Full wwPDB X-ray Structure Validation Report (i)

Jun 11, 2024 – 10:38 PM EDT

PDB ID	:	1DML
Title	:	CRYSTAL STRUCTURE OF HERPES SIMPLEX UL42 BOUND TO THE C-TERMINUS OF HSV POL
Authors	:	Zuccola, H.J.; Filman, D.J.; Coen, D.M.; Hogle, J.M.
Deposited on	:	1999-12-14
Resolution	:	2.70 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp
with specific help available everywhere you see the (i) 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 (1)) were used in the production of this report:

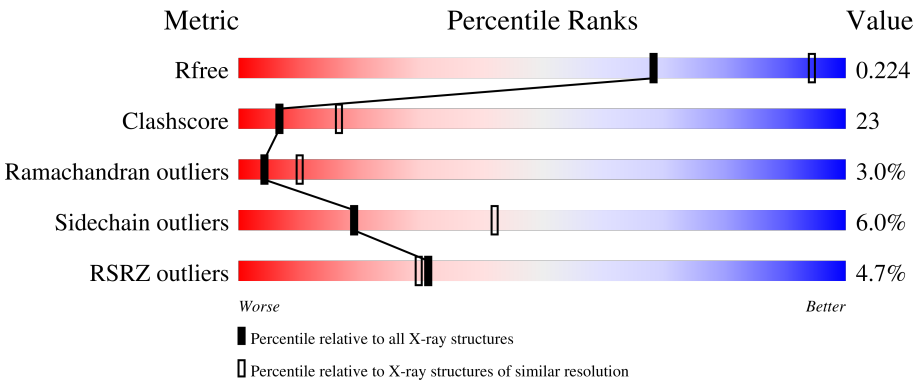
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	319	3%, 50%, 29%, •, •, 16%
1	C	319	4%, 51%, 29%, 5%, 15%
1	E	319	3%, 52%, 30%, •, 14%
1	G	319	6%, 51%, 31%, •, 14%
2	B	36	3%, 56%, 39%, 6%

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Mol	Chain	Length	Quality of chain
2	D	36	3% 53% 42% 6%
2	F	36	3% 44% 47% 8%
2	H	36	8% 42% 50% 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 9414 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 DNA POLYMERASE PROCESSIVITY FACTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	267	2059	1309	362	381	7	0	0	0
1	C	272	2087	1325	368	387	7	0	0	0
1	E	275	2108	1336	370	395	7	0	0	0
1	G	275	2108	1336	370	395	7	0	0	0

- Molecule 2 is a protein called DNA POLYMERASE.

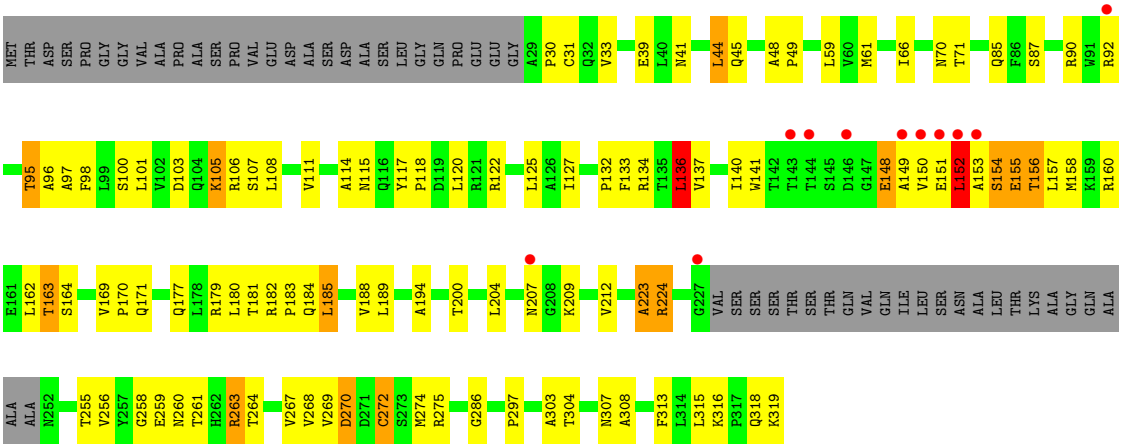
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	36	263	159	53	50	1	0	0	0
2	D	36	263	159	53	50	1	0	0	0
2	F	36	263	159	53	50	1	0	0	0
2	H	36	263	159	53	50	1	0	0	0

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 electron 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 dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

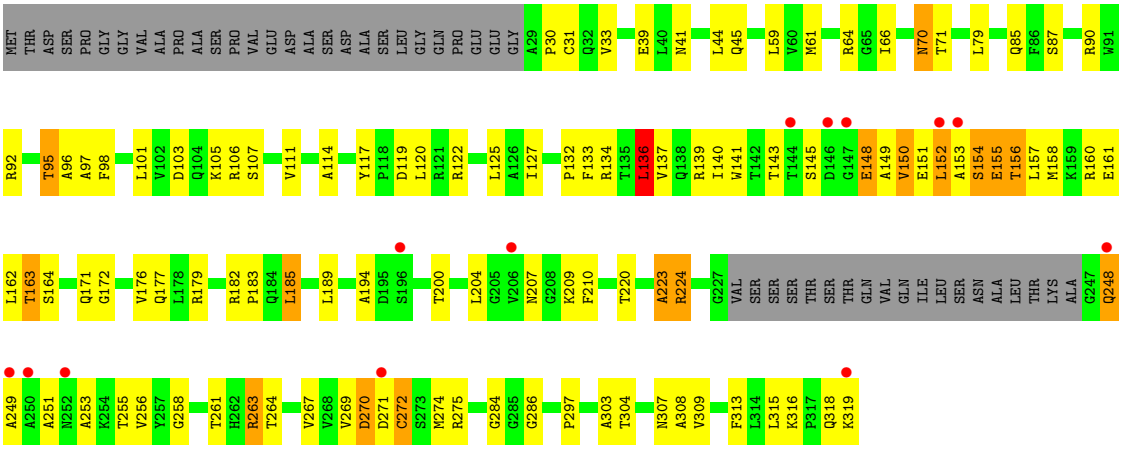
• Molecule 1: DNA POLYMERASE PROCESSIVITY FACTOR

Chain A:



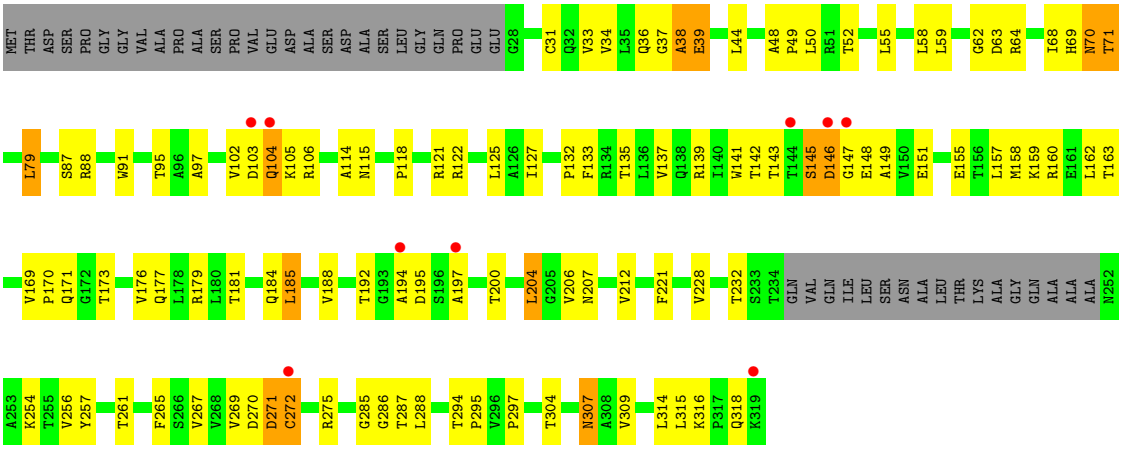
• Molecule 1: DNA POLYMERASE PROCESSIVITY FACTOR

