2:N:8:LYS:HD2	2:N:78:ILE:HD13	2.00	0.43
3:O:455:VAL:O	3:O:459:ILE:HG13	2.18	0.43
3:O:1045:ASN:OD1	3:O:1048:ILE:HG22	2.19	0.43
3:O:1277:LYS:O	3:O:1281:LEU:HD23	2.18	0.43
3:O:1905:ARG:O	3:O:1909:LEU:HD23	2.19	0.43
3:O:1911:PHE:CG	3:O:1945:ARG:HD3	2.53	0.43
3:O:2187:LYS:NZ	15:O:3000:ANP:O1A	2.24	0.43
6:R:27:ARG:NH2	6:R:88:LEU:O	2.52	0.43
1:B:257:GLU:C	1:B:258:LEU:HD22	2.43	0.43
3:A:1376:ASP:OD1	3:A:1376:ASP:N	2.51	0.43
9:C:810:GLN:O	9:C:814:VAL:HG23	2.18	0.43
9:C:1048:PHE:CZ	9:C:1084:LEU:HD22	2.54	0.43
3:O:425:LYS:HE2	3:O:425:LYS:HA	2.00	0.43
9:U:1214:VAL:O	9:U:1214:VAL:HG13	2.18	0.43
10:V:223:HIS:HE1	10:V:282:TYR:CE2	2.37	0.43
3:A:1277:LYS:O	3:A:1281:LEU:HD23	2.18	0.43
9:C:923:PHE:CD1	10:E:224:SER:HB3	2.53	0.43
1:M:164:GLN:C	1:M:165:LEU:HD22	2.43	0.43
2:N:65:ASP:OD1	2:N:67:TYR:N	2.51	0.43
3:O:165:ARG:O	3:O:169:VAL:HG23	2.18	0.43
4:P:11:LEU:HD11	4:P:85:VAL:HG21	2.01	0.43
3:A:1262:THR:HG22	3:A:1266:GLN:OE1	2.19	0.43
3:A:2324:LEU:HD23	3:A:2387:MET:CE	2.48	0.43
6:H:16:VAL:CG1	6:H:19:LEU:HD23	2.49	0.43
3:O:935:LEU:HD22	3:O:1363:PHE:CE1	2.54	0.43
3:O:938:MET:HE3	3:O:941:LEU:HB2	1.99	0.43
3:O:1031:MET:HE3	3:O:1035:VAL:CG1	2.49	0.43
3:O:1694:PRO:HB3	3:O:1724:MET:CE	2.48	0.43
3:O:2324:LEU:HD23	3:O:2387:MET:CE	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:195:ALA:HB2	4:P:203:VAL:HG21	2.00	0.43
3:A:583:THR:HG23	3:A:621:GLU:HG3	2.00	0.43
3:A:1423:LEU:HD23	3:A:2314:PHE:CZ	2.53	0.43
4:D:67:ASP:OD1	4:D:68:THR:N	2.52	0.43
9:C:689:GLU:OE1	9:C:690:LYS:NZ	2.42	0.43
9:C:796:LEU:HD12	9:C:796:LEU:O	2.17	0.43
2:N:12:LEU:HD23	2:N:61:THR:HG21	2.01	0.43
6:R:68:ASN:OD1	6:R:69:LYS:N	2.51	0.43
9:U:1048:PHE:CZ	9:U:1084:LEU:HD22	2.54	0.43
9:U:1178:ARG:O	9:U:1180:LEU:N	2.52	0.43
3:A:146:GLU:OE2	3:A:1286:ARG:NH2	2.51	0.43
3:A:165:ARG:O	3:A:169:VAL:HG23	2.18	0.43
3:A:303:LEU:HD22	3:A:579:VAL:HG12	2.00	0.43
3:A:814:ARG:O	3:A:817:VAL:HG12	2.19	0.43
4:D:46:GLU:OE2	9:C:597:ARG:NH1	2.51	0.43
10:E:183:LEU:O	10:E:188:LYS:NZ	2.46	0.43
3:O:1514:ARG:HD2	3:O:1542:ASP:HB3	2.01	0.43
3:O:1653:TRP:HE3	3:O:1672:THR:HG23	1.84	0.43
5:Q:6:ALA:O	5:Q:10:VAL:HG23	2.19	0.43
6:R:16:VAL:CG1	6:R:19:LEU:HD23	2.48	0.43
1:B:255:MET:O	1:B:255:MET:HG2	2.19	0.42
3:A:521:LEU:HD22	3:A:535:ILE:HG23	2.01	0.42
3:A:624:ARG:O	3:A:628:ARG:HG3	2.19	0.42
3:A:1345:LEU:HD21	3:A:1357:LEU:HB3	2.01	0.42
3:A:1552:LEU:HD12	3:A:1560:ALA:CB	2.49	0.42
3:A:2308:PRO:HD2	3:A:2312:VAL:HG11	2.01	0.42
9:C:1214:VAL:O	9:C:1214:VAL:HG13	2.18	0.42
10:E:327:TYR:OH	10:E:329:LYS:NZ	2.39	0.42
3:O:1564:ILE:HG12	3:O:1599:LEU:HD23	2.01	0.42
7:S:64:VAL:HG11	11:W:129:LEU:CD1	2.42	0.42
3:A:935:LEU:HD22	3:A:1363:PHE:CE1	2.54	0.42
3:A:1653:TRP:HE3	3:A:1672:THR:HG23	1.84	0.42
3:A:2172:LEU:HD21	3:A:2174:LEU:CD1	2.49	0.42
4:D:19:GLY:HA2	17:D:401:GTP:H5"	2.01	0.42
10:V:139:ALA:CB	10:V:236:LEU:HD11	2.49	0.42
10:V:192:GLN:HB2	10:V:217:LEU:HD21	2.01	0.42
2:L:8:LYS:HD2	2:L:78:ILE:HD13	2.01	0.42
3:A:115:LEU:HD12	3:A:167:ALA:HB1	2.00	0.42
3:A:1031:MET:HE3	3:A:1035:VAL:HG13	2.01	0.42
3:A:1427:GLU:OE2	3:A:2322:ARG:NE	2.49	0.42
3:A:1784:ARG:O	3:A:1790:TRP:NE1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:2215:SER:HB2	3:A:2220:LEU:HD12	2.01	0.42
9:C:1035:THR:O	9:C:1037:CYS:N	2.52	0.42
9:C:1205:MET:HE1	9:C:1207:TYR:CE2	2.55	0.42
3:O:169:VAL:HG13	3:O:209:ALA:HA	2.01	0.42
3:O:424:VAL:HG23	3:O:425:LYS:HD2	2.01	0.42
3:O:1345:LEU:HD21	3:O:1357:LEU:HB3	2.02	0.42
9:U:1029:VAL:HG23	9:U:1306:CYS:SG	2.59	0.42
10:V:358:CYS:SG	11:W:65:ILE:HD13	2.60	0.42
3:A:33:ASN:OD1	3:A:36:THR:N	2.46	0.42
3:A:269:ASN:OD1	3:A:398:ARG:NE	2.53	0.42
3:A:690:ALA:HB2	3:A:725:PHE:HE2	1.83	0.42
5:G:86:VAL:HG12	5:G:87:ALA:N	2.34	0.42
9:C:499:LEU:HB3	9:C:541:VAL:HG11	2.01	0.42
1:M:255:MET:O	1:M:255:MET:HG2	2.20	0.42
3:O:269:ASN:OD1	3:O:398:ARG:NE	2.52	0.42
10:V:327:TYR:OH	10:V:329:LYS:NZ	2.39	0.42
12:X:75:LEU:C	12:X:76:LEU:HD12	2.45	0.42
3:A:1548:ALA:O	3:A:1552:LEU:HD13	2.20	0.42
6:H:27:ARG:NH2	6:H:88:LEU:O	2.52	0.42
9:C:184:THR:OG1	9:C:213:ARG:NH2	2.43	0.42
9:C:607:LEU:HD22	9:C:615:VAL:CG1	2.50	0.42
4:P:19:GLY:HA2	17:P:401:GTP:H5''	2.02	0.42
9:U:27:PRO:O	9:U:1133:GLN:NE2	2.47	0.42
9:U:1272:SER:OG	9:U:1273:VAL:N	2.52	0.42
1:B:224:LEU:HD23	1:B:274:TRP:CZ3	2.54	0.42
3:A:935:LEU:HD22	3:A:1363:PHE:CZ	2.54	0.42
9:C:1178:ARG:O	9:C:1180:LEU:N	2.52	0.42
3:O:44:LEU:CD2	3:O:93:LEU:HD21	2.50	0.42
3:O:680:ASP:OD1	3:O:681:GLU:N	2.46	0.42
3:O:935:LEU:HD22	3:O:1363:PHE:CZ	2.54	0.42
3:O:1691:THR:O	3:O:1691:THR:HG22	2.20	0.42
9:U:981:GLU:O	9:U:982:SER:OG	2.35	0.42
3:A:169:VAL:HG13	3:A:209:ALA:HA	2.01	0.42
3:A:2058:MET:HE3	3:A:2058:MET:HA	2.01	0.42
9:C:1301:VAL:HG22	9:C:1302:GLY:N	2.34	0.42
1:M:224:LEU:HD23	1:M:274:TRP:CZ3	2.54	0.42
3:O:531:LEU:HD23	3:O:531:LEU:H	1.84	0.42
3:O:1520:ALA:HB3	3:O:1529:MET:HG2	2.01	0.42
3:O:1546:TYR:O	3:O:1550:LEU:HD23	2.19	0.42
4:P:67:ASP:OD1	4:P:68:THR:N	2.52	0.42
2:L:16:SER:O	13:L:201:GSP:H5'1	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:11:LEU:HD11	4:D:85:VAL:HG21	2.00	0.42
5:G:6:ALA:O	5:G:10:VAL:HG23	2.19	0.42
12:I:75:LEU:C	12:I:76:LEU:HD12	2.44	0.42
3:O:1933:ASP:OD1	3:O:1933:ASP:N	2.52	0.42
9:U:646:MET:O	9:U:650:GLN:NE2	2.53	0.42
3:A:142:ALA:O	3:A:146:GLU:HG3	2.19	0.42
5:G:78:GLU:OE1	5:G:78:GLU:N	2.53	0.42
6:H:4:ASP:OD1	6:H:5:LEU:N	2.53	0.42
9:C:1197:MET:O	9:C:1197:MET:HG3	2.20	0.42
3:O:1427:GLU:OE2	3:O:2322:ARG:NE	2.49	0.42
6:R:4:ASP:OD1	6:R:5:LEU:N	2.53	0.42
9:U:624:GLY:O	9:U:627:VAL:HG22	2.20	0.42
10:V:114:ILE:HG22	10:V:115:TRP:N	2.35	0.42
3:A:410:THR:HG22	3:A:410:THR:O	2.20	0.42
3:A:1049:GLN:OE1	3:A:1092:VAL:HG11	2.20	0.42
9:C:138:ARG:HH21	9:C:146:VAL:HG12	1.85	0.42
10:E:174:GLU:CD	10:E:232:VAL:HG22	2.45	0.42
3:O:142:ALA:O	3:O:146:GLU:HG3	2.20	0.42
3:O:441:SER:CB	3:O:489:LEU:HD23	2.49	0.42
3:O:521:LEU:HD22	3:O:535:ILE:HG23	2.01	0.42
3:O:1262:THR:HG22	3:O:1266:GLN:OE1	2.19	0.42
3:O:2215:SER:HB2	3:O:2220:LEU:HD12	2.01	0.42
4:P:190:ASN:OD1	4:P:300:LEU:HD21	2.19	0.42
9:U:118:ARG:NH2	9:U:137:LEU:HD23	2.35	0.42
9:U:1301:VAL:HG22	9:U:1302:GLY:N	2.34	0.42
3:A:269:ASN:HA	3:A:395:LEU:HD13	2.02	0.41
3:A:1136:LEU:O	3:A:1139:VAL:HG12	2.20	0.41
3:A:1910:TRP:CH2	3:A:1957:ILE:HD13	2.55	0.41
9:C:327:VAL:HG12	9:C:371:PRO:CG	2.49	0.41
9:C:560:ALA:O	9:C:564:GLU:OE1	2.38	0.41
10:E:288:MET:HG3	10:E:318:ILE:HD12	2.02	0.41
10:E:358:CYS:SG	11:F:65:ILE:HD13	2.60	0.41
9:U:315:ILE:HG22	9:U:319:ILE:HD12	2.02	0.41
2:L:65:ASP:OD1	2:L:67:TYR:N	2.52	0.41
3:A:1514:ARG:HD2	3:A:1542:ASP:HB3	2.02	0.41
3:A:1907:LEU:HD11	3:A:1938:VAL:HB	2.03	0.41
9:C:53:ASP:OD1	9:C:55:MET:HE2	2.20	0.41
9:C:664:VAL:HG22	9:C:818:LEU:HD13	2.02	0.41
9:C:1029:VAL:HG23	9:C:1306:CYS:SG	2.59	0.41
1:M:221:ARG:HG3	1:M:240:ALA:HB3	2.01	0.41
3:O:624:ARG:O	3:O:628:ARG:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:2027:TRP:O	3:O:2031:LEU:HD23	2.19	0.41
5:Q:84:THR:HG22	5:Q:85:ARG:N	2.36	0.41
9:U:392:GLN:OE1	9:U:404:ARG:N	2.53	0.41
10:V:165:TYR:O	10:V:165:TYR:CD1	2.73	0.41
10:V:348:ARG:HH12	11:W:68:VAL:HG13	1.85	0.41
3:A:757:LEU:O	3:A:761:VAL:HG23	2.20	0.41
3:A:1045:ASN:OD1	3:A:1048:ILE:HG22	2.19	0.41
3:A:2085:CYS:SG	3:A:2089:MET:HE1	2.61	0.41
5:G:84:THR:HG22	5:G:85:ARG:N	2.36	0.41
3:O:269:ASN:HA	3:O:395:LEU:HD13	2.01	0.41
3:O:741:LEU:O	3:O:782:LYS:NZ	2.53	0.41
3:O:1276:SER:OG	3:O:1278:ASP:OD1	2.14	0.41
10:V:174:GLU:CD	10:V:232:VAL:HG22	2.45	0.41
1:B:221:ARG:HG3	1:B:240:ALA:HB3	2.01	0.41
2:L:66:GLU:HA	2:L:98:VAL:HG11	2.02	0.41
2:L:69:ILE:HD13	3:A:969:THR:CG2	2.50	0.41
3:A:1111:LEU:HD11	3:A:1115:LEU:HD13	2.02	0.41
