



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:36 AM GMT

PDB ID : 2HTM
Title : Crystal structure of TTHA0676 from *Thermus thermophilus* HB8
Authors : Sugahara, M.; Kunishima, N.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on : 2006-07-26
Resolution : 2.30 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

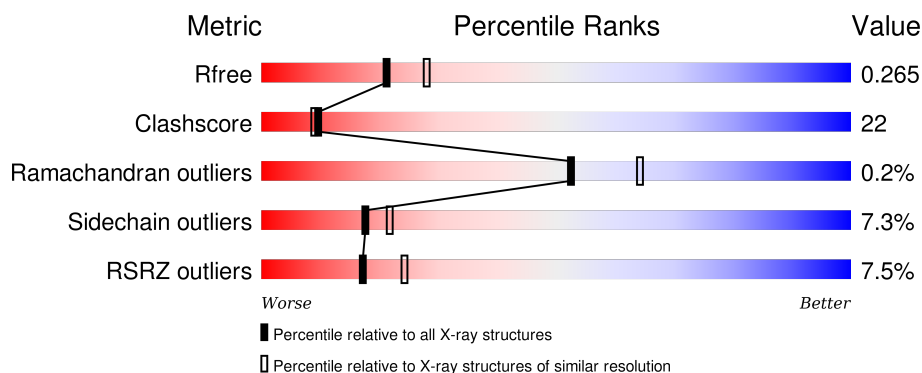
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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}	91344	3852 (2.30-2.30)
Clashscore	102246	4452 (2.30-2.30)
Ramachandran outliers	100387	4410 (2.30-2.30)
Sidechain outliers	100360	4409 (2.30-2.30)
RSRZ outliers	91569	3857 (2.30-2.30)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	268	<div> <div>5%</div> <div>49% 35% 13%</div> </div>
1	B	268	<div> <div>5%</div> <div>53% 29% 13%</div> </div>
1	C	268	<div> <div>6%</div> <div>50% 36% 10%</div> </div>
1	D	268	<div> <div>6%</div> <div>52% 32% 13%</div> </div>
2	E	64	<div> <div>14%</div> <div>70% 27%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	64	<div><div>8%</div><div><div></div><div>61%</div><div>38%</div></div><div></div></div>
2	G	64	<div><div>11%</div><div><div></div><div>70%</div><div>27%</div></div><div></div></div>
2	H	64	<div><div>16%</div><div><div></div><div>67%</div><div>30%</div></div><div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9392 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 Thiazole biosynthesis protein thiG.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	234	Total	C	N	O	S	0	0	0
			1759	1127	305	320	7			
1	B	233	Total	C	N	O	S	0	0	0
			1750	1122	304	317	7			
1	C	241	Total	C	N	O	S	0	0	0
			1809	1160	315	327	7			
1	D	234	Total	C	N	O	S	0	0	0
			1759	1127	305	320	7			

- Molecule 2 is a protein called Putative thiamine biosynthesis protein ThiS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	64	Total	C	N	O	Se	0	0	0
			489	311	80	95	3			
2	F	64	Total	C	N	O	Se	0	0	0
			489	311	80	95	3			
2	G	64	Total	C	N	O	Se	0	0	0
			489	311	80	95	3			
2	H	64	Total	C	N	O	Se	0	0	0
			489	311	80	95	3			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	1	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
E	23	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
E	61	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
F	1	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
F	23	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
F	61	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
G	1	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
G	23	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8

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Chain	Residue	Modelled	Actual	Comment	Reference
G	61	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
H	1	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
H	23	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8
H	61	MSE	MET	MODIFIED RESIDUE	UNP Q5SKG8