Chain C:



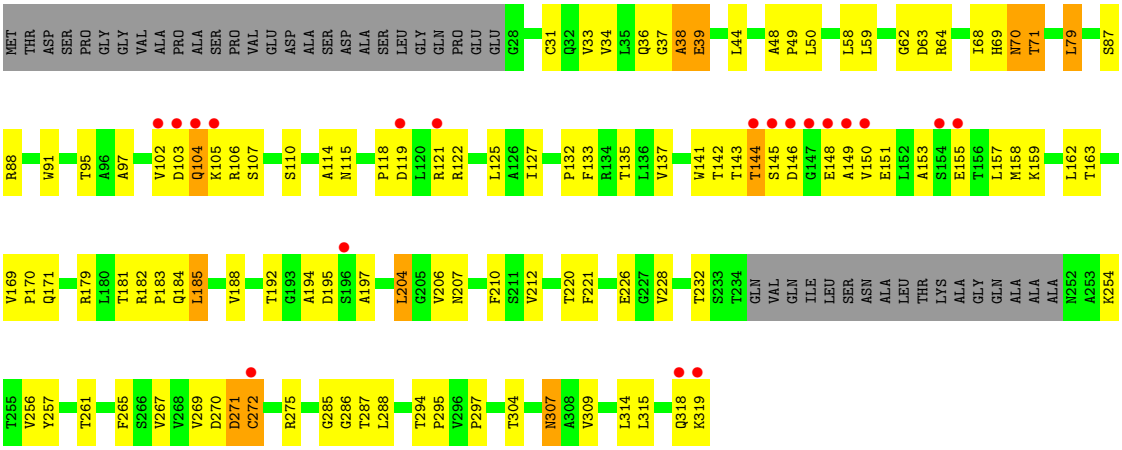
• Molecule 1: DNA POLYMERASE PROCESSIVITY FACTOR

Chain E:



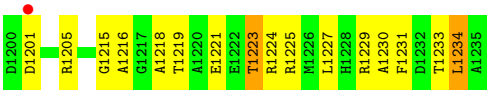
• Molecule 1: DNA POLYMERASE PROCESSIVITY FACTOR

Chain G:



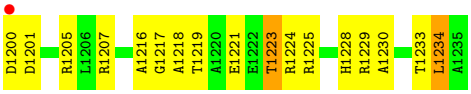
• Molecule 2: DNA POLYMERASE

Chain B:



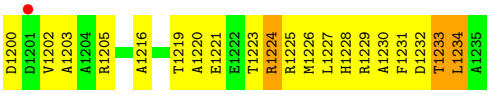
• Molecule 2: DNA POLYMERASE

Chain D:



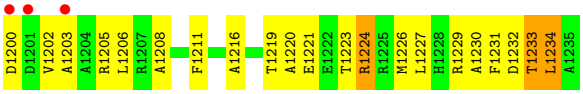
• Molecule 2: DNA POLYMERASE

Chain F:



• Molecule 2: DNA POLYMERASE

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	54.32Å 100.07Å 129.53Å 90.00° 100.62° 90.00°	Depositor
Resolution (Å)	12.00 – 2.70 29.87 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.6 (12.00-2.70) 99.9 (29.87-2.50)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.21 (at 2.51Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.230 , 0.281 0.190 , 0.224	Depositor DCC
R_{free} test set	1140 reflections (2.42%)	wwPDB-VP
Wilson B-factor (Å^2)	30.9	Xtriage
Anisotropy	0.174	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 44.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	9414	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 56.37 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.7625e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality (i)

5.1 Standard geometry (i)

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	A	0.41	0/2097	0.71	2/2851 (0.1%)
1	C	0.41	0/2125	0.70	2/2889 (0.1%)
1	E	0.39	0/2146	0.65	0/2918
1	G	0.38	0/2146	0.64	0/2918
2	B	0.41	0/265	0.56	0/354
2	D	0.40	0/265	0.56	0/354
2	F	0.38	0/265	0.52	0/354
2	H	0.39	0/265	0.55	0/354
All	All	0.40	0/9574	0.66	4/12992 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	155	GLU	N-CA-C	-6.85	92.49	111.00
1	C	155	GLU	N-CA-C	-6.85	92.50	111.00
1	A	136	LEU	CA-CB-CG	5.30	127.49	115.30
1	C	136	LEU	CA-CB-CG	5.27	127.43	115.30

There are no chirality outliers.

There are no planarity outliers.

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	A	2059	0	2104	100	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2087	0	2130	96	0
1	E	2108	0	2150	104	0
1	G	2108	0	2150	104	0
2	B	263	0	256	18	0
2	D	263	0	256	20	0
2	F	263	0	256	25	0
2	H	263	0	256	22	0
All	All	9414	0	9558	444	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 23.