9:C:476:VAL:HG11	9:C:494:ILE:HG21	2.02	0.41
9:C:646:MET:O	9:C:650:GLN:NE2	2.53	0.41
3:O:170:LEU:O	3:O:174:GLU:OE1	2.39	0.41
3:O:2210:ALA:HA	3:O:2216:LEU:HD13	2.02	0.41
9:U:550:GLN:NE2	9:U:583:ARG:O	2.54	0.41
1:B:126:GLN:OE1	1:B:126:GLN:HA	2.20	0.41
3:A:990:LEU:HD21	3:A:1023:VAL:HG21	2.01	0.41
10:E:239:GLN:O	10:E:242:THR:HG22	2.20	0.41
10:E:348:ARG:HH12	11:F:68:VAL:HG13	1.86	0.41
3:O:2308:PRO:HD2	3:O:2312:VAL:HG11	2.02	0.41
9:U:664:VAL:HG22	9:U:818:LEU:HD13	2.03	0.41
3:A:1505:ASN:OD1	3:A:1506:ASP:N	2.54	0.41
3:A:1520:ALA:HB3	3:A:1529:MET:HG2	2.01	0.41
4:D:190:ASN:OD1	4:D:300:LEU:HD21	2.20	0.41
10:E:114:ILE:HG22	10:E:115:TRP:N	2.35	0.41
2:N:16:SER:O	13:N:201:GSP:H5'1	2.20	0.41
3:O:483:PHE:HB3	3:O:520:VAL:HG21	2.01	0.41
3:O:589:LEU:HD22	3:O:629:LEU:HD11	2.01	0.41
3:O:994:MET:HE1	3:O:1019:LEU:HD22	2.02	0.41
3:O:1944:ALA:O	3:O:1987:ARG:NH2	2.53	0.41
5:Q:86:VAL:HG12	5:Q:87:ALA:N	2.35	0.41
9:U:667:LEU:HD22	9:U:811:ILE:HD12	2.02	0.41
3:A:90:ILE:CG2	3:A:94:ILE:HD11	2.51	0.41
3:A:417:MET:O	3:A:421:LEU:HD23	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:1675:LEU:C	3:A:1675:LEU:HD23	2.46	0.41
6:H:34:LYS:HE2	6:H:36:ALA:HB3	2.03	0.41
3:O:583:THR:HG23	3:O:621:GLU:HG3	2.02	0.41
3:O:1948:THR:HG22	3:O:1950:ARG:H	1.85	0.41
3:O:2241:PRO:O	3:O:2242:HIS:ND1	2.54	0.41
5:Q:78:GLU:OE1	5:Q:78:GLU:N	2.53	0.41
9:U:607:LEU:HD22	9:U:615:VAL:CG1	2.50	0.41
3:A:1546:TYR:O	3:A:1550:LEU:HD23	2.20	0.41
3:A:1798:PHE:HD1	3:A:1909:LEU:HD21	1.84	0.41
9:C:1093:ILE:CD1	9:C:1127:MET:HE1	2.51	0.41
2:N:135:LYS:O	2:N:139:GLU:OE1	2.38	0.41
4:P:130:ASP:CG	17:P:401:GTP:HN1	2.28	0.41
5:Q:76:CYS:HB2	6:R:65:LEU:HD22	2.03	0.41
6:R:34:LYS:HE2	6:R:36:ALA:HB3	2.03	0.41
9:U:60:VAL:HB	9:U:119:TYR:CD1	2.56	0.41
9:U:689:GLU:OE1	9:U:690:LYS:NZ	2.44	0.41
2:L:8:LYS:CD	2:L:78:ILE:HD13	2.51	0.41
3:A:262:HIS:CE1	3:A:387:LEU:HD13	2.56	0.41
3:A:731:ARG:NH2	9:C:383:ASP:HB2	2.35	0.41
3:A:1623:LEU:CD2	3:A:1652:THR:HG23	2.51	0.41
5:G:78:GLU:HG2	6:H:65:LEU:HD23	2.03	0.41
5:G:118:PRO:CB	11:F:155:VAL:HG21	2.51	0.41
6:H:44:ALA:C	6:H:45:LEU:HD22	2.46	0.41
9:C:118:ARG:NH2	9:C:137:LEU:HD23	2.35	0.41
9:C:315:ILE:HG22	9:C:319:ILE:HD12	2.01	0.41
9:C:355:ARG:NH2	9:C:383:ASP:OD2	2.46	0.41
9:C:926:THR:HG22	10:E:283:GLU:OE2	2.21	0.41
9:C:1237:ARG:HG2	9:C:1239:PHE:CE1	2.55	0.41
2:N:7:ARG:NH2	3:O:154:GLU:OE2	2.53	0.41
2:N:69:ILE:HD13	3:O:969:THR:CG2	2.50	0.41
2:N:115:MET:CE	2:N:159:VAL:HG23	2.46	0.41
3:O:56:SER:OG	3:O:57:GLN:N	2.52	0.41
3:O:200:ASP:OD2	3:O:201:PRO:HD2	2.21	0.41
3:O:587:ARG:HG3	3:O:621:GLU:OE2	2.21	0.41
3:O:962:GLN:O	3:O:965:SER:OG	2.37	0.41
3:O:1188:TYR:OH	3:O:1195:VAL:HG11	2.21	0.41
5:Q:59:ASN:OD1	5:Q:60:GLY:N	2.54	0.41
9:U:560:ALA:O	9:U:564:GLU:OE1	2.38	0.41
9:U:1093:ILE:HD11	9:U:1127:MET:HE1	2.03	0.41
9:U:1093:ILE:CD1	9:U:1127:MET:HE1	2.50	0.41
11:W:111:LEU:HD21	12:X:63:PHE:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:200:ASP:OD2	3:A:201:PRO:HD2	2.21	0.41
3:A:483:PHE:HB3	3:A:520:VAL:HG21	2.02	0.41
3:A:1101:GLN:HE22	3:A:1138:THR:HG22	1.86	0.41
3:A:1726:GLN:HA	3:A:1726:GLN:OE1	2.21	0.41
3:A:1878:LEU:HD23	3:A:1878:LEU:O	2.21	0.41
3:A:2241:PRO:O	3:A:2242:HIS:ND1	2.54	0.41
5:G:59:ASN:OD1	5:G:60:GLY:N	2.53	0.41
5:G:68:ASN:OD1	5:G:70:LYS:NZ	2.36	0.41
9:C:1245:GLU:N	9:C:1245:GLU:OE1	2.54	0.41
3:O:2085:CYS:SG	3:O:2089:MET:HE1	2.61	0.41
9:U:184:THR:OG1	9:U:213:ARG:NH2	2.43	0.41
3:A:170:LEU:O	3:A:174:GLU:OE1	2.39	0.40
3:A:1116:PRO:HG2	3:A:1117:PRO:HD3	2.02	0.40
3:A:1144:GLU:N	3:A:1144:GLU:OE1	2.54	0.40
9:C:928:LYS:NZ	9:C:931:ASP:OD1	2.55	0.40
3:O:203:GLN:OE1	3:O:387:LEU:HD11	2.20	0.40
3:O:410:THR:HG22	3:O:410:THR:O	2.20	0.40
3:O:783:LEU:HD23	3:O:795:ILE:HD12	2.03	0.40
3:O:1907:LEU:HD11	3:O:1938:VAL:HB	2.03	0.40
3:O:2033:GLU:OE1	3:O:2050:VAL:HG11	2.21	0.40
3:O:2038:TYR:HE1	3:O:2097:LEU:HD21	1.83	0.40
3:O:2375:ILE:HD11	3:O:2545:TRP:CZ2	2.57	0.40
5:Q:114:TYR:CD2	11:W:148:VAL:HG13	2.56	0.40
6:R:44:ALA:C	6:R:45:LEU:HD22	2.46	0.40
6:R:92:PHE:HD2	6:R:103:ILE:HD12	1.84	0.40
3:A:203:GLN:OE1	3:A:387:LEU:HD11	2.21	0.40
3:A:2299:LEU:CD2	3:A:2383:LEU:HD23	2.52	0.40
4:D:49:HIS:ND1	9:C:564:GLU:OE2	2.53	0.40
9:C:302:LEU:H	9:C:302:LEU:HD12	1.86	0.40
9:C:1272:SER:OG	9:C:1273:VAL:N	2.53	0.40
11:F:61:THR:O	11:F:65:ILE:HG12	2.21	0.40
3:O:1675:LEU:C	3:O:1675:LEU:HD23	2.46	0.40
3:O:1797:ASN:HB3	3:O:1884:ALA:HB2	2.03	0.40
9:U:306:ARG:O	9:U:405:HIS:NE2	2.51	0.40
9:U:476:VAL:HG11	9:U:494:ILE:HG21	2.02	0.40
10:V:156:ARG:HA	10:V:159:ILE:HG12	2.03	0.40
3:A:943:LEU:HA	3:A:946:PHE:HB3	2.04	0.40
3:A:1372:LEU:O	3:A:1374:LEU:N	2.54	0.40
3:A:2152:ARG:O	3:A:2177:SER:N	2.49	0.40
3:A:2375:ILE:HD11	3:A:2545:TRP:CZ2	2.57	0.40
4:D:32:ILE:HD12	4:D:34:ARG:HG2	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:114:TYR:CD2	11:F:148:VAL:HG13	2.56	0.40
9:C:88:ILE:HD13	9:C:101:THR:HG22	2.02	0.40
9:C:667:LEU:HD22	9:C:811:ILE:HD12	2.02	0.40
11:F:61:THR:O	11:F:64:ASN:N	2.51	0.40
3:O:262:HIS:CE1	3:O:387:LEU:HD13	2.57	0.40
3:O:1784:ARG:O	3:O:1790:TRP:NE1	2.53	0.40
5:Q:89:LEU:HD22	5:Q:119:LEU:HD13	2.02	0.40
9:U:138:ARG:HH21	9:U:146:VAL:HG12	1.86	0.40
9:U:1035:THR:O	9:U:1037:CYS:N	2.52	0.40
1:B:92:GLY:N	1:B:101:TYR:O	2.53	0.40
2:L:156:ALA:O	2:L:159:VAL:HG12	2.21	0.40
3:A:784:LYS:HD2	3:A:823:ILE:HD11	2.04	0.40
3:A:2379:LEU:HD21	3:A:2392:LEU:CD1	2.51	0.40
9:C:1093:ILE:HD11	9:C:1127:MET:HE1	2.03	0.40
3:O:1194:MET:SD	3:O:1194:MET:N	2.79	0.40
3:O:1505:ASN:OD1	3:O:1506:ASP:N	2.54	0.40
3:O:1623:LEU:HD23	3:O:1652:THR:HG23	2.02	0.40
3:O:2321:THR:HG21	3:O:2395:ASN:HB3	2.03	0.40
9:U:283:CYS:SG	9:U:284:VAL:N	2.94	0.40
9:U:1137:LEU:HD22	9:U:1149:ILE:HG22	2.04	0.40
3:A:507:PRO:O	3:A:511:VAL:HG23	2.21	0.40
3:A:1711:ILE:HG22	3:A:1715:GLN:OE1	2.21	0.40
3:A:2210:ALA:HA	3:A:2216:LEU:HD13	2.02	0.40
6:H:6:LYS:HD3	6:H:6:LYS:N	2.37	0.40
9:C:550:GLN:NE2	9:C:583:ARG:O	2.54	0.40
3:O:664:ILE:HG23	3:O:698:VAL:CG1	2.48	0.40
3:O:730:LEU:HB3	3:O:767:LEU:HD22	2.03	0.40
3:O:1391:ARG:HB3	3:O:1578:MET:SD	2.61	0.40
4:P:32:ILE:HD12	4:P:34:ARG:HG2	2.02	0.40
9:U:302:LEU:H	9:U:302:LEU:HD12	1.87	0.40
9:U:432:GLN:HA	9:U:435:ILE:HD13	2.03	0.40
9:U:979:ASP:OD1	9:U:980:LEU:N	2.55	0.40
9:U:1245:GLU:N	9:U:1245:GLU:OE1	2.54	0.40
10:V:348:ARG:NE	10:V:351:LEU:HD11	2.34	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	B	315/326 (97%)	293 (93%)	22 (7%)	0	100	100
1	M	315/326 (97%)	294 (93%)	21 (7%)	0	100	100
2	L	168/184 (91%)	155 (92%)	13 (8%)	0	100	100
2	N	168/184 (91%)	155 (92%)	13 (8%)	0	100	100
3	A	2291/2549 (90%)	2219 (97%)	72 (3%)	0	100	100
3	O	2291/2549 (90%)	2218 (97%)	73 (3%)	0	100	100
4	D	296/313 (95%)	280 (95%)	16 (5%)	0	100	100
4	P	296/313 (95%)	280 (95%)	16 (5%)	0	100	100
5	G	122/125 (98%)	108 (88%)	14 (12%)	0	100	100
5	Q	122/125 (98%)	110 (90%)	12 (10%)	0	100	100
6	H	118/124 (95%)	108 (92%)	10 (8%)	0	100	100
6	R	118/124 (95%)	108 (92%)	10 (8%)	0	100	100
7	J	87/91 (96%)	81 (93%)	6 (7%)	0	100	100
7	S	87/91 (96%)	83 (95%)	4 (5%)	0	100	100
8	K	6/118 (5%)	6 (100%)	0	0	100	100
8	T	6/118 (5%)	6 (100%)	0	0	100	100
9	C	1134/1335 (85%)	1056 (93%)	74 (6%)	4 (0%)	30	60
9	U	1134/1335 (85%)	1052 (93%)	78 (7%)	4 (0%)	30	60
10	E	275/399 (69%)	255 (93%)	19 (7%)	1 (0%)	30	60
10	V	275/399 (69%)	255 (93%)	19 (7%)	1 (0%)	30	60
11	F	107/161 (66%)	103 (96%)	3 (3%)	1 (1%)	14	44
11	W	107/161 (66%)	103 (96%)	3 (3%)	1 (1%)	14	44
12	I	80/99 (81%)	73 (91%)	7 (9%)	0	100	100
12	X	80/99 (81%)	72 (90%)	8 (10%)	0	100	100
All	All	9998/11648 (86%)	9473 (95%)	513 (5%)	12 (0%)	49	77