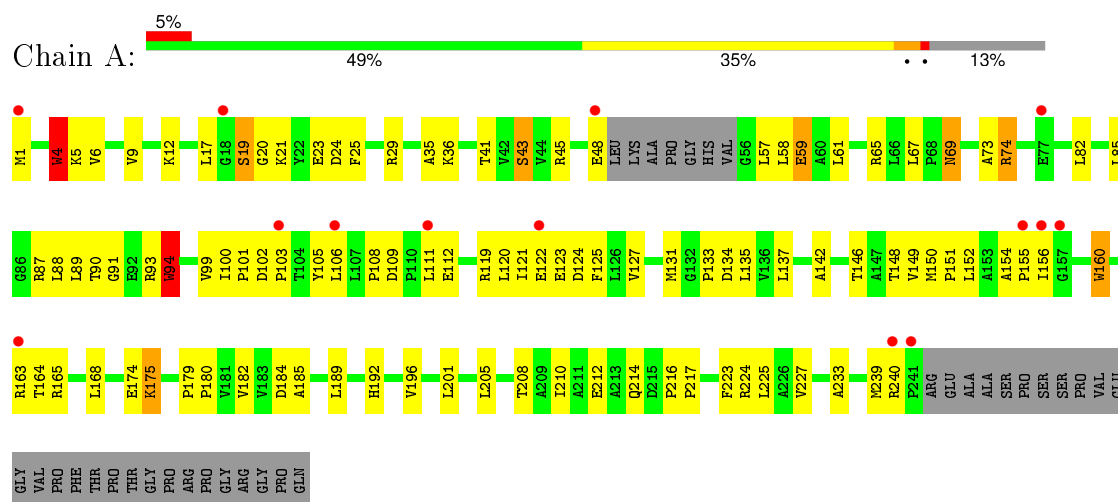
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	89	Total O 89 89	0	0
3	B	60	Total O 60 60	0	0
3	C	94	Total O 94 94	0	0
3	D	58	Total O 58 58	0	0
3	E	10	Total O 10 10	0	0
3	F	14	Total O 14 14	0	0
3	G	30	Total O 30 30	0	0
3	H	4	Total O 4 4	0	0

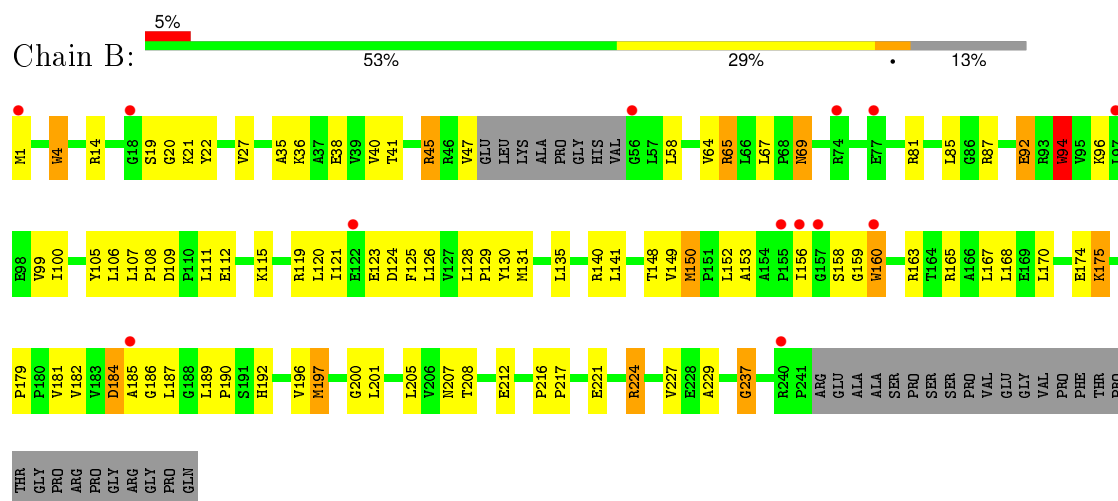
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Thiazole biosynthesis protein thiG



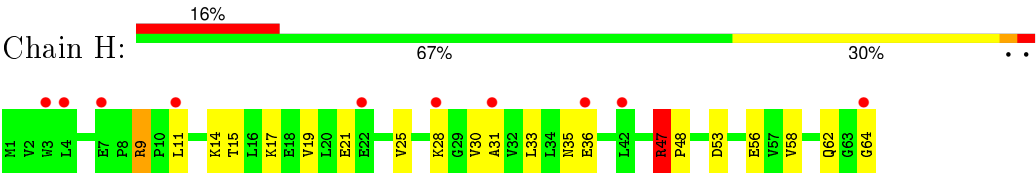
• Molecule 1: Thiazole biosynthesis protein thiG