All (444) 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)
1:G:121:ARG:HH11	1:G:143:THR:HG22	1.18	1.06
1:A:267:VAL:HG11	1:A:315:LEU:HD13	1.34	1.05
1:G:171:GLN:HA	2:H:1233:THR:HG21	1.39	1.04
1:C:149:ALA:HB3	1:C:152:LEU:HD22	1.41	0.99
1:E:286:GLY:HA2	1:E:304:THR:HG23	1.44	0.99
1:C:267:VAL:HG11	1:C:315:LEU:HD13	1.41	0.99
1:G:307:ASN:HD21	1:G:309:VAL:HG22	1.28	0.98
1:E:307:ASN:HD21	1:E:309:VAL:HG22	1.32	0.95
1:C:248:GLN:HG3	1:C:249:ALA:H	1.33	0.93
1:G:286:GLY:HA2	1:G:304:THR:HG23	1.51	0.92
1:E:171:GLN:HA	2:F:1233:THR:HG21	1.53	0.91
1:E:307:ASN:HD22	1:E:309:VAL:H	1.18	0.90
1:G:121:ARG:NH1	1:G:143:THR:HG22	1.89	0.88
1:G:70:ASN:ND2	1:G:71:THR:H	1.72	0.88
1:G:307:ASN:HD22	1:G:309:VAL:H	1.19	0.87
1:C:303:ALA:HB3	1:C:308:ALA:HB1	1.54	0.86
1:E:70:ASN:ND2	1:E:71:THR:H	1.73	0.85
1:A:303:ALA:HB3	1:A:308:ALA:HB1	1.57	0.85
1:G:144:THR:HG22	1:G:145:SER:H	1.40	0.84
1:C:200:THR:HB	1:C:269:VAL:HG12	1.60	0.83
1:A:200:THR:HB	1:A:269:VAL:HG12	1.61	0.83
1:E:228:VAL:O	1:E:232:THR:HG23	1.80	0.81
1:E:171:GLN:HE22	2:F:1226:MET:CE	1.94	0.80
1:E:102:VAL:HG22	1:E:159:LYS:HD3	1.63	0.80
1:E:50:LEU:HD21	1:E:309:VAL:HG11	1.65	0.78
1:G:307:ASN:ND2	1:G:309:VAL:HG22	1.97	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:102:VAL:HG22	1:G:159:LYS:HD3	1.66	0.77
1:E:267:VAL:HA	1:E:318:GLN:NE2	2.00	0.77
1:E:307:ASN:ND2	1:E:309:VAL:H	1.82	0.77
1:G:228:VAL:O	1:G:232:THR:HG23	1.83	0.77
1:G:267:VAL:HA	1:G:318:GLN:NE2	1.99	0.76
1:A:122:ARG:CZ	1:A:148:GLU:HG2	2.16	0.76
1:G:307:ASN:ND2	1:G:309:VAL:H	1.84	0.75
1:E:307:ASN:ND2	1:E:309:VAL:HG22	2.01	0.74
1:A:207:ASN:HD21	1:A:209:LYS:HB2	1.52	0.74
1:C:31:CYS:HB2	1:C:127:ILE:HB	1.69	0.74
1:G:50:LEU:HD21	1:G:309:VAL:HG11	1.69	0.74
1:A:31:CYS:HB2	1:A:127:ILE:HB	1.69	0.74
1:G:70:ASN:HD22	1:G:71:THR:H	1.36	0.74
2:B:1230:ALA:O	2:B:1234:LEU:HB2	1.88	0.73
1:A:141:TRP:HE1	1:A:152:LEU:HD21	1.53	0.73
1:A:267:VAL:HG11	1:A:315:LEU:CD1	2.17	0.73
1:C:132:PRO:HB2	1:C:163:THR:HA	1.71	0.73
1:C:39:GLU:HG3	1:C:87:SER:N	2.04	0.72
1:G:121:ARG:HH11	1:G:143:THR:CG2	1.99	0.72
1:G:171:GLN:HE22	2:H:1226:MET:CE	2.03	0.72
1:A:39:GLU:HG3	1:A:87:SER:N	2.05	0.71
1:C:207:ASN:HD21	1:C:209:LYS:HB2	1.55	0.71
2:D:1230:ALA:O	2:D:1234:LEU:HB2	1.91	0.70
1:C:162:LEU:O	1:C:164:SER:N	2.22	0.70
1:C:179:ARG:O	1:C:256:VAL:HG23	1.91	0.70
1:A:179:ARG:O	1:A:256:VAL:HG23	1.91	0.70
2:B:1201:ASP:O	2:B:1205:ARG:HG3	1.92	0.69
1:A:162:LEU:O	1:A:164:SER:N	2.22	0.69
1:G:155:GLU:O	1:G:157:LEU:HD22	1.93	0.69
1:A:132:PRO:HB2	1:A:163:THR:HA	1.75	0.68
1:A:118:PRO:HB3	2:F:1225:ARG:HH21	1.56	0.68
1:E:62:GLY:HA2	1:E:91:TRP:CE2	2.29	0.68
1:E:70:ASN:HD22	1:E:71:THR:H	1.40	0.68
1:E:294:THR:HB	1:E:295:PRO:HD2	1.76	0.67
1:G:62:GLY:HA2	1:G:91:TRP:CE2	2.29	0.67
1:C:297:PRO:HB2	1:C:315:LEU:HB2	1.76	0.66
2:D:1201:ASP:O	2:D:1205:ARG:HG3	1.95	0.66
1:A:39:GLU:H	1:A:39:GLU:CD	1.99	0.66
1:A:286:GLY:HA2	1:A:304:THR:HG23	1.77	0.66
1:C:39:GLU:H	1:C:39:GLU:CD	1.99	0.66
1:C:151:GLU:O	1:C:153:ALA:N	2.29	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1219:THR:O	2:H:1223:THR:HG22	1.95	0.66
1:C:140:ILE:O	1:C:154:SER:HA	1.96	0.65
1:E:127:ILE:N	1:E:127:ILE:HD12	2.12	0.65
1:A:140:ILE:O	1:A:154:SER:HA	1.96	0.65
1:C:41:ASN:O	1:C:45:GLN:HG3	1.96	0.65
1:C:153:ALA:O	1:C:154:SER:HB3	1.97	0.65
1:A:41:ASN:O	1:A:45:GLN:HG3	1.97	0.65
1:C:194:ALA:HB2	1:C:275:ARG:HH21	1.61	0.65
1:C:286:GLY:HA2	1:C:304:THR:HG23	1.78	0.65
1:E:143:THR:HA	1:E:148:GLU:O	1.96	0.65
1:A:297:PRO:HB2	1:A:315:LEU:HB2	1.77	0.65
2:F:1219:THR:O	2:F:1223:THR:HG22	1.97	0.64
1:G:144:THR:HB	1:G:150:VAL:HG21	1.80	0.64
1:A:39:GLU:HG3	1:A:87:SER:CA	2.27	0.64
1:G:267:VAL:HA	1:G:318:GLN:HE22	1.61	0.64
1:G:148:GLU:HG3	1:G:149:ALA:H	1.62	0.64
1:G:294:THR:HB	1:G:295:PRO:HD2	1.80	0.64
1:A:153:ALA:O	1:A:154:SER:HB3	1.97	0.64
1:C:39:GLU:HG3	1:C:87:SER:CA	2.29	0.63
1:E:188:VAL:HG13	1:E:212:VAL:HG21	1.81	0.63
1:G:171:GLN:CA	2:H:1233:THR:HG21	2.23	0.63