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
9	C	224	PRO
9	C	288	PRO
9	C	525	PRO
9	C	983	GLN
10	E	169	PRO
9	U	224	PRO
9	U	288	PRO
9	U	525	PRO
9	U	983	GLN
10	V	169	PRO
11	F	66	ILE
11	W	66	ILE

5.3.2 Protein sidechains [i](#)

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	B	269/276 (98%)	269 (100%)	0	100	100
1	M	269/276 (98%)	269 (100%)	0	100	100
2	L	149/161 (92%)	149 (100%)	0	100	100
2	N	149/161 (92%)	149 (100%)	0	100	100
3	A	2027/2220 (91%)	2027 (100%)	0	100	100
3	O	2027/2220 (91%)	2027 (100%)	0	100	100
4	D	271/287 (94%)	271 (100%)	0	100	100
4	P	271/287 (94%)	271 (100%)	0	100	100
5	G	97/98 (99%)	97 (100%)	0	100	100
5	Q	97/98 (99%)	97 (100%)	0	100	100
6	H	105/108 (97%)	105 (100%)	0	100	100
6	R	105/108 (97%)	105 (100%)	0	100	100
7	J	76/77 (99%)	76 (100%)	0	100	100
7	S	76/77 (99%)	76 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
8	K	8/102 (8%)	8 (100%)	0	100	100
8	T	8/102 (8%)	8 (100%)	0	100	100
9	C	1007/1163 (87%)	1007 (100%)	0	100	100
9	U	1007/1163 (87%)	1007 (100%)	0	100	100
10	E	255/340 (75%)	255 (100%)	0	100	100
10	V	255/340 (75%)	255 (100%)	0	100	100
11	F	97/141 (69%)	97 (100%)	0	100	100
11	W	97/141 (69%)	97 (100%)	0	100	100
12	I	71/83 (86%)	71 (100%)	0	100	100
12	X	71/83 (86%)	71 (100%)	0	100	100
All	All	8864/10112 (88%)	8864 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (66) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	74	ASN
1	B	122	GLN
1	B	264	ASN
3	A	292	GLN
3	A	372	GLN
3	A	418	ASN
3	A	554	HIS
3	A	605	HIS
3	A	763	ASN
3	A	878	GLN
3	A	973	GLN
3	A	999	ASN
3	A	1026	HIS
3	A	1112	HIS
3	A	1311	ASN
3	A	1758	GLN
3	A	1937	GLN
3	A	2161	GLN
3	A	2180	HIS
3	A	2189	HIS
4	D	30	ASN

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Mol	Chain	Res	Type
5	G	20	GLN
7	J	30	ASN
9	C	380	GLN
9	C	428	ASN
9	C	575	GLN
9	C	797	ASN
9	C	1226	HIS
10	E	83	HIS
10	E	234	GLN
1	M	73	ASN
1	M	74	ASN
1	M	122	GLN
1	M	264	ASN
3	O	292	GLN
3	O	372	GLN
3	O	414	GLN
3	O	418	ASN
3	O	554	HIS
3	O	605	HIS
3	O	689	GLN
3	O	703	GLN
3	O	736	GLN
3	O	878	GLN
3	O	973	GLN
3	O	999	ASN
3	O	1157	HIS
3	O	1206	HIS
3	O	1311	ASN
3	O	1758	GLN
3	O	1937	GLN
3	O	2161	GLN
3	O	2180	HIS
3	O	2189	HIS
4	P	30	ASN
5	Q	20	GLN
5	Q	121	GLN
9	U	303	ASN
9	U	380	GLN
9	U	557	ASN
9	U	575	GLN
9	U	805	ASN
9	U	978	HIS

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Mol	Chain	Res	Type
9	U	1226	HIS
10	V	83	HIS
10	V	234	GLN

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](#)

Of 18 ligands modelled in this entry, 8 are monoatomic - leaving 10 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
13	GSP	L	201	14	33,34,34	1.91	3 (9%)	47,54,54	1.77	9 (19%)
17	GTP	D	401	14	33,34,34	0.91	1 (3%)	50,54,54	1.65	10 (20%)
15	ANP	O	3000	14	33,33,33	3.61	20 (60%)	45,52,52	2.98	11 (24%)
17	GTP	P	401	14	33,34,34	0.91	1 (3%)	50,54,54	1.65	10 (20%)
18	GDP	V	401	-	29,30,30	1.16	3 (10%)	45,47,47	1.78	7 (15%)
16	IHP	A	3003	-	36,36,36	2.07	6 (16%)	60,60,60	1.23	5 (8%)
15	ANP	A	3000	14	33,33,33	3.61	20 (60%)	45,52,52	2.99	11 (24%)
13	GSP	N	201	14	33,34,34	1.91	3 (9%)	47,54,54	1.77	9 (19%)
16	IHP	O	3003	-	36,36,36	2.08	6 (16%)	60,60,60	1.23	6 (10%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
18	GDP	E	401	-	29,30,30	1.16	3 (10%)	45,47,47	1.79	7 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
13	GSP	L	201	14	-	3/21/38/38	0/3/3/3
17	GTP	D	401	14	-	6/22/38/38	0/3/3/3
15	ANP	O	3000	14	-	1/18/38/38	0/3/3/3
17	GTP	P	401	14	-	6/22/38/38	0/3/3/3
18	GDP	V	401	-	-	2/16/32/32	0/3/3/3
16	IHP	A	3003	-	-	7/30/54/54	0/1/1/1
15	ANP	A	3000	14	-	1/18/38/38	0/3/3/3
13	GSP	N	201	14	-	2/21/38/38	0/3/3/3
16	IHP	O	3003	-	-	7/30/54/54	0/1/1/1
18	GDP	E	401	-	-	3/16/32/32	0/3/3/3

All (66) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	O	3000	ANP	C2'-C3'	-10.86	1.23	1.53
15	A	3000	ANP	C2'-C3'	-10.86	1.23	1.53
13	L	201	GSP	PG-S1G	-9.56	1.69	1.90
13	N	201	GSP	PG-S1G	-9.55	1.69	1.90
15	O	3000	ANP	O4'-C4'	-6.55	1.30	1.45
15	A	3000	ANP	O4'-C4'	-6.54	1.30	1.45
15	O	3000	ANP	PA-O3A	6.16	1.66	1.59
15	A	3000	ANP	PA-O3A	6.16	1.66	1.59
15	O	3000	ANP	PB-O3A	6.07	1.66	1.59
15	A	3000	ANP	PB-O3A	6.06	1.66	1.59
15	O	3000	ANP	C3'-C4'	5.36	1.66	1.53
15	A	3000	ANP	C3'-C4'	5.36	1.66	1.53
16	O	3003	IHP	P5-O15	4.95	1.68	1.59
16	A	3003	IHP	P5-O15	4.95	1.68	1.59
16	O	3003	IHP	P6-O16	4.77	1.67	1.59
16	O	3003	IHP	P3-O13	4.76	1.67	1.59
16	A	3003	IHP	P3-O13	4.76	1.67	1.59
16	A	3003	IHP	P6-O16	4.76	1.67	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	A	3000	ANP	C1'-N9	-4.74	1.33	1.46
15	O	3000	ANP	C1'-N9	-4.74	1.33	1.46
16	O	3003	IHP	P1-O11	4.64	1.67	1.59
16	O	3003	IHP	P4-O14	4.63	1.67	1.59
16	A	3003	IHP	P4-O14	4.63	1.67	1.59
15	A	3000	ANP	C6-N6	4.62	1.46	1.34
16	A	3003	IHP	P1-O11	4.61	1.67	1.59
15	O	3000	ANP	C6-N6	4.61	1.46	1.34
16	O	3003	IHP	P2-O12	4.53	1.67	1.59
16	A	3003	IHP	P2-O12	4.50	1.67	1.59
15	A	3000	ANP	O4'-C1'	4.01	1.51	1.42
15	O	3000	ANP	O4'-C1'	3.98	1.51	1.42
15	A	3000	ANP	PB-O1B	3.49	1.51	1.46
15	O	3000	ANP	PB-O1B	3.49	1.51	1.46
15	A	3000	ANP	PG-O1G	3.38	1.51	1.46
15	O	3000	ANP	PG-O1G	3.37	1.51	1.46
15	O	3000	ANP	O2'-C2'	3.13	1.50	1.43
15	A	3000	ANP	O2'-C2'	3.12	1.50	1.43
15	O	3000	ANP	PB-N3B	3.09	1.71	1.63
15	A	3000	ANP	PB-N3B	3.09	1.71	1.63
15	O	3000	ANP	PG-N3B	3.05	1.71	1.63
15	A	3000	ANP	PG-N3B	3.04	1.71	1.63
18	V	401	GDP	C5-C4	3.04	1.47	1.38
18	E	401	GDP	C5-C4	3.03	1.47	1.38
15	O	3000	ANP	C5-N7	-3.02	1.33	1.39
15	A	3000	ANP	C5-N7	-2.99	1.33	1.39
18	E	401	GDP	C6-N1	-2.66	1.33	1.38
15	A	3000	ANP	C5-C4	-2.65	1.34	1.39
15	O	3000	ANP	C5-C4	-2.64	1.34	1.39
18	V	401	GDP	C6-N1	-2.64	1.33	1.38
15	O	3000	ANP	C2'-C1'	2.20	1.60	1.53
15	A	3000	ANP	C2'-C1'	2.19	1.60	1.53
13	L	201	GSP	C2-N3	2.18	1.38	1.33
13	N	201	GSP	C2-N3	2.17	1.38	1.33
18	E	401	GDP	C5-N7	-2.16	1.34	1.39
18	V	401	GDP	C5-N7	-2.13	1.34	1.39
17	P	401	GTP	C2-N3	2.10	1.38	1.33
17	D	401	GTP	C2-N3	2.09	1.38	1.33
15	O	3000	ANP	PA-O5'	2.08	1.67	1.59
15	A	3000	ANP	PA-O5'	2.08	1.67	1.59
13	L	201	GSP	C5-N7	-2.07	1.34	1.39
13	N	201	GSP	C5-N7	-2.06	1.34	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
15	A	3000	ANP	C8-N9	-2.03	1.34	1.37
15	O	3000	ANP	O3'-C3'	2.02	1.48	1.43
15	A	3000	ANP	O3'-C3'	2.02	1.48	1.43
15	O	3000	ANP	C8-N9	-2.02	1.34	1.37
15	A	3000	ANP	PG-O2G	-2.02	1.51	1.56
15	O	3000	ANP	PG-O2G	-2.02	1.51	1.56