1:A:207:ASN:ND2	1:A:209:LYS:HB2	2.13	0.63
1:C:200:THR:HB	1:C:269:VAL:CG1	2.29	0.63
1:G:122:ARG:HB3	1:G:141:TRP:HB2	1.81	0.63
1:E:102:VAL:O	1:E:106:ARG:HB2	1.99	0.63
1:G:39:GLU:HG3	1:G:87:SER:CA	2.30	0.62
1:E:297:PRO:HG2	1:E:315:LEU:HB2	1.81	0.62
1:A:223:ALA:O	1:A:224:ARG:HB2	1.99	0.62
1:G:102:VAL:O	1:G:106:ARG:HB2	2.00	0.62
1:E:70:ASN:HD22	1:E:71:THR:N	1.98	0.61
1:C:207:ASN:ND2	1:C:209:LYS:HB2	2.14	0.61
1:G:314:LEU:HD12	2:H:1205:ARG:CZ	2.30	0.61
1:A:61:MET:HG2	1:A:66:ILE:HG12	1.83	0.61
1:C:248:GLN:HG3	1:C:249:ALA:N	2.11	0.61
1:A:101:LEU:HD23	1:A:107:SER:HB2	1.82	0.61
1:C:223:ALA:O	1:C:224:ARG:HB2	2.00	0.61
1:E:122:ARG:HB3	1:E:141:TRP:HB2	1.81	0.61
1:G:127:ILE:N	1:G:127:ILE:HD12	2.16	0.61
1:A:200:THR:HB	1:A:269:VAL:CG1	2.30	0.61
1:E:267:VAL:HA	1:E:318:GLN:HE22	1.62	0.61
1:G:70:ASN:HD22	1:G:71:THR:N	1.98	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:39:GLU:HG3	1:E:87:SER:CA	2.31	0.60
1:A:39:GLU:HG2	1:A:87:SER:OG	2.00	0.60
1:A:194:ALA:HB2	1:A:275:ARG:HH21	1.67	0.60
1:C:122:ARG:HB3	1:C:141:TRP:HB2	1.82	0.60
1:G:103:ASP:HB3	1:G:106:ARG:HD3	1.82	0.60
1:C:101:LEU:HD23	1:C:107:SER:HB2	1.83	0.60
1:C:267:VAL:HG11	1:C:315:LEU:CD1	2.23	0.60
1:E:36:GLN:NE2	1:E:122:ARG:NH1	2.49	0.60
1:E:103:ASP:HB3	1:E:106:ARG:HD3	1.84	0.60
1:E:155:GLU:O	1:E:157:LEU:HD22	2.01	0.59
1:G:36:GLN:NE2	1:G:122:ARG:NH1	2.50	0.59
1:A:127:ILE:HD12	1:A:127:ILE:N	2.18	0.59
1:C:61:MET:HG2	1:C:66:ILE:HG12	1.85	0.59
1:C:39:GLU:HG2	1:C:87:SER:OG	2.01	0.59
2:B:1225:ARG:O	2:B:1229:ARG:HG3	2.03	0.59
1:G:179:ARG:O	1:G:256:VAL:HG13	2.03	0.59
1:A:115:ASN:HD22	2:F:1228:HIS:CG	2.21	0.58
1:C:103:ASP:OD2	1:C:106:ARG:HD3	2.04	0.58
1:A:286:GLY:CA	1:A:304:THR:HG23	2.33	0.58
1:A:115:ASN:ND2	2:F:1228:HIS:CE1	2.72	0.58
1:E:314:LEU:HD12	2:F:1205:ARG:CZ	2.33	0.58
1:C:127:ILE:N	1:C:127:ILE:HD12	2.19	0.58
1:E:37:GLY:O	1:E:38:ALA:CB	2.52	0.58
2:H:1200:ASP:OD1	2:H:1202:VAL:HG22	2.03	0.58
1:G:297:PRO:HG2	1:G:315:LEU:HB2	1.84	0.58
2:H:1220:ALA:O	2:H:1224:ARG:HB3	2.04	0.58
1:G:37:GLY:O	1:G:38:ALA:CB	2.51	0.57
1:G:162:LEU:O	1:G:163:THR:HB	2.04	0.57
2:F:1200:ASP:OD1	2:F:1202:VAL:HG22	2.03	0.57
1:A:149:ALA:HB3	1:A:152:LEU:HD13	1.86	0.57
1:A:103:ASP:OD2	1:A:106:ARG:HD3	2.04	0.57
1:C:39:GLU:CG	1:C:87:SER:OG	2.52	0.57
1:G:221:PHE:HA	1:G:254:LYS:HG2	1.87	0.57
1:A:263:ARG:HG3	1:A:263:ARG:HH11	1.69	0.57
1:E:145:SER:O	1:E:146:ASP:HB2	2.05	0.56
1:E:179:ARG:O	1:E:256:VAL:HG13	2.04	0.56
2:D:1225:ARG:O	2:D:1229:ARG:HG3	2.04	0.56
1:E:221:PHE:HA	1:E:254:LYS:HG2	1.87	0.56
1:C:286:GLY:CA	1:C:304:THR:HG23	2.35	0.56
1:E:169:VAL:HG23	1:E:170:PRO:HD2	1.86	0.56
1:A:39:GLU:CG	1:A:87:SER:OG	2.53	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:318:GLN:O	1:C:319:LYS:HB2	2.06	0.56
1:A:122:ARG:HB3	1:A:141:TRP:HB2	1.88	0.56
1:C:139:ARG:NE	1:C:150:VAL:HG13	2.21	0.56
2:D:1221:GLU:O	2:D:1225:ARG:HG2	2.05	0.56
1:E:185:LEU:HD12	1:E:285:GLY:HA2	1.87	0.56
1:G:206:VAL:HG12	1:G:207:ASN:ND2	2.21	0.56
1:E:121:ARG:CZ	1:E:149:ALA:HB2	2.36	0.56
1:C:33:VAL:HB	1:C:125:LEU:HB2	1.88	0.55
1:E:39:GLU:HG3	1:E:87:SER:N	2.21	0.55
1:G:195:ASP:OD2	1:G:197:ALA:HB3	2.06	0.55
2:F:1220:ALA:O	2:F:1224:ARG:HB3	2.06	0.55
1:A:177:GLN:O	1:A:258:GLY:HA3	2.05	0.55
1:E:162:LEU:O	1:E:163:THR:HB	2.04	0.55
1:E:195:ASP:OD2	1:E:197:ALA:HB3	2.07	0.55
1:E:267:VAL:HG21	1:E:315:LEU:HD13	1.89	0.55
1:A:318:GLN:O	1:A:319:LYS:HB2	2.06	0.55
1:E:79:LEU:HG	1:E:309:VAL:HG12	1.89	0.55
1:C:122:ARG:NH2	1:C:148:GLU:HG2	2.21	0.55
1:G:185:LEU:HD12	1:G:285:GLY:HA2	1.89	0.55
1:A:162:LEU:C	1:A:164:SER:H	2.10	0.55
1:C:162:LEU:C	1:C:164:SER:H	2.10	0.55
1:C:267:VAL:CG1	1:C:315:LEU:HD22	2.37	0.54
1:A:115:ASN:HD21	2:F:1228:HIS:CE1	2.26	0.54
2:D:1225:ARG:HG3	2:D:1225:ARG:HH11	1.72	0.54
1:G:63:ASP:O	1:G:64:ARG:HB3	2.08	0.54
1:C:263:ARG:HG3	1:C:263:ARG:HH11	1.72	0.54
1:G:132:PRO:HB2	1:G:163:THR:HA	1.88	0.54
2:B:1221:GLU:O	2:B:1225:ARG:HG2	2.08	0.54
1:C:156:THR:C	1:C:157:LEU:HD12	2.28	0.54
1:C:194:ALA:HB2	1:C:275:ARG:NH2	2.23	0.54
1:C:151:GLU:C	1:C:152:LEU:HD23	2.28	0.54
1:G:295:PRO:HG2	2:H:1208:ALA:O	2.07	0.54
1:G:79:LEU:HG	1:G:309:VAL:HG12	1.90	0.54
1:G:70:ASN:ND2	1:G:71:THR:N	2.49	0.53
1:G:169:VAL:HG23	1:G:170:PRO:HD2	1.89	0.53
2:H:1202:VAL:HG23	2:H:1203:ALA:N	2.23	0.53
1:E:70:ASN:ND2	1:E:71:THR:N	2.49	0.53
1:E:121:ARG:HD3	1:E:143:THR:OG1	2.09	0.53
1:E:132:PRO:HB2	1:E:163:THR:HA	1.89	0.53
1:C:251:ALA:C	1:C:253:ALA:H	2.11	0.53
1:G:39:GLU:HG3	1:G:87:SER:N	2.23	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:206:VAL:HG12	1:E:207:ASN:ND2	2.23	0.53
1:A:171:GLN:HB2	2:B:1229:ARG:NH1	2.24	0.53
1:C:85:GLN:HG3	1:C:307:ASN:OD1	2.08	0.53
1:A:33:VAL:HB	1:A:125:LEU:HB2	1.90	0.53
1:A:141:TRP:HE1	1:A:152:LEU:CD2	2.21	0.53
1:G:188:VAL:HG13	1:G:212:VAL:HG21	1.90	0.53
2:B:1225:ARG:HG3	2:B:1225:ARG:HH11	1.74	0.53
1:A:156:THR:C	1:A:157:LEU:HD12	2.29	0.53
1:C:171:GLN:HB2	2:D:1229:ARG:NH1	2.24	0.52
1:A:223:ALA:O	1:A:224:ARG:CB	2.57	0.52
1:C:223:ALA:O	1:C:224:ARG:CB	2.57	0.52
1:E:63:ASP:O	1:E:64:ARG:HB3	2.09	0.52
1:A:85:GLN:HG3	1:A:307:ASN:OD1	2.09	0.52
1:A:270:ASP:HA	1:A:316:LYS:HE3	1.90	0.52
1:C:177:GLN:O	1:C:258:GLY:HA3	2.09	0.52
1:E:31:CYS:HB2	1:E:127:ILE:HB	1.91	0.52
1:A:30:PRO:CB	1:A:92:ARG:HD3	2.40	0.52
1:G:314:LEU:HB2	2:H:1205:ARG:NH2	2.24	0.52
1:G:31:CYS:HB2	1:G:127:ILE:HB	1.91	0.52
1:A:150:VAL:N	1:A:152:LEU:HD22	2.25	0.52
1:E:121:ARG:NH2	1:E:149:ALA:HB2	2.25	0.52
1:E:185:LEU:HD12	1:E:285:GLY:CA	2.40	0.52
1:E:261:THR:HG22	1:E:261:THR:O	2.10	0.51
1:A:90:ARG:NH2	1:A:92:ARG:HD2	2.25	0.51
1:A:163:THR:HB	1:G:133:PHE:CG	2.46	0.51
1:G:39:GLU:HG3	1:G:87:SER:HA	1.92	0.51
1:G:115:ASN:O	1:G:118:PRO:HD3	2.11	0.51
1:E:269:VAL:HG13	1:E:269:VAL:O	2.10	0.51
1:G:171:GLN:HA	2:H:1233:THR:CG2	2.27	0.51
1:C:90:ARG:NH2	1:C:92:ARG:HD2	2.26	0.51
1:E:39:GLU:HG3	1:E:87:SER:HA	1.93	0.51
1:E:69:HIS:CD2	1:E:70:ASN:N	2.79	0.50
1:G:71:THR:HG22	1:G:71:THR:O	2.11	0.50
2:F:1202:VAL:HG23	2:F:1203:ALA:N	2.24	0.50
1:C:145:SER:HB3	1:C:153:ALA:HB2	1.93	0.50
1:C:152:LEU:HG	1:C:153:ALA:N	2.27	0.50
2:D:1221:GLU:OE1	2:D:1224:ARG:HD3	2.11	0.50
1:G:69:HIS:CD2	1:G:70:ASN:N	2.80	0.50
1:G:269:VAL:HG13	1:G:269:VAL:O	2.12	0.50
1:A:267:VAL:CG1	1:A:315:LEU:HD22	2.42	0.50
1:E:104:GLN:OE1	1:E:105:LYS:HE3	2.12	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:256:VAL:HG12	1:G:257:TYR:N	2.26	0.50
1:C:248:GLN:O	1:C:251:ALA:HB3	2.11	0.50
1:G:169:VAL:HG21	2:H:1230:ALA:HB1	1.92	0.50
1:C:270:ASP:HA	1:C:316:LYS:HE3	1.94	0.49
1:G:185:LEU:HD12	1:G:285:GLY:CA	2.42	0.49
1:C:164:SER:OG	1:E:160:ARG:NE	2.40	0.49
1:E:288:LEU:HD23	1:E:288:LEU:N	2.27	0.49
1:C:59:LEU:O	1:C:97:ALA:HA	2.13	0.49
1:G:261:THR:HG22	1:G:261:THR:O	2.12	0.49
1:A:115:ASN:ND2	2:F:1228:HIS:CD2	2.80	0.49
1:G:169:VAL:HG21	2:H:1230:ALA:CB	2.43	0.49
1:E:256:VAL:HG12	1:E:257:TYR:N	2.28	0.49
1:G:34:VAL:HG21	1:G:88:ARG:HH21	1.78	0.49
1:C:152:LEU:HG	1:C:153:ALA:H	1.78	0.49
1:E:34:VAL:HG21	1:E:88:ARG:HH21	1.78	0.49
1:A:59:LEU:O	1:A:97:ALA:HA	2.13	0.48
1:A:194:ALA:HB2	1:A:275:ARG:NH2	2.28	0.48
2:D:1217:GLY:HA3	1:E:137:VAL:HG21	1.95	0.48
1:G:267:VAL:HG21	1:G:315:LEU:HD13	1.94	0.48
1:C:30:PRO:CB	1:C:92:ARG:HD3	2.43	0.48
1:G:48:ALA:HB3	1:G:49:PRO:CD	2.43	0.48
1:E:33:VAL:HB	1:E:125:LEU:HB2	1.95	0.48
1:G:104:GLN:OE1	1:G:105:LYS:HE3	2.13	0.48
1:G:270:ASP:O	1:G:271:ASP:O	2.32	0.48
1:A:133:PHE:HB3	1:A:160:ARG:HH22	1.77	0.48
1:E:171:GLN:HE22	2:F:1226:MET:HE1	1.78	0.48
1:G:48:ALA:HB3	1:G:49:PRO:HD3	1.96	0.48
1:G:58:LEU:HD11	1:G:97:ALA:HB1	1.96	0.48
1:A:286:GLY:N	1:A:304:THR:HG23	2.29	0.47
1:E:270:ASP:O	1:E:271:ASP:O	2.32	0.47
2:B:1221:GLU:OE1	2:B:1224:ARG:HD3	2.14	0.47
1:G:33:VAL:HB	1:G:125:LEU:HB2	1.97	0.47
1:E:58:LEU:HD11	1:E:97:ALA:HB1	1.95	0.47
2:D:1219:THR:O	2:D:1223:THR:HG23	2.14	0.47
2:D:1225:ARG:HG3	2:D:1225:ARG:NH1	2.30	0.47
1:E:71:THR:O	1:E:71:THR:HG22	2.13	0.47