All (85) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	O	3000	ANP	N6-C6-N1	-9.60	96.99	118.38
15	A	3000	ANP	N6-C6-N1	-9.60	97.00	118.38
15	O	3000	ANP	C5-C6-N6	7.82	142.65	123.29
15	A	3000	ANP	C5-C6-N6	7.82	142.65	123.29
15	O	3000	ANP	C5-C4-N3	-6.37	117.94	126.72
15	A	3000	ANP	C5-C4-N3	-6.35	117.97	126.72
18	E	401	GDP	C5-C4-N3	-6.25	118.45	128.39
15	A	3000	ANP	C4-N9-C1'	-6.22	112.08	126.63
18	V	401	GDP	C5-C4-N3	-6.22	118.49	128.39
15	O	3000	ANP	C4-N9-C1'	-6.19	112.15	126.63
15	A	3000	ANP	C1'-N9-C8	6.18	140.80	127.09
15	O	3000	ANP	C1'-N9-C8	6.15	140.74	127.09
15	O	3000	ANP	N3-C2-N1	-5.72	119.92	128.58
15	A	3000	ANP	N3-C2-N1	-5.72	119.92	128.58
13	N	201	GSP	C5-C4-N3	-5.14	120.21	128.39
13	L	201	GSP	C5-C4-N3	-5.14	120.21	128.39
17	P	401	GTP	C5-C4-N3	-5.10	120.27	128.39
17	D	401	GTP	C5-C4-N3	-5.07	120.31	128.39
18	V	401	GDP	C2-N3-C4	5.05	121.00	112.30
18	E	401	GDP	C2-N3-C4	5.03	120.97	112.30
17	P	401	GTP	C2-N3-C4	4.69	120.38	112.30
17	D	401	GTP	C2-N3-C4	4.68	120.36	112.30
13	N	201	GSP	C2-N3-C4	4.63	120.27	112.30
13	L	201	GSP	C2-N3-C4	4.61	120.25	112.30
18	E	401	GDP	N9-C4-N3	4.61	135.16	125.95
18	V	401	GDP	N9-C4-N3	4.53	135.00	125.95
15	O	3000	ANP	N3-C4-N9	4.43	134.71	127.17
15	A	3000	ANP	N3-C4-N9	4.42	134.69	127.17
13	L	201	GSP	PB-O3B-PG	-4.42	117.01	133.17
13	N	201	GSP	PB-O3B-PG	-4.40	117.08	133.17
16	O	3003	IHP	C6-C1-C2	4.30	119.86	110.43
16	A	3003	IHP	C6-C1-C2	4.28	119.83	110.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
15	O	3000	ANP	C2-N3-C4	3.87	121.29	111.83
15	A	3000	ANP	C2-N3-C4	3.87	121.27	111.83
15	O	3000	ANP	N9-C8-N7	-3.39	109.12	113.94
15	A	3000	ANP	N9-C8-N7	-3.39	109.13	113.94
13	L	201	GSP	N9-C4-N3	3.33	132.60	125.95
18	V	401	GDP	C6-C5-N7	3.32	136.33	130.29
13	N	201	GSP	N9-C4-N3	3.30	132.56	125.95
18	E	401	GDP	C6-C5-N7	3.24	136.18	130.29
17	P	401	GTP	N9-C4-N3	3.23	132.42	125.95
17	D	401	GTP	N9-C4-N3	3.22	132.40	125.95
16	O	3003	IHP	O11-C1-C6	3.18	115.54	108.76
16	A	3003	IHP	O11-C1-C6	3.17	115.51	108.76
13	L	201	GSP	C2-N1-C6	-3.06	119.56	125.11
13	N	201	GSP	C2-N1-C6	-3.06	119.57	125.11
17	P	401	GTP	C2-N1-C6	-3.02	119.63	125.11
16	A	3003	IHP	C3-C2-C1	3.02	117.05	110.43
16	O	3003	IHP	C3-C2-C1	2.99	117.00	110.43
17	D	401	GTP	C2-N1-C6	-2.99	119.69	125.11
15	O	3000	ANP	C6-C5-C4	2.70	120.87	117.18
15	A	3000	ANP	C6-C5-C4	2.70	120.87	117.18
17	P	401	GTP	N9-C8-N7	-2.68	108.44	113.40
17	D	401	GTP	N9-C8-N7	-2.67	108.45	113.40
17	P	401	GTP	C5-C6-N1	2.65	120.01	113.25
17	D	401	GTP	C5-C6-N1	2.65	120.00	113.25
18	V	401	GDP	C4-C5-N7	-2.64	106.48	110.67
15	A	3000	ANP	C5-N7-C8	2.62	107.56	103.45
15	O	3000	ANP	C5-N7-C8	2.61	107.56	103.45
18	E	401	GDP	C4-C5-N7	-2.59	106.57	110.67
13	L	201	GSP	N9-C8-N7	-2.57	108.63	113.40
13	N	201	GSP	N9-C8-N7	-2.57	108.64	113.40
13	N	201	GSP	C5-C6-N1	2.56	119.77	113.25
13	L	201	GSP	C5-C6-N1	2.56	119.77	113.25
13	L	201	GSP	O6-C6-C5	-2.54	119.82	126.53
13	N	201	GSP	O6-C6-C5	-2.53	119.84	126.53
17	P	401	GTP	C8-N7-C5	2.53	108.76	104.26
17	D	401	GTP	C8-N7-C5	2.51	108.73	104.26
17	P	401	GTP	O6-C6-C5	-2.50	119.94	126.53
17	D	401	GTP	O6-C6-C5	-2.49	119.96	126.53
13	N	201	GSP	C8-N7-C5	2.44	108.60	104.26
13	L	201	GSP	C8-N7-C5	2.43	108.58	104.26
18	V	401	GDP	C3'-C2'-C1'	2.30	105.82	101.46
18	E	401	GDP	C3'-C2'-C1'	2.28	105.78	101.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
18	E	401	GDP	O6-C6-C5	-2.15	120.87	126.53
17	P	401	GTP	C3'-C2'-C1'	2.12	105.47	101.46
17	D	401	GTP	C3'-C2'-C1'	2.11	105.46	101.46
18	V	401	GDP	O6-C6-C5	-2.10	120.98	126.53
16	A	3003	IHP	C5-C4-C3	-2.08	105.86	110.43
16	O	3003	IHP	C5-C4-C3	-2.05	105.92	110.43
16	O	3003	IHP	O13-C3-C4	2.04	113.09	108.76
16	A	3003	IHP	O13-C3-C4	2.03	113.08	108.76
17	D	401	GTP	O3G-PG-O3B	2.03	111.44	104.64
17	P	401	GTP	O3G-PG-O3B	2.01	111.38	104.64
16	O	3003	IHP	P1-O11-C1	2.01	128.79	123.43

There are no chirality outliers.

All (38) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
13	L	201	GSP	PB-O3B-PG-O2G
13	L	201	GSP	PB-O3B-PG-O3G
13	N	201	GSP	PB-O3B-PG-O2G
13	N	201	GSP	PB-O3B-PG-O3G
15	A	3000	ANP	PB-N3B-PG-O1G
15	O	3000	ANP	PB-N3B-PG-O1G
16	A	3003	IHP	C6-C1-O11-P1
16	A	3003	IHP	C4-C3-O13-P3
16	A	3003	IHP	C3-C4-O14-P4
16	A	3003	IHP	C4-C5-O15-P5
16	O	3003	IHP	C6-C1-O11-P1
16	O	3003	IHP	C4-C3-O13-P3
16	O	3003	IHP	C3-C4-O14-P4
16	O	3003	IHP	C4-C5-O15-P5
17	D	401	GTP	PB-O3B-PG-O3G
17	P	401	GTP	PB-O3B-PG-O3G
18	E	401	GDP	C3'-C4'-C5'-O5'
18	V	401	GDP	O4'-C4'-C5'-O5'
18	V	401	GDP	C3'-C4'-C5'-O5'
18	E	401	GDP	O4'-C4'-C5'-O5'
17	D	401	GTP	O4'-C4'-C5'-O5'
17	D	401	GTP	C3'-C4'-C5'-O5'
17	P	401	GTP	O4'-C4'-C5'-O5'
17	P	401	GTP	C3'-C4'-C5'-O5'
17	P	401	GTP	PG-O3B-PB-O1B
16	A	3003	IHP	C5-C4-O14-P4

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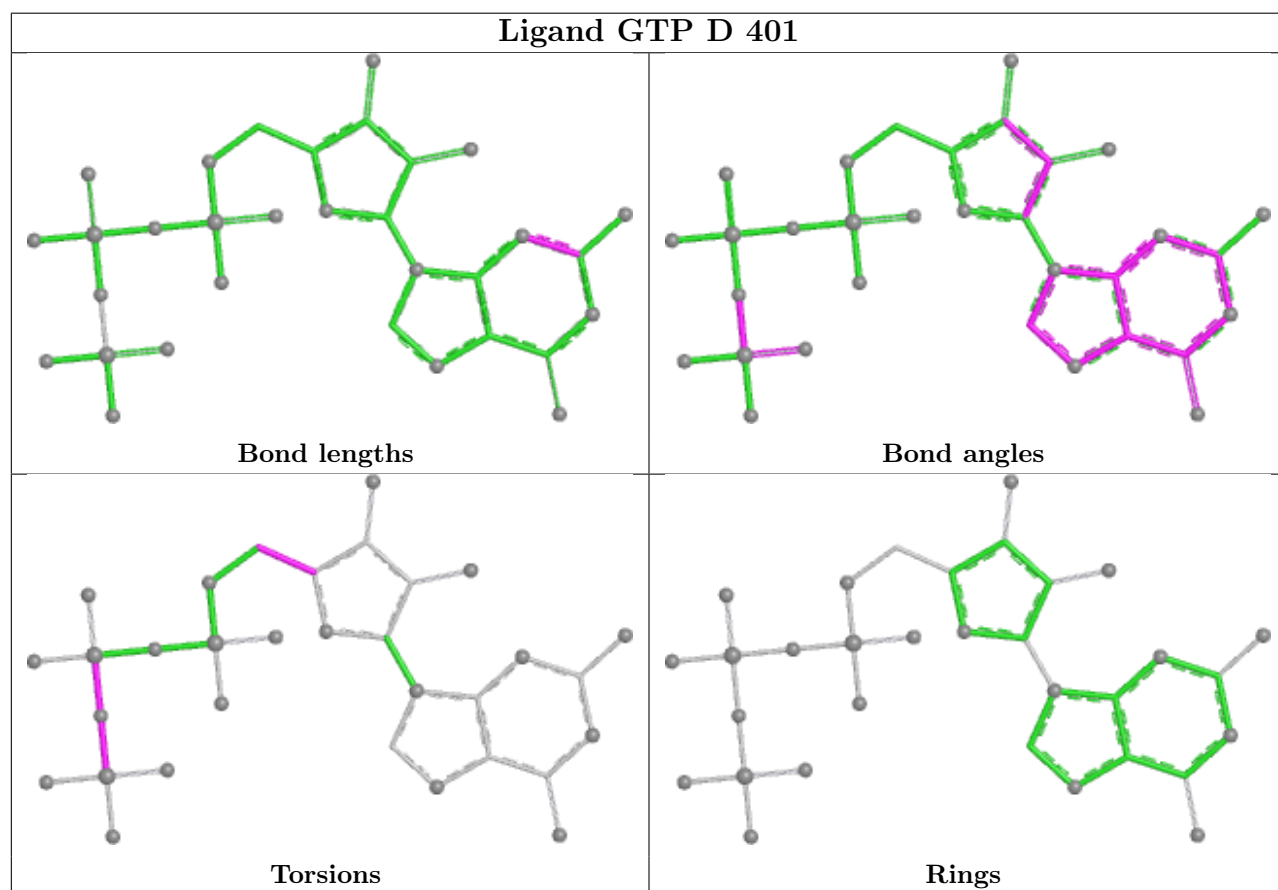
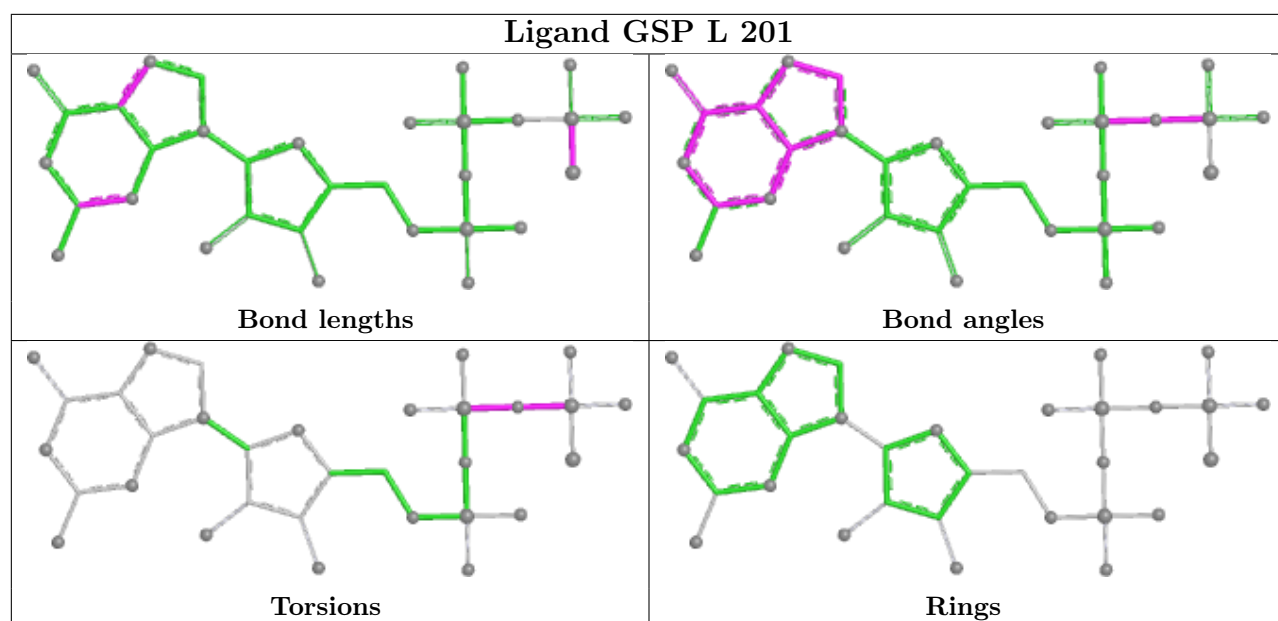
Mol	Chain	Res	Type	Atoms
16	O	3003	IHP	C5-C4-O14-P4
17	D	401	GTP	PG-O3B-PB-O1B
18	E	401	GDP	C5'-O5'-PA-O1A
16	A	3003	IHP	C4-O14-P4-O34
16	O	3003	IHP	C4-O14-P4-O34
17	D	401	GTP	PB-O3B-PG-O1G
17	P	401	GTP	PB-O3B-PG-O1G
16	A	3003	IHP	C6-C5-O15-P5
16	O	3003	IHP	C6-C5-O15-P5
13	L	201	GSP	PG-O3B-PB-O2B
17	D	401	GTP	PG-O3B-PB-O2B
17	P	401	GTP	PG-O3B-PB-O2B