1:G:144:THR:HB	1:G:150:VAL:CG2	2.45	0.47
1:E:195:ASP:N	1:E:272:CYS:HB3	2.29	0.47
1:G:36:GLN:NE2	1:G:122:ARG:HH11	2.12	0.47
1:G:104:GLN:HG2	1:G:105:LYS:HG3	1.97	0.47
1:G:195:ASP:N	1:G:272:CYS:HB3	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:169:VAL:HG21	2:F:1230:ALA:HB1	1.97	0.47
1:C:98:PHE:CE2	1:C:136:LEU:HB2	2.49	0.47
1:C:171:GLN:C	2:D:1233:THR:HG21	2.35	0.47
2:B:1225:ARG:HG3	2:B:1225:ARG:NH1	2.31	0.46
1:C:117:TYR:HB3	1:C:120:LEU:HB2	1.97	0.46
1:C:153:ALA:O	1:C:154:SER:CB	2.62	0.46
1:C:139:ARG:HE	1:C:150:VAL:HG13	1.80	0.46
1:E:36:GLN:NE2	1:E:122:ARG:HH11	2.13	0.46
1:E:63:ASP:OD1	2:F:1224:ARG:NE	2.48	0.46
1:A:98:PHE:CE2	1:A:136:LEU:HB2	2.50	0.46
1:A:133:PHE:HB3	1:A:160:ARG:NH2	2.30	0.46
1:G:39:GLU:CG	1:G:87:SER:OG	2.63	0.46
1:G:288:LEU:HD23	1:G:288:LEU:N	2.30	0.46
1:A:105:LYS:HG3	1:E:173:THR:HB	1.97	0.46
1:A:263:ARG:HD3	1:A:264:THR:O	2.15	0.46
1:C:267:VAL:CG1	1:C:315:LEU:HB3	2.46	0.46
2:F:1221:GLU:OE1	2:F:1221:GLU:N	2.40	0.46
1:G:170:PRO:HG3	2:H:1234:LEU:HD11	1.97	0.46
1:A:137:VAL:HG22	1:A:158:MET:HG2	1.97	0.46
1:C:133:PHE:HB3	1:C:160:ARG:HH22	1.80	0.46
1:G:39:GLU:HG2	1:G:87:SER:OG	2.16	0.46
1:A:269:VAL:HG13	1:A:272:CYS:HB2	1.98	0.46
2:B:1229:ARG:O	2:B:1233:THR:HG23	2.16	0.46
1:A:171:GLN:C	2:B:1233:THR:HG21	2.37	0.46
2:B:1219:THR:O	2:B:1223:THR:HG23	2.16	0.46
1:E:115:ASN:O	1:E:118:PRO:HD3	2.15	0.46
1:E:169:VAL:HG21	2:F:1230:ALA:CB	2.46	0.46
1:G:179:ARG:NH2	1:G:226:GLU:OE2	2.48	0.46
1:G:204:LEU:HB2	1:G:265:PHE:CE2	2.51	0.46
2:H:1229:ARG:O	2:H:1232:ASP:HB2	2.16	0.46
1:A:267:VAL:HG13	1:A:315:LEU:HB3	1.98	0.45
1:G:63:ASP:O	1:G:64:ARG:CB	2.64	0.45
2:B:1218:ALA:HB3	2:B:1223:THR:HG22	1.98	0.45
2:D:1218:ALA:HB3	2:D:1223:THR:HG22	1.98	0.45
1:A:96:ALA:HB2	1:A:134:ARG:NH2	2.31	0.45
1:C:286:GLY:N	1:C:304:THR:HG23	2.32	0.45
2:F:1229:ARG:O	2:F:1232:ASP:HB2	2.16	0.45
2:H:1227:LEU:O	2:H:1231:PHE:HD1	1.99	0.45
1:A:150:VAL:N	1:A:152:LEU:CD2	2.80	0.45
1:A:263:ARG:HD3	1:A:263:ARG:C	2.36	0.45
1:A:274:MET:HA	1:A:313:PHE:CE2	2.52	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:188:VAL:O	1:G:192:THR:HG23	2.16	0.45
1:A:185:LEU:HD22	1:A:189:LEU:HG	1.99	0.45
1:C:137:VAL:HG22	1:C:158:MET:HG2	1.97	0.45
1:C:269:VAL:HG13	1:C:272:CYS:HB2	1.98	0.45
1:A:171:GLN:OE1	2:B:1229:ARG:NH1	2.50	0.45
1:A:267:VAL:CG1	1:A:315:LEU:HB3	2.47	0.45
1:C:90:ARG:HG3	1:C:90:ARG:HH11	1.82	0.45
1:C:133:PHE:HB3	1:C:160:ARG:NH2	2.32	0.45
1:G:206:VAL:HG12	1:G:207:ASN:CG	2.37	0.45
1:C:185:LEU:HD22	1:C:189:LEU:HG	1.99	0.45
1:G:107:SER:HB3	1:G:110:SER:OG	2.16	0.45
1:G:137:VAL:HG22	1:G:158:MET:HG2	1.99	0.45
1:A:90:ARG:HH11	1:A:90:ARG:HG3	1.82	0.45
1:E:206:VAL:HG12	1:E:207:ASN:CG	2.36	0.45
2:F:1224:ARG:HH11	2:F:1224:ARG:CG	2.30	0.45
1:A:39:GLU:CD	1:A:39:GLU:N	2.70	0.44
1:C:274:MET:HA	1:C:313:PHE:CE2	2.52	0.44
1:G:59:LEU:HD22	1:G:68:ILE:HG12	1.98	0.44
1:E:52:THR:HB	1:E:55:LEU:HD12	1.99	0.44
1:C:267:VAL:HG13	1:C:315:LEU:HB3	1.99	0.44
1:C:96:ALA:HB2	1:C:134:ARG:NH2	2.33	0.44
1:E:184:GLN:O	1:E:188:VAL:HG23	2.18	0.44
1:G:184:GLN:O	1:G:188:VAL:HG23	2.17	0.44
1:C:122:ARG:CZ	1:C:148:GLU:HG2	2.48	0.44
1:E:104:GLN:HG2	1:E:105:LYS:HG3	1.99	0.44
1:E:137:VAL:HG22	1:E:158:MET:HG2	2.00	0.44
1:G:151:GLU:O	1:G:153:ALA:N	2.50	0.44
2:H:1221:GLU:OE1	2:H:1221:GLU:N	2.42	0.43
1:C:207:ASN:HD21	1:C:209:LYS:HE2	1.83	0.43
2:F:1227:LEU:O	2:F:1231:PHE:HD1	2.01	0.43
1:A:224:ARG:HD2	1:A:255:THR:CG2	2.48	0.43
1:A:207:ASN:HD21	1:A:209:LYS:HE2	1.84	0.43
2:D:1207:ARG:HH21	1:E:158:MET:CE	2.31	0.43
1:E:48:ALA:HB3	1:E:49:PRO:CD	2.48	0.43
1:E:169:VAL:CG2	1:E:170:PRO:HD2	2.49	0.43
1:C:149:ALA:O	1:C:150:VAL:HB	2.19	0.43
1:E:204:LEU:HB2	1:E:265:PHE:CE2	2.53	0.43
1:C:79:LEU:HD13	1:C:309:VAL:HG12	2.00	0.43
1:A:115:ASN:ND2	2:F:1228:HIS:NE2	2.67	0.43
1:A:223:ALA:HB1	1:A:261:THR:HB	2.01	0.43
1:C:263:ARG:HD3	1:C:264:THR:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:63:ASP:OD1	2:H:1224:ARG:NE	2.52	0.42