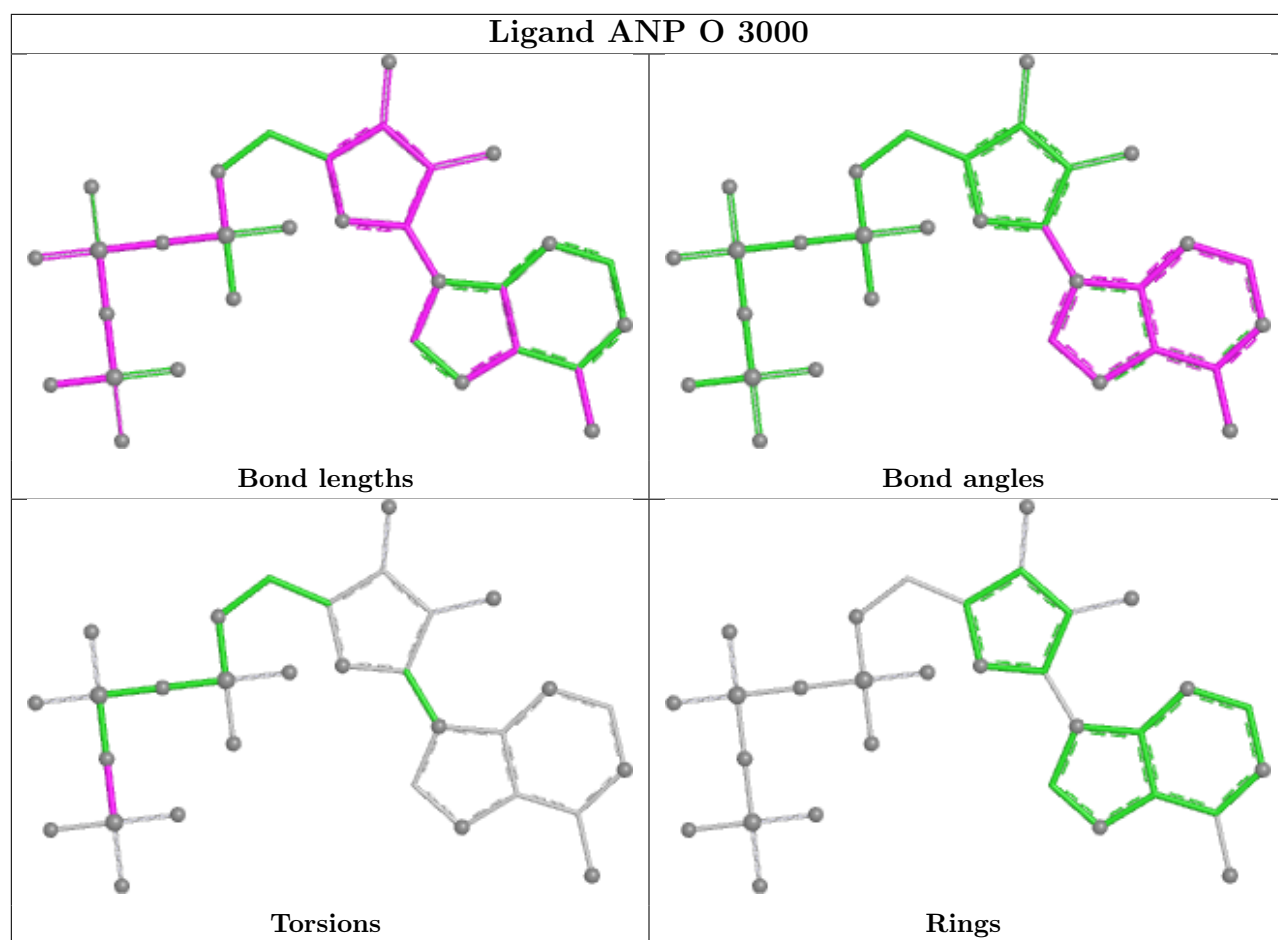
There are no ring outliers.

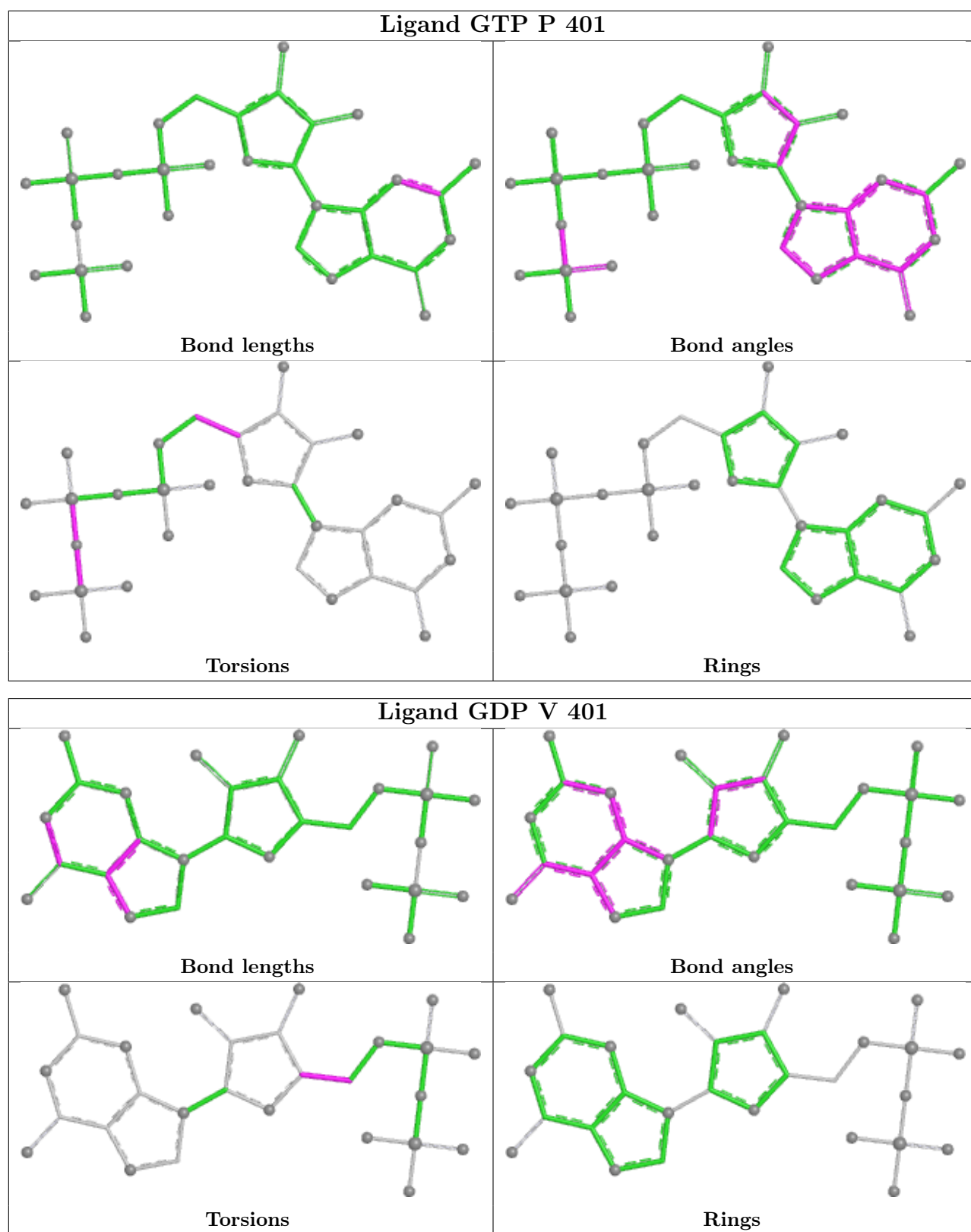
10 monomers are involved in 30 short contacts:

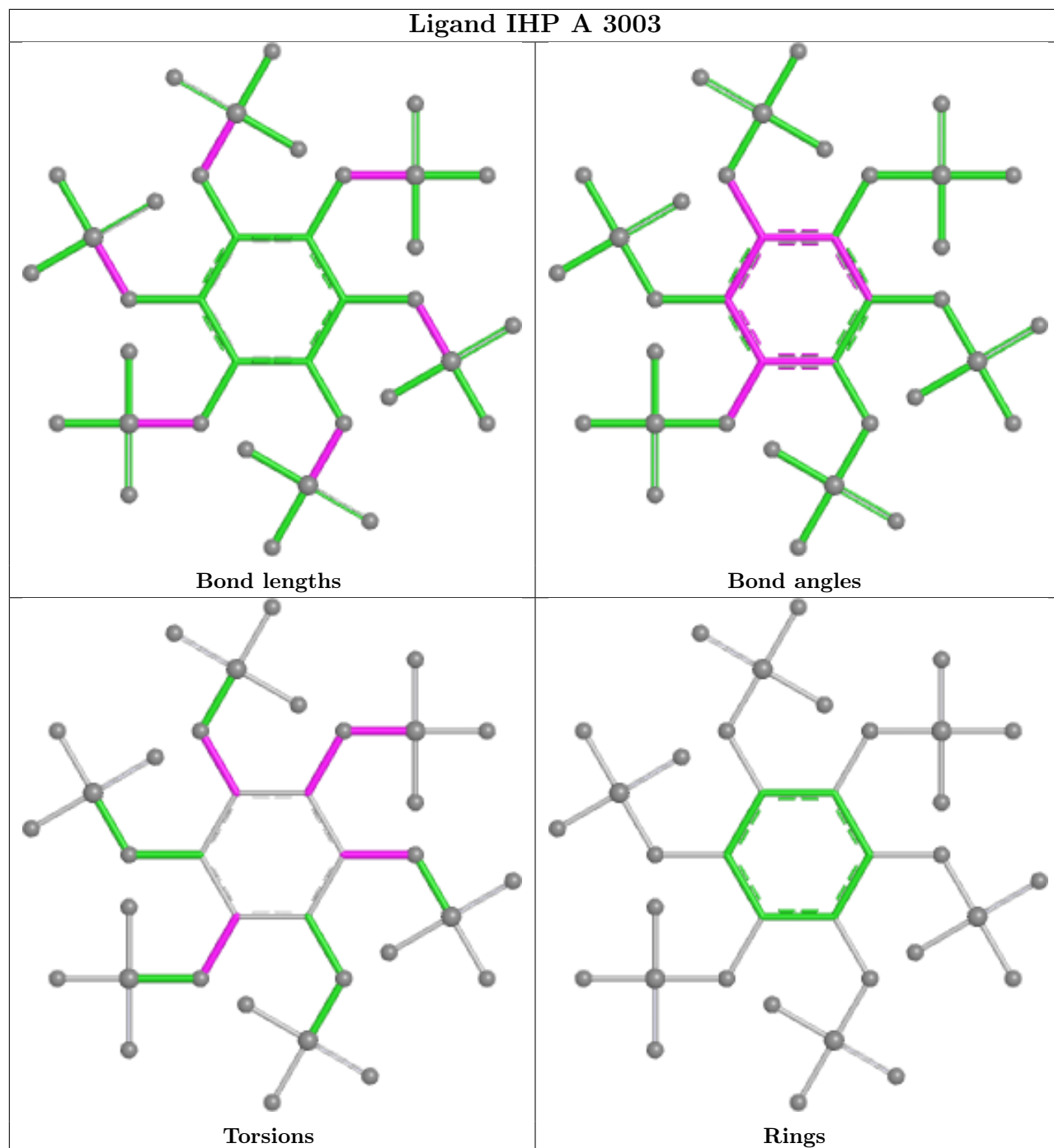
Mol	Chain	Res	Type	Clashes	Symm-Clashes
13	L	201	GSP	5	0
17	D	401	GTP	5	0
15	O	3000	ANP	1	0
17	P	401	GTP	5	0
18	V	401	GDP	3	0
16	A	3003	IHP	1	0
15	A	3000	ANP	1	0
13	N	201	GSP	5	0
16	O	3003	IHP	1	0
18	E	401	GDP	3	0

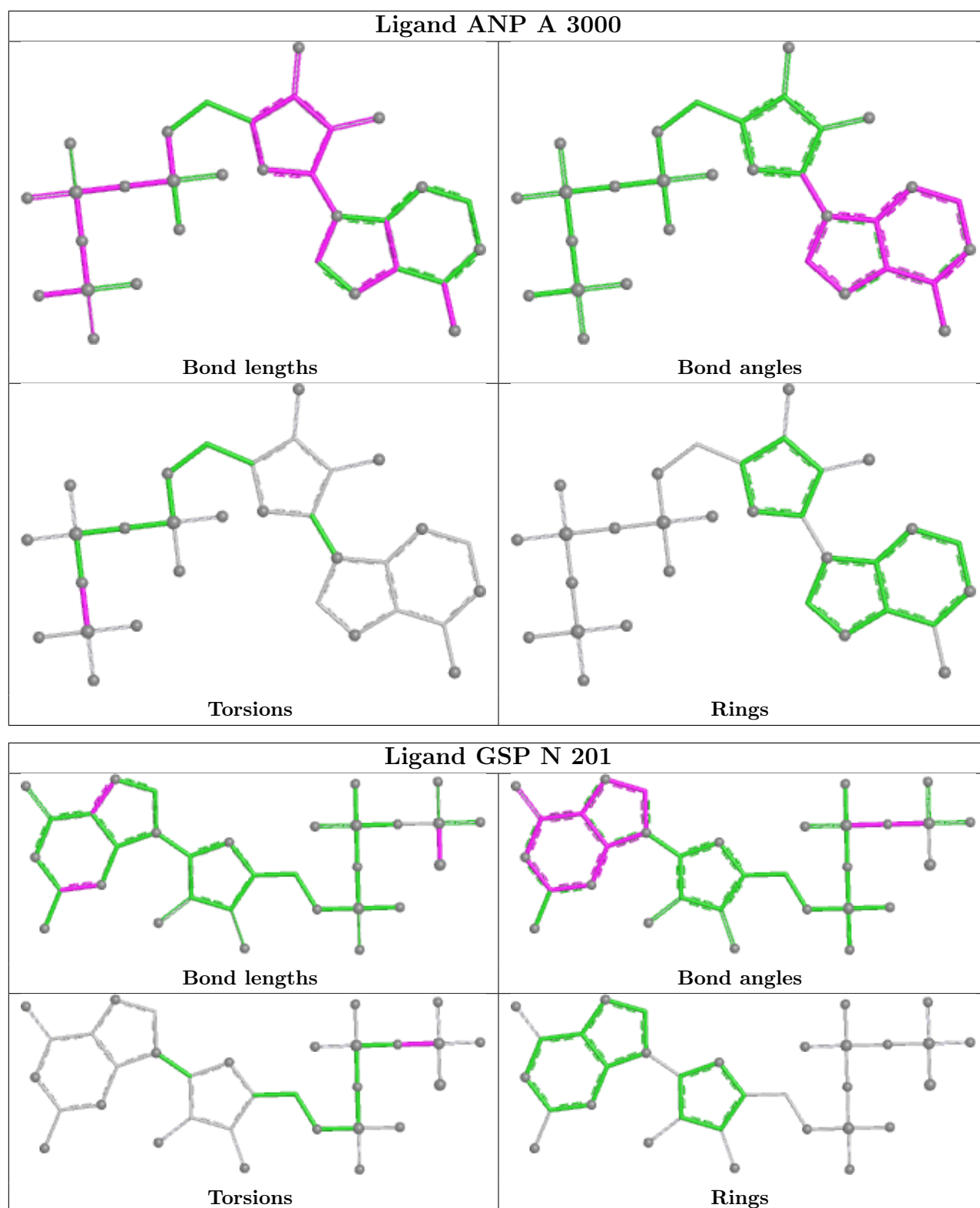
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

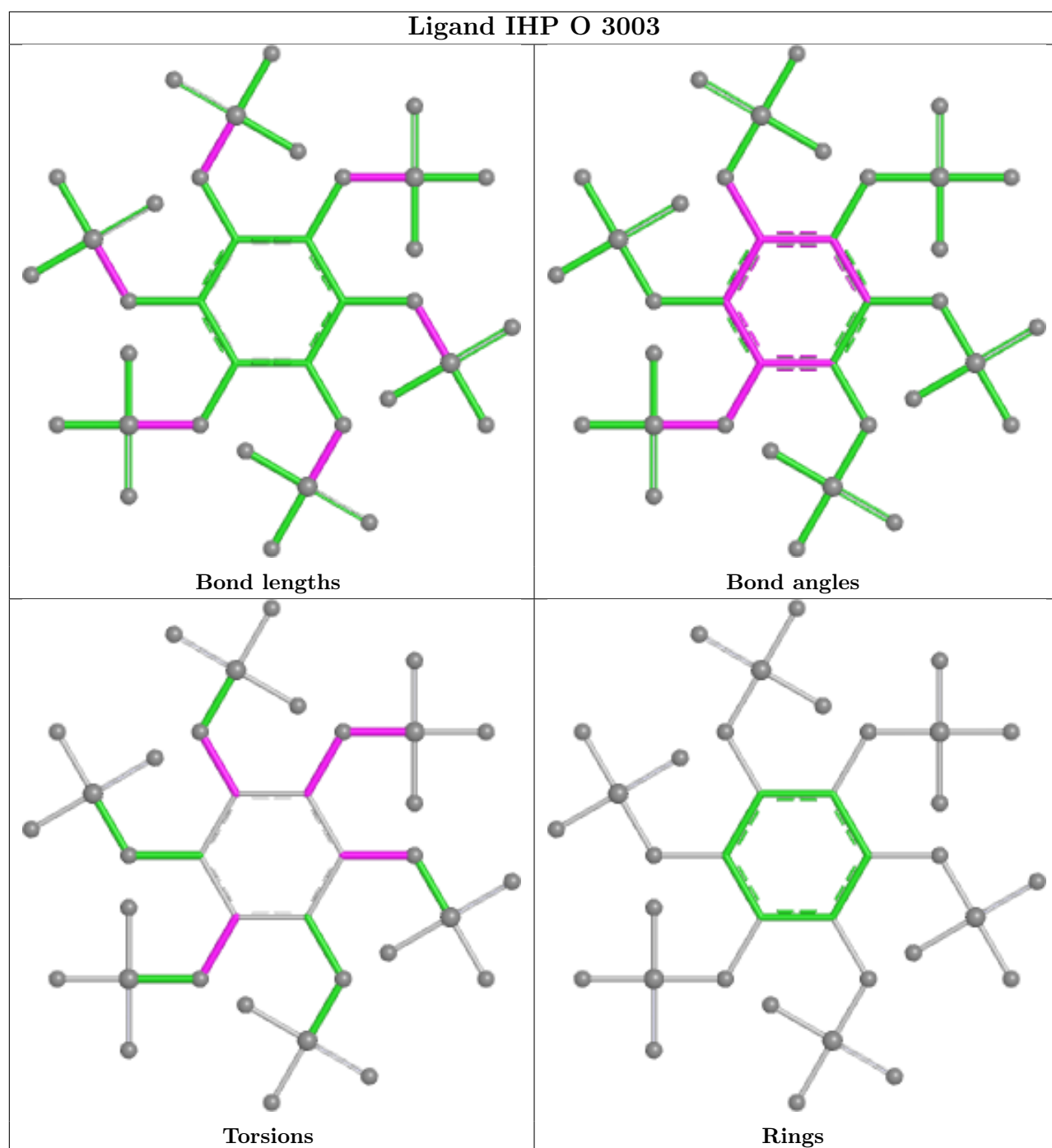


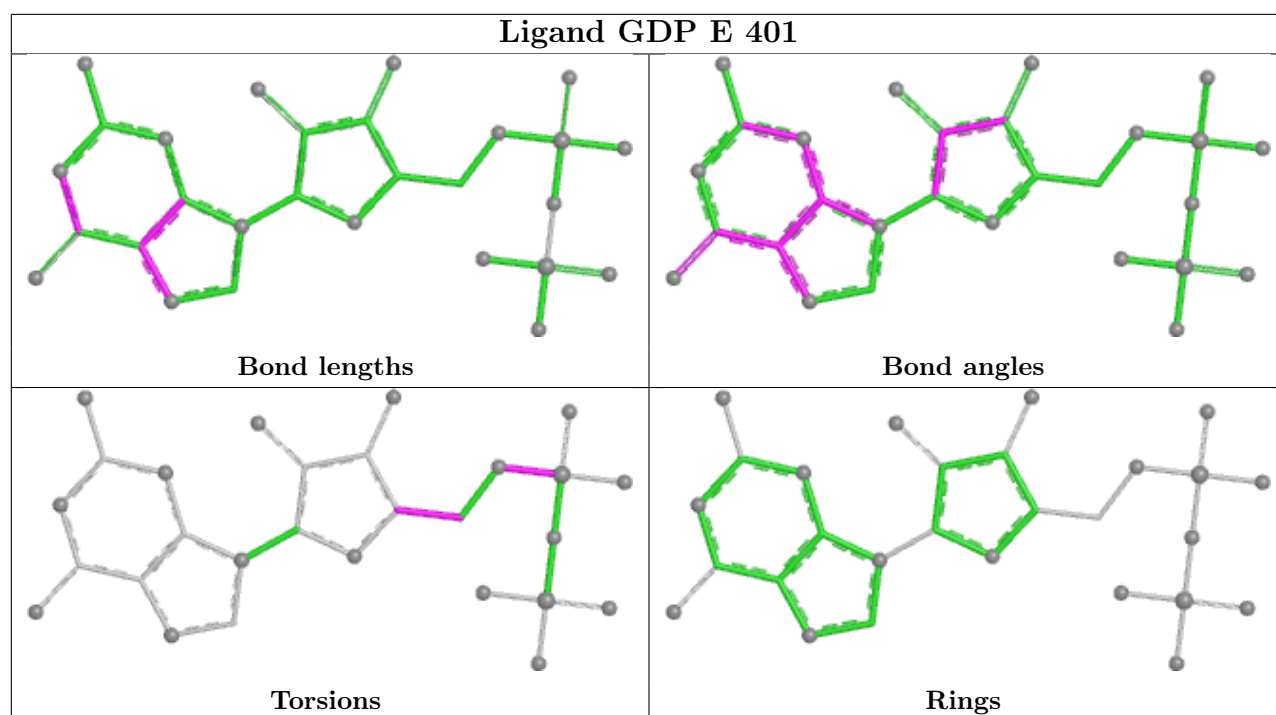












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

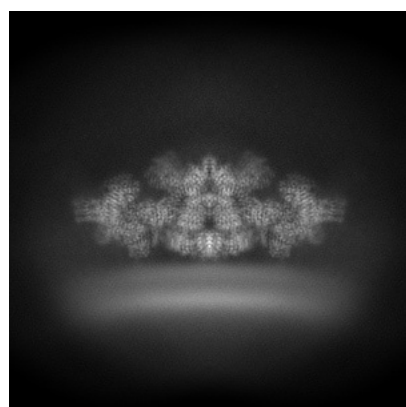
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-47932. These allow visual inspection of the internal detail of the map and identification of artifacts.