1:C:119:ASP:HB3	1:C:143:THR:OG1	2.18	0.42
1:C:267:VAL:HG11	1:C:315:LEU:HD22	2.00	0.42
1:E:64:ARG:HA	1:E:64:ARG:HD2	1.82	0.42
1:A:95:THR:HG21	2:B:1223:THR:OG1	2.19	0.42
1:A:180:LEU:HD23	1:A:256:VAL:CG2	2.49	0.42
2:B:1215:GLY:H	2:B:1223:THR:CG2	2.32	0.42
1:C:149:ALA:C	1:C:151:GLU:H	2.22	0.42
1:C:176:VAL:HG12	1:C:177:GLN:N	2.35	0.42
1:E:48:ALA:HB3	1:E:49:PRO:HD3	2.02	0.42
2:D:1207:ARG:HH21	1:E:158:MET:HE2	1.84	0.42
1:E:63:ASP:O	1:E:64:ARG:CB	2.66	0.42
1:E:141:TRP:CE2	1:E:151:GLU:HG3	2.55	0.42
1:E:176:VAL:HG12	1:E:177:GLN:N	2.35	0.42
1:A:48:ALA:HB3	1:A:49:PRO:CD	2.49	0.42
1:C:185:LEU:O	1:C:189:LEU:HG	2.19	0.42
1:G:144:THR:HG22	1:G:145:SER:N	2.20	0.42
1:E:139:ARG:HD2	1:E:151:GLU:OE2	2.19	0.42
1:G:170:PRO:CG	2:H:1234:LEU:HD11	2.50	0.42
1:G:318:GLN:HB2	1:G:319:LYS:H	1.62	0.42
1:A:100:SER:HA	1:A:108:LEU:HD12	2.02	0.42
1:C:30:PRO:CA	1:C:92:ARG:HD3	2.50	0.42
1:E:181:THR:OG1	1:E:184:GLN:HG3	2.20	0.42
1:A:117:TYR:HB3	1:A:120:LEU:HB2	2.02	0.42
1:A:169:VAL:CG2	1:A:170:PRO:HD2	2.50	0.42
1:C:95:THR:HG21	2:D:1223:THR:OG1	2.20	0.42
1:A:180:LEU:HD23	1:A:256:VAL:HG23	2.00	0.42
1:E:39:GLU:HG2	1:E:87:SER:OG	2.20	0.42
1:G:181:THR:OG1	1:G:184:GLN:HG3	2.20	0.42
1:A:115:ASN:HD22	2:F:1228:HIS:CD2	2.38	0.41
1:A:188:VAL:HG13	1:A:212:VAL:HG21	2.02	0.41
2:B:1227:LEU:O	2:B:1231:PHE:HD1	2.02	0.41
1:E:59:LEU:HD22	1:E:68:ILE:HG12	2.02	0.41
1:C:171:GLN:HB2	2:D:1229:ARG:HH11	1.85	0.41
1:E:142:THR:O	1:E:149:ALA:HA	2.20	0.41
2:H:1202:VAL:CG2	2:H:1203:ALA:N	2.83	0.41
1:A:151:GLU:O	1:A:152:LEU:O	2.38	0.41
1:C:224:ARG:HD2	1:C:255:THR:CG2	2.50	0.41
1:C:263:ARG:HD3	1:C:263:ARG:C	2.41	0.41
1:E:267:VAL:CG2	1:E:315:LEU:HD13	2.49	0.41
1:E:307:ASN:ND2	1:E:309:VAL:HG13	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:1206:LEU:O	2:H:1211:PHE:HB2	2.21	0.41
1:E:170:PRO:HG3	2:F:1234:LEU:HD11	2.03	0.41
1:A:185:LEU:O	1:A:189:LEU:HG	2.20	0.41
1:G:127:ILE:N	1:G:127:ILE:CD1	2.84	0.41
1:G:265:PHE:CD1	1:G:265:PHE:C	2.93	0.41
1:A:182:ARG:N	1:A:183:PRO:HD2	2.35	0.41
1:E:307:ASN:ND2	1:E:307:ASN:C	2.74	0.41
1:A:181:THR:HG23	1:A:184:GLN:OE1	2.20	0.41
1:C:172:GLY:O	2:D:1233:THR:CG2	2.68	0.41
1:G:307:ASN:ND2	1:G:307:ASN:C	2.74	0.41
1:A:30:PRO:CA	1:A:92:ARG:HD3	2.50	0.41
1:A:162:LEU:C	1:A:164:SER:N	2.72	0.41
1:C:70:ASN:HD22	1:C:70:ASN:HA	1.52	0.41
1:C:162:LEU:C	1:C:164:SER:N	2.71	0.41
1:C:223:ALA:HB1	1:C:261:THR:HB	2.03	0.41
1:C:271:ASP:OD1	1:C:271:ASP:O	2.38	0.41
1:E:102:VAL:O	1:E:103:ASP:HB3	2.21	0.41
1:E:192:THR:HG22	1:E:200:THR:HG21	2.03	0.41
1:G:169:VAL:CG2	1:G:170:PRO:HD2	2.51	0.41
1:A:148:GLU:C	1:A:150:VAL:H	2.23	0.41
1:A:200:THR:O	1:A:268:VAL:HA	2.20	0.41
1:E:265:PHE:CD1	1:E:265:PHE:C	2.93	0.41
2:F:1202:VAL:CG2	2:F:1203:ALA:N	2.84	0.41
1:G:194:ALA:HB2	1:G:275:ARG:HD3	2.02	0.41
1:A:44:LEU:HD12	1:A:44:LEU:HA	1.98	0.41
1:C:210:PHE:O	1:C:220:THR:HA	2.21	0.41
2:D:1200:ASP:CG	2:D:1201:ASP:N	2.74	0.41
1:E:143:THR:HG23	1:E:147:GLY:HA2	2.02	0.41
1:G:64:ARG:HA	1:G:64:ARG:HD2	1.82	0.41
1:G:210:PHE:O	1:G:220:THR:HA	2.21	0.41
1:A:169:VAL:HG22	1:A:170:PRO:HD2	2.03	0.40
1:E:194:ALA:HB2	1:E:275:ARG:HD3	2.03	0.40
1:G:182:ARG:N	1:G:183:PRO:HD2	2.36	0.40
1:A:171:GLN:HB2	2:B:1229:ARG:HH11	1.86	0.40
2:B:1215:GLY:H	2:B:1223:THR:HG21	1.85	0.40
1:C:182:ARG:N	1:C:183:PRO:HD2	2.36	0.40
1:E:188:VAL:O	1:E:192:THR:HG23	2.21	0.40
1:C:64:ARG:HD3	2:D:1228:HIS:CE1	2.57	0.40
1:E:132:PRO:HD2	1:E:133:PHE:CE1	2.57	0.40
1:E:315:LEU:O	1:E:316:LYS:C	2.59	0.40
1:A:39:GLU:HG3	1:A:87:SER:HA	2.01	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:GLU:HG2	1:A:260:ASN:ND2	2.36	0.40
2:D:1234:LEU:HD12	2:D:1234:LEU:HA	1.97	0.40
1:E:314:LEU:HB2	2:F:1205:ARG:NH2	2.36	0.40
1:G:119:ASP:HB2	1:G:142:THR:OG1	2.21	0.40
1:G:132:PRO:HD2	1:G:133:PHE:CE1	2.56	0.40
1:E:39:GLU:CG	1:E:87:SER:OG	2.69	0.40
1:G:142:THR:O	1:G:149:ALA:HA	2.21	0.40
2:H:1224:ARG:CG	2:H:1224:ARG:HH11	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