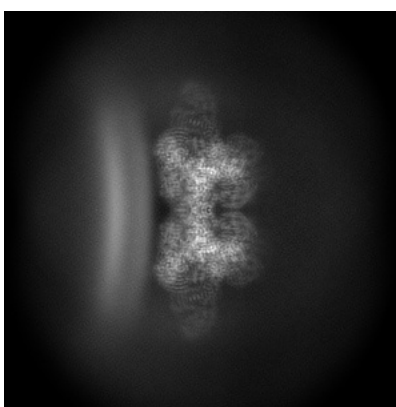
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

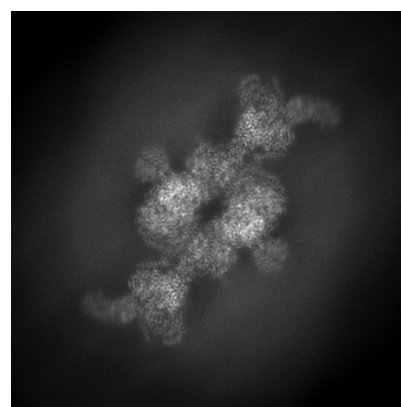
6.1.1 Primary map



X



Y

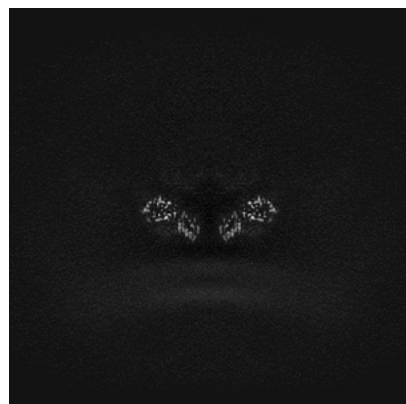


Z

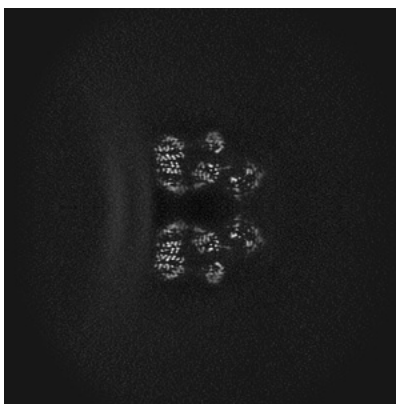
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

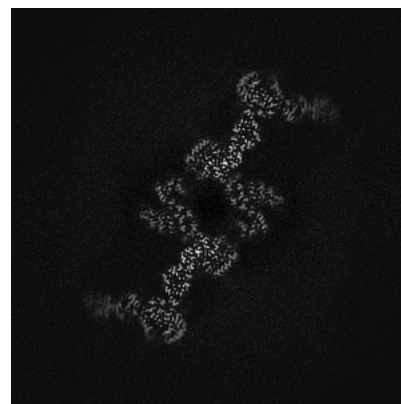
6.2.1 Primary map



X Index: 224



Y Index: 224

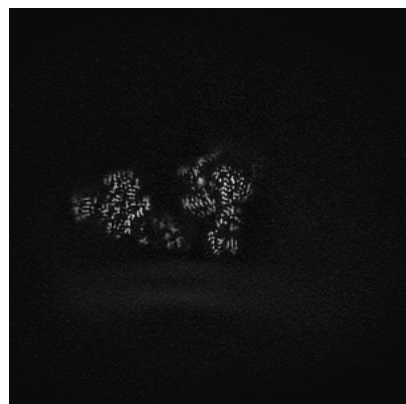


Z Index: 224

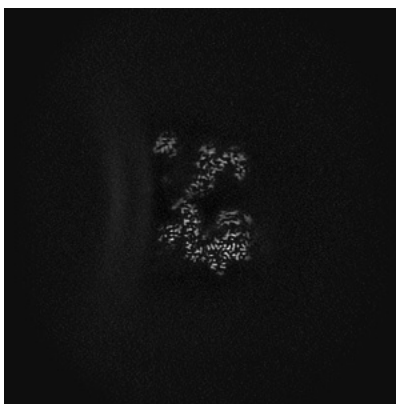
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

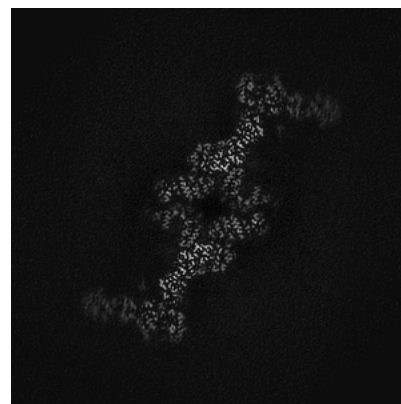
6.3.1 Primary map



X Index: 178



Y Index: 241

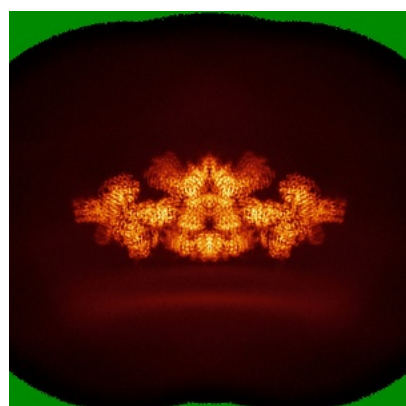


Z Index: 216

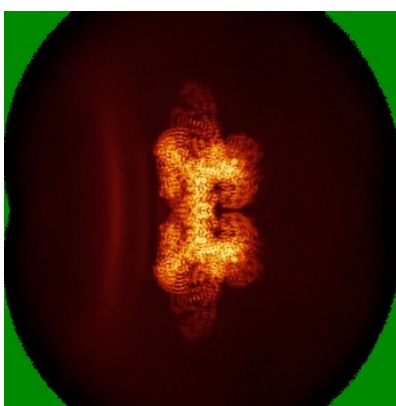
The images above show the largest variance slices of the map in three orthogonal directions.

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

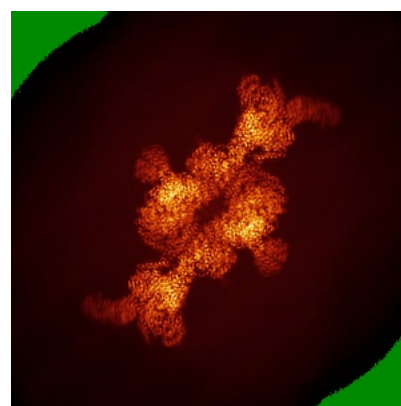
6.4.1 Primary map



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

This section was not generated.

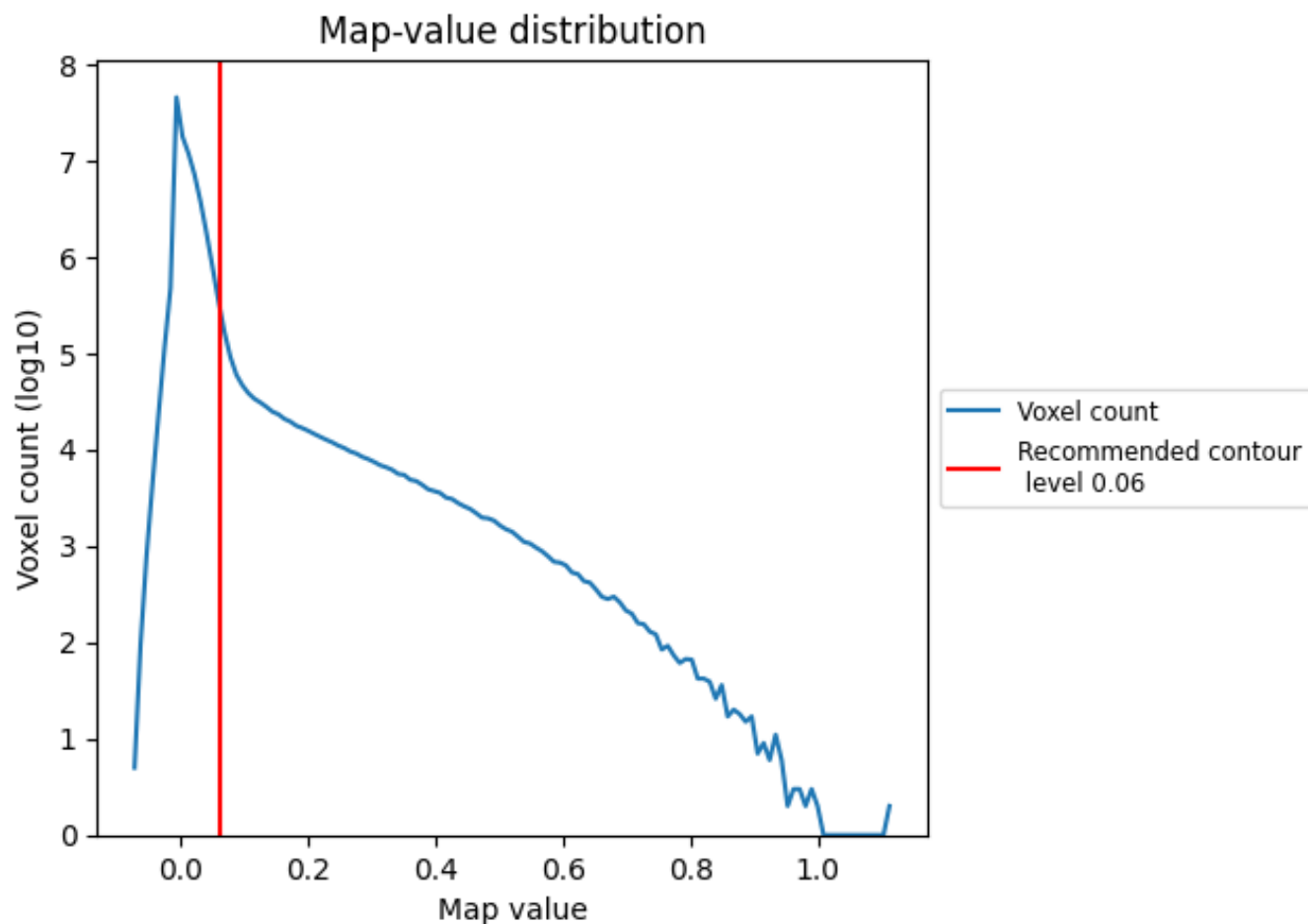
6.6 Mask visualisation

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

7 Map analysis [i](#)

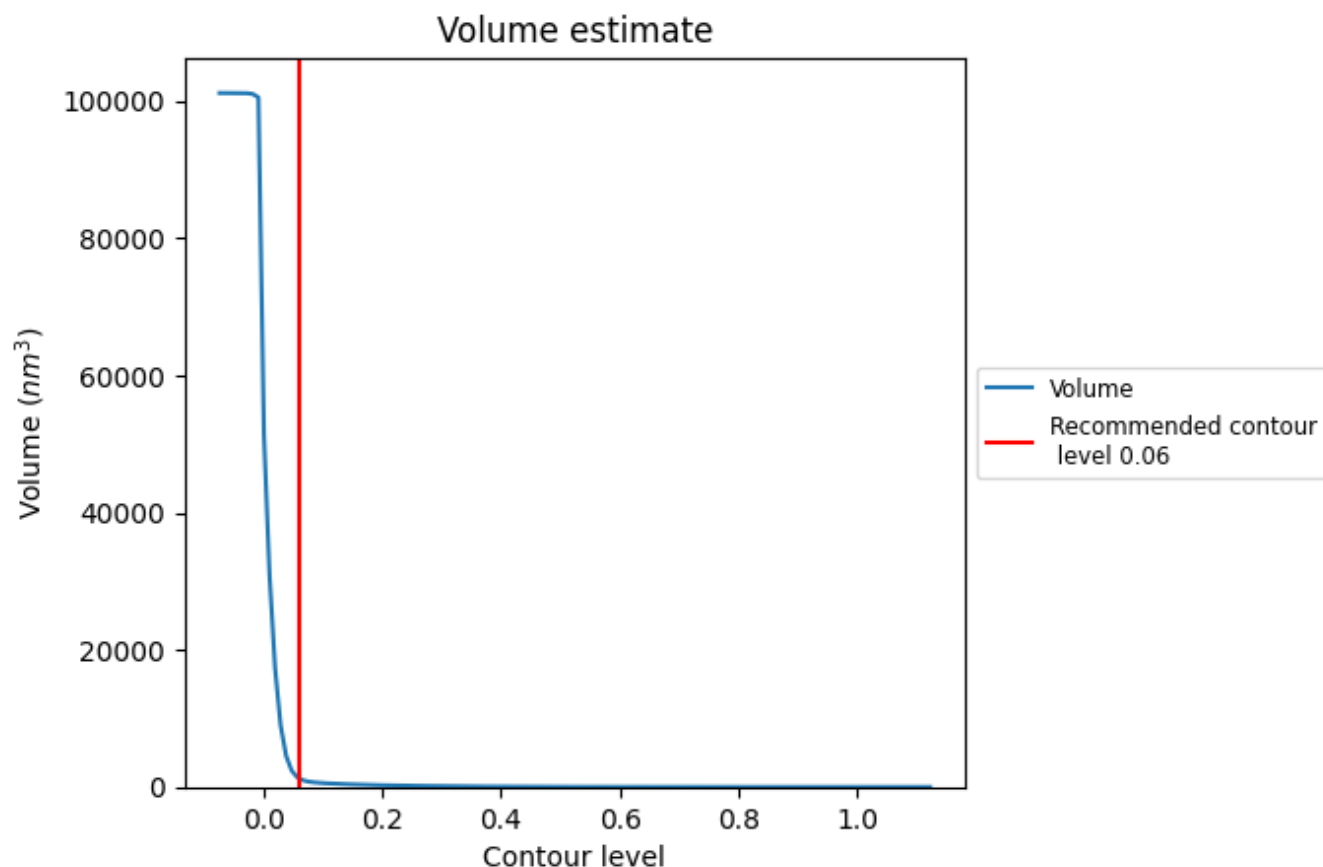
This section contains the results of statistical analysis of the map.

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.