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	A	263/319 (82%)	237 (90%)	18 (7%)	8 (3%)	4 10
1	C	268/319 (84%)	240 (90%)	16 (6%)	12 (4%)	2 5
1	E	271/319 (85%)	243 (90%)	21 (8%)	7 (3%)	5 13
1	G	271/319 (85%)	238 (88%)	28 (10%)	5 (2%)	8 21
2	B	34/36 (94%)	33 (97%)	0	1 (3%)	4 10
2	D	34/36 (94%)	33 (97%)	0	1 (3%)	4 10
2	F	34/36 (94%)	31 (91%)	2 (6%)	1 (3%)	4 10
2	H	34/36 (94%)	30 (88%)	3 (9%)	1 (3%)	4 10
All	All	1209/1420 (85%)	1085 (90%)	88 (7%)	36 (3%)	4 10

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	LEU
1	A	223	ALA

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Mol	Chain	Res	Type
1	A	270	ASP
1	A	272	CYS
2	B	1216	ALA
1	C	152	LEU
1	C	223	ALA
1	C	270	ASP
1	C	272	CYS
2	D	1216	ALA
1	E	38	ALA
1	E	145	SER
1	E	271	ASP
1	G	38	ALA
1	G	271	ASP
1	A	114	ALA
1	A	224	ARG
1	C	114	ALA
1	C	224	ARG
1	C	248	GLN
1	E	272	CYS
2	F	1216	ALA
1	G	272	CYS
2	H	1216	ALA
1	A	154	SER
1	A	163	THR
1	C	154	SER
1	C	161	GLU
1	E	104	GLN
1	E	146	ASP
1	G	104	GLN
1	G	114	ALA
1	C	150	VAL
1	C	163	THR
1	E	114	ALA
1	C	284	GLY

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 X-ray entries followed by that with respect to entries of similar resolution.

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	A	228/266 (86%)	214 (94%)	14 (6%)	18	41
1	C	229/266 (86%)	216 (94%)	13 (6%)	20	44
1	E	235/266 (88%)	224 (95%)	11 (5%)	26	54
1	G	235/266 (88%)	222 (94%)	13 (6%)	21	46
2	B	22/22 (100%)	20 (91%)	2 (9%)	9	21
2	D	22/22 (100%)	20 (91%)	2 (9%)	9	21
2	F	22/22 (100%)	19 (86%)	3 (14%)	3	8
2	H	22/22 (100%)	19 (86%)	3 (14%)	3	8
All	All	1015/1152 (88%)	954 (94%)	61 (6%)	19	42

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	LEU
1	A	70	ASN
1	A	71	THR
1	A	95	THR
1	A	105	LYS
1	A	111	VAL
1	A	136	LEU
1	A	148	GLU
1	A	152	LEU
1	A	155	GLU
1	A	156	THR
1	A	185	LEU
1	A	204	LEU
1	A	263	ARG
2	B	1223	THR
2	B	1234	LEU
1	C	44	LEU
1	C	70	ASN
1	C	71	THR
1	C	95	THR
1	C	105	LYS
1	C	111	VAL
1	C	136	LEU
1	C	148	GLU
1	C	155	GLU
1	C	156	THR
1	C	185	LEU

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Mol	Chain	Res	Type
1	C	204	LEU
1	C	263	ARG
2	D	1223	THR
2	D	1234	LEU
1	E	39	GLU
1	E	44	LEU
1	E	70	ASN
1	E	71	THR
1	E	79	LEU
1	E	95	THR
1	E	135	THR
1	E	185	LEU
1	E	204	LEU
1	E	287	THR
1	E	307	ASN
2	F	1224	ARG
2	F	1233	THR
2	F	1234	LEU
1	G	39	GLU
1	G	44	LEU
1	G	70	ASN
1	G	71	THR
1	G	79	LEU
1	G	95	THR
1	G	135	THR
1	G	144	THR
1	G	146	ASP
1	G	185	LEU
1	G	204	LEU
1	G	287	THR
1	G	307	ASN
2	H	1224	ARG
2	H	1233	THR
2	H	1234	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	70	ASN
1	A	115	ASN
1	A	190	ASN
1	A	282	GLN

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Mol	Chain	Res	Type
1	C	70	ASN
1	C	138	GLN
1	C	190	ASN
1	E	36	GLN
1	E	70	ASN
1	E	171	GLN
1	E	207	ASN
1	E	252	ASN
1	E	307	ASN
1	G	36	GLN
1	G	70	ASN
1	G	171	GLN
1	G	207	ASN
1	G	252	ASN
1	G	307	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	267/319 (83%)	-0.19	11 (4%)	37	36	5, 19, 64, 85	0
1	C	272/319 (85%)	-0.09	13 (4%)	30	28	5, 23, 67, 87	0
1	E	275/319 (86%)	-0.02	9 (3%)	46	46	8, 29, 69, 90	0
1	G	275/319 (86%)	0.15	19 (6%)	16	15	8, 33, 76, 91	0
2	B	36/36 (100%)	-0.28	1 (2%)	53	54	9, 23, 45, 69	0
2	D	36/36 (100%)	-0.16	1 (2%)	53	54	11, 23, 48, 71	0
2	F	36/36 (100%)	0.27	1 (2%)	53	54	11, 46, 68, 82	0
2	H	36/36 (100%)	0.43	3 (8%)	11	9	15, 48, 71, 86	0
All	All	1233/1420 (86%)	-0.02	58 (4%)	31	30	5, 27, 69, 91	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	144	THR	6.9
1	E	146	ASP	6.1
1	G	146	ASP	6.1
1	C	152	LEU	5.9
2	H	1200	ASP	5.8
1	E	319	LYS	5.3
1	C	249	ALA	5.1
1	E	104	GLN	5.1
1	G	154	SER	4.9
1	G	105	LYS	4.6
1	G	148	GLU	4.6
1	C	146	ASP	4.6
1	C	248	GLN	4.5
1	G	319	LYS	4.5
1	A	146	ASP	4.3
1	C	319	LYS	4.2

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Mol	Chain	Res	Type	RSRZ
1	G	103	ASP	4.1
1	G	104	GLN	4.1
1	G	150	VAL	4.1
1	C	144	THR	4.0
1	E	103	ASP	3.9
1	G	147	GLY	3.9
1	A	227	GLY	3.8
1	C	250	ALA	3.7
1	G	272	CYS	3.5
1	C	252	ASN	3.4
1	E	194	ALA	3.4
2	F	1201	ASP	3.4
1	E	272	CYS	3.3
1	A	151	GLU	3.3
2	H	1201	ASP	3.3
1	A	144	THR	3.3
1	C	206	VAL	3.2
1	A	153	ALA	3.1
2	H	1203	ALA	3.1
1	E	144	THR	3.1
1	A	143	THR	3.1
2	D	1200	ASP	3.0
1	A	207	ASN	3.0
1	G	149	ALA	2.8
1	A	152	LEU	2.7
1	E	147	GLY	2.7
1	G	121	ARG	2.6
1	G	145	SER	2.6
1	C	271	ASP	2.5
1	C	153	ALA	2.5
1	C	196	SER	2.4
1	G	155	GLU	2.4
1	E	197	ALA	2.3
1	G	102	VAL	2.3
1	A	149	ALA	2.3
2	B	1201	ASP	2.3
1	G	318	GLN	2.2
1	G	196	SER	2.2
1	C	147	GLY	2.2
1	A	92	ARG	2.2
1	G	119	ASP	2.1
1	A	150	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.