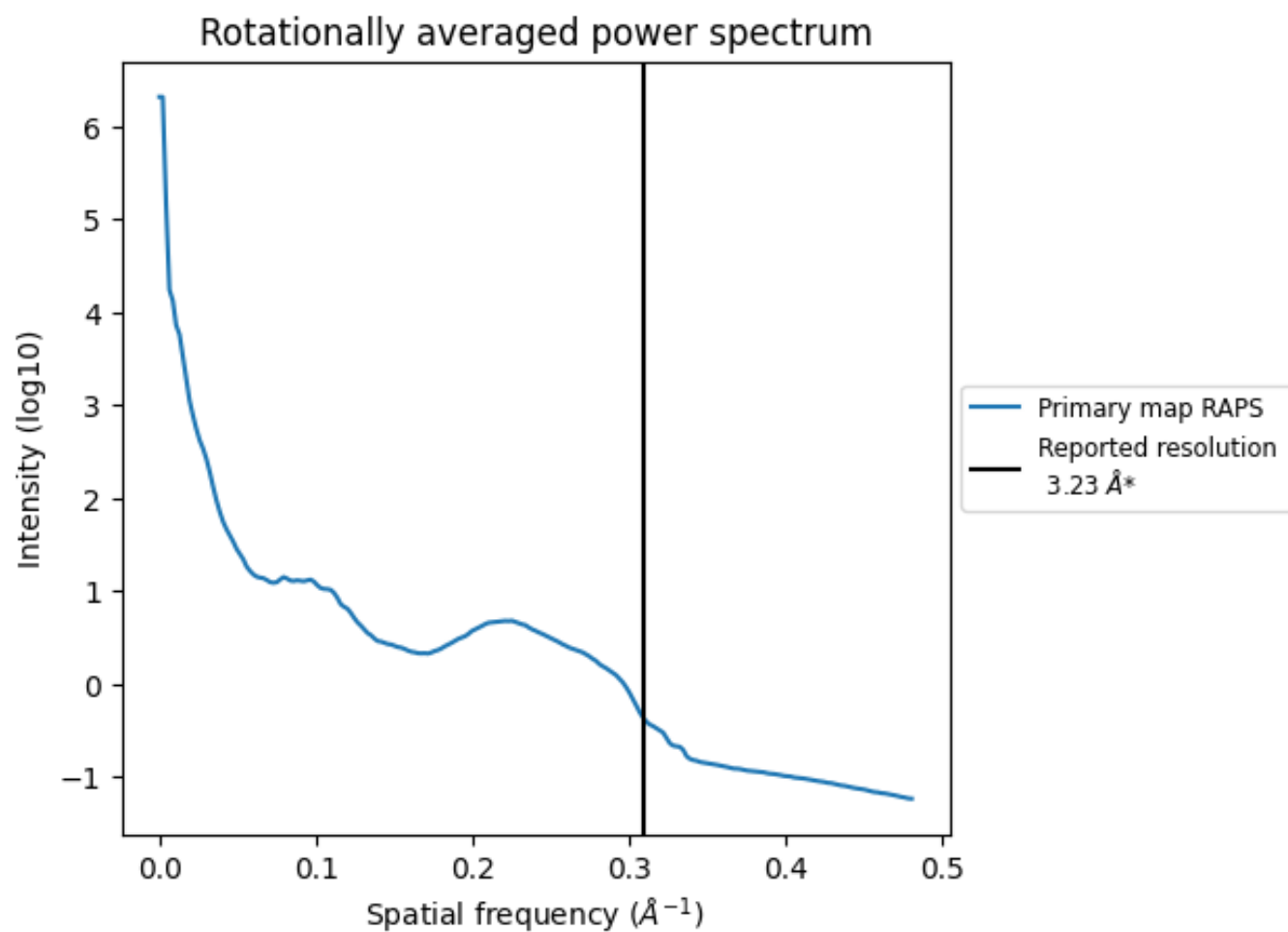
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1293 nm^3 ; this corresponds to an approximate mass of 1168 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 0.310 Å⁻¹

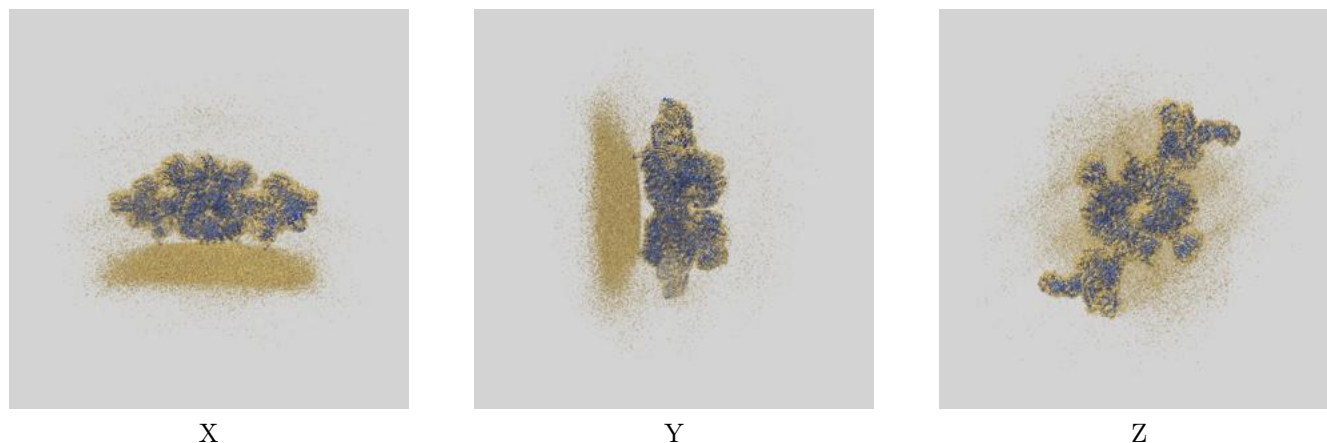
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

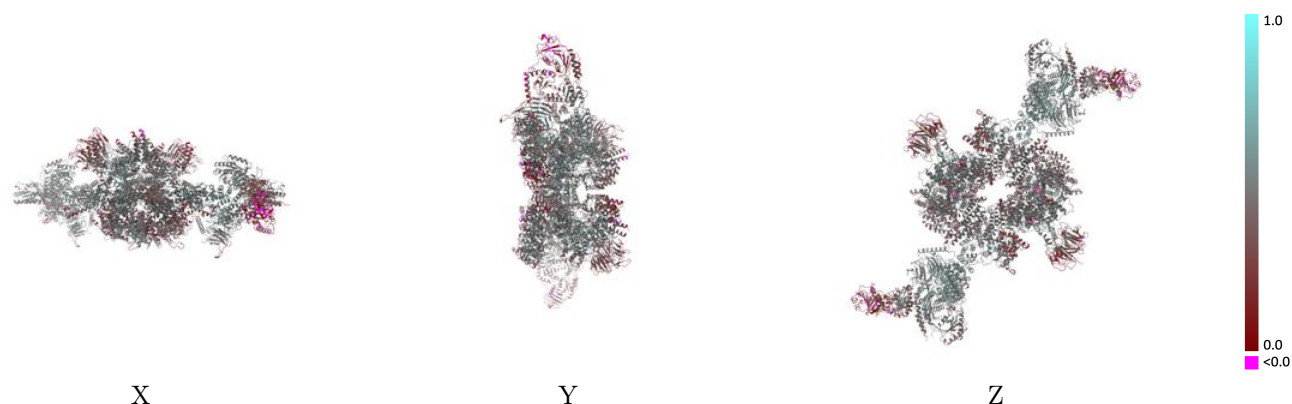
This section contains information regarding the fit between EMDB map EMD-47932 and PDB model 9ED4. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



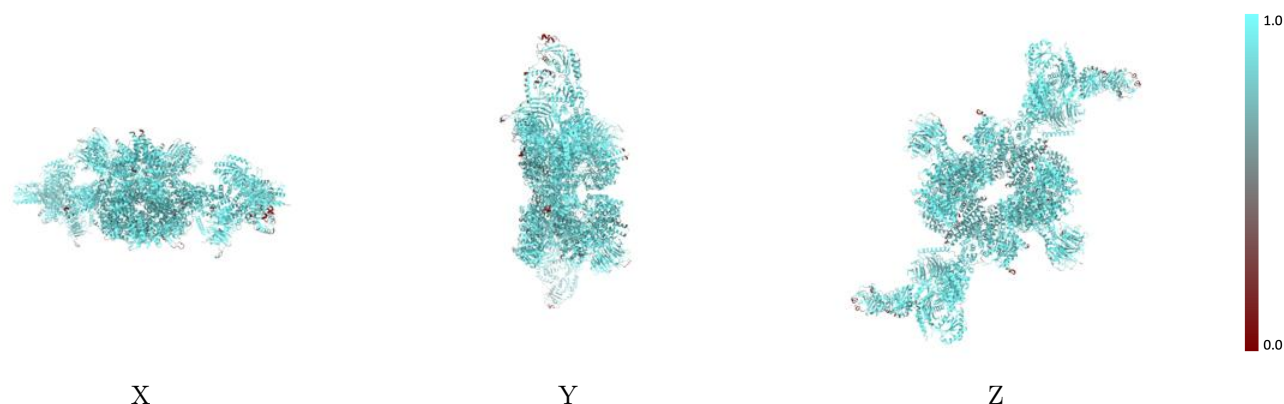
The images above show the 3D surface view of the map at the recommended contour level 0.06 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



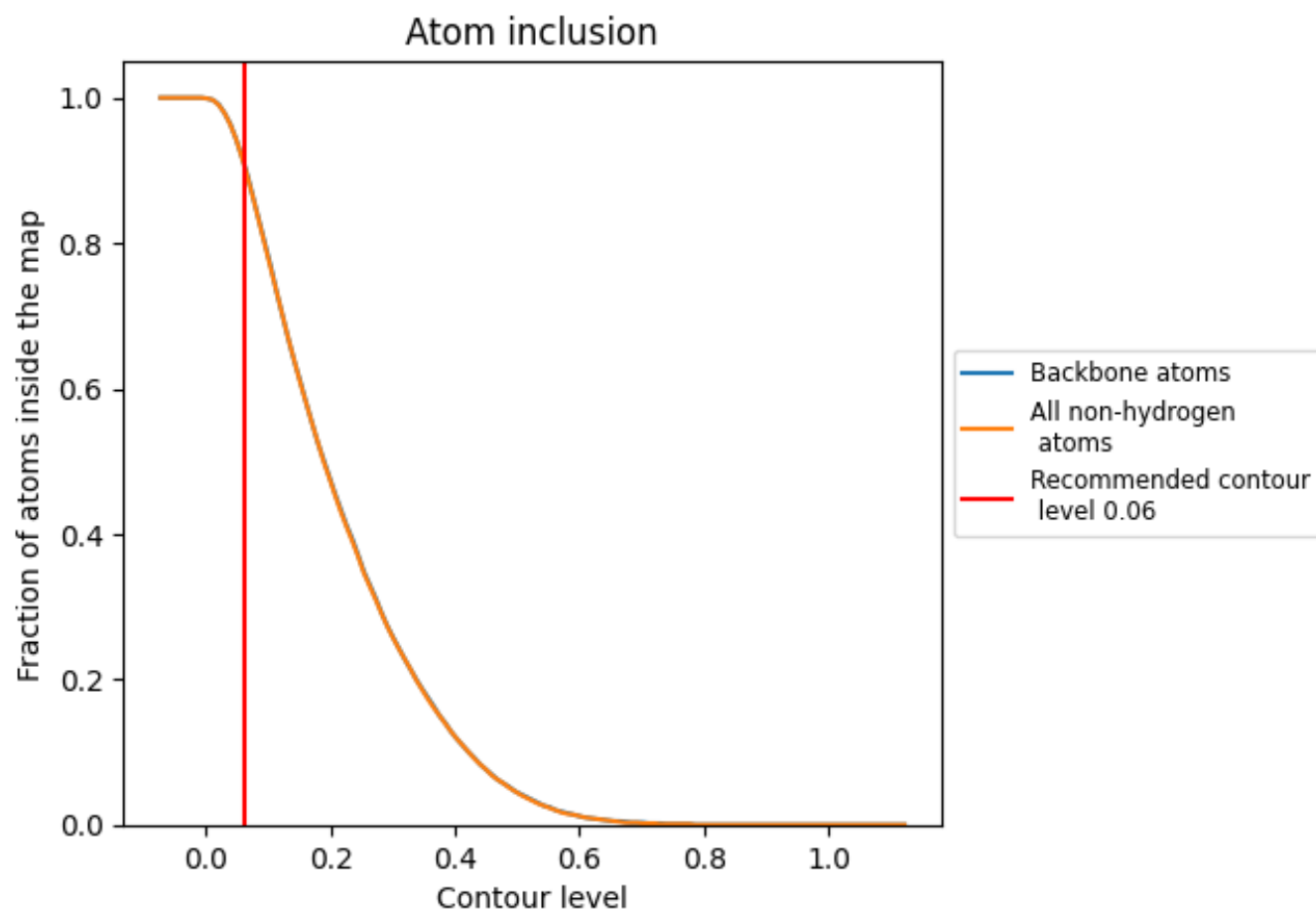
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.06).



















































9.4 Atom inclusion [i](#)



At the recommended contour level, 91% of all backbone atoms, 91% 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 (0.06) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9110	 0.4270
A	 0.9120	 0.4250
B	 0.8730	 0.3160
C	 0.9490	 0.4890
D	 0.9670	 0.5040
E	 0.9480	 0.4580
F	 0.7390	 0.2440
G	 0.9150	 0.3910
H	 0.8290	 0.2810
I	 0.6790	 0.1580
J	 0.8160	 0.2490
K	 0.7830	 0.4120
L	 0.9400	 0.4870
M	 0.8730	 0.3170
N	 0.9400	 0.4850
O	 0.9120	 0.4240
P	 0.9670	 0.5030
Q	 0.9140	 0.3950
R	 0.8290	 0.2840
S	 0.8180	 0.2540
T	 0.7830	 0.4070
U	 0.9500	 0.4910
V	 0.9480	 0.4570
W	 0.7360	 0.2470
X	 0.6800	 0.1600