• Molecule 1: Thiazole biosynthesis protein thiG



● Molecule 2: Putative thiamine biosynthesis protein ThiS



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	47.34Å 73.51Å 100.91Å 68.64° 80.16° 79.09°	Depositor
Resolution (Å)	19.96 – 2.30 20.06 – 2.31	Depositor EDS
% Data completeness (in resolution range)	97.7 (19.96-2.30) 86.6 (20.06-2.31)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.67 (at 2.30Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.253 , 0.266 0.252 , 0.265	Depositor DCC
R_{free} test set	2670 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	40.9	Xtriage
Anisotropy	0.536	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 55.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 53298 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9392	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.69% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.76	3/1789 (0.2%)	1.04	0/2433
1	B	0.75	3/1780 (0.2%)	1.04	0/2421
1	C	0.60	2/1842 (0.1%)	0.90	0/2507
1	D	0.81	3/1789 (0.2%)	1.00	2/2433 (0.1%)
2	E	0.92	1/493 (0.2%)	1.02	0/662
2	F	0.93	1/493 (0.2%)	1.05	0/662
2	G	0.64	0/493	0.80	0/662
2	H	0.62	0/493	0.81	1/662 (0.2%)
All	All	0.75	13/9172 (0.1%)	0.98	3/12442 (0.0%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	94	TRP	NE1-CE2	8.94	1.49	1.37
1	A	94	TRP	NE1-CE2	8.88	1.49	1.37
1	A	4	TRP	NE1-CE2	8.75	1.49	1.37
1	B	160	TRP	NE1-CE2	8.75	1.49	1.37
1	B	4	TRP	NE1-CE2	8.74	1.49	1.37
2	F	3	TRP	NE1-CE2	8.74	1.49	1.37
1	A	160	TRP	NE1-CE2	8.74	1.49	1.37
1	B	94	TRP	NE1-CE2	8.72	1.48	1.37
1	D	160	TRP	NE1-CE2	8.72	1.48	1.37
1	D	4	TRP	NE1-CE2	8.70	1.48	1.37
1	C	4	TRP	NE1-CE2	8.70	1.48	1.37
1	C	160	TRP	NE1-CE2	8.70	1.48	1.37
2	E	3	TRP	NE1-CE2	8.63	1.48	1.37

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	101	PRO	N-CD-CG	7.21	114.02	103.20
2	H	47	ARG	CD-NE-CZ	-5.44	115.98	123.60
1	D	165	ARG	CD-NE-CZ	-5.10	116.46	123.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1759	0	1844	102	0
1	B	1750	0	1838	77	0
1	C	1809	0	1900	109	0
1	D	1759	0	1844	92	0
2	E	489	0	503	21	0
2	F	489	0	503	17	0
2	G	489	0	503	19	0
2	H	489	0	503	20	0
3	A	89	0	0	5	0
3	B	60	0	0	0	0
3	C	94	0	0	11	0
3	D	58	0	0	6	0
3	E	10	0	0	0	0
3	F	14	0	0	0	0
3	G	30	0	0	1	0
3	H	4	0	0	1	0
All	All	9392	0	9438	413	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 22.

All (413) 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:B:40:VAL:HG23	1:B:64:VAL:HG11	1.38	1.06
1:A:45:ARG:HG2	1:A:45:ARG:HH11	1.30	0.95
1:A:156:ILE:HG12	1:A:185:ALA:HB1	1.51	0.92
2:F:36:GLU:OE1	2:F:36:GLU:HA	1.69	0.90
1:A:196:VAL:HG13	1:A:201:LEU:HD12	1.55	0.87
1:B:111:LEU:HD23	1:B:111:LEU:O	1.76	0.85
1:C:28:MET:CE	1:C:61:LEU:HD21	2.07	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:100:ILE:HG21	1:D:106:LEU:HA	1.58	0.84
1:A:120:LEU:O	1:A:125:PHE:HB2	1.77	0.83
1:D:18:GLY:HA2	1:D:41:THR:HG22	1.61	0.82
1:A:88:LEU:HD13	2:E:40:LEU:HD23	1.61	0.82
1:A:111:LEU:HD13	1:D:111:LEU:HD13	1.62	0.82
1:B:40:VAL:CG2	1:B:64:VAL:HG11	2.10	0.81
2:H:9:ARG:HB3	2:H:11:LEU:HG	1.63	0.80
1:D:88:LEU:HD12	1:D:89:LEU:N	1.97	0.79
1:C:164:THR:HG22	1:C:164:THR:O	1.81	0.79
1:C:54:HIS:CE1	1:C:55:VAL:HG23	2.19	0.78
1:A:164:THR:O	1:A:164:THR:HG22	1.83	0.78
1:B:152:LEU:HA	1:B:184:ASP:O	1.84	0.78
1:B:106:LEU:HB3	1:B:156:ILE:HD12	1.66	0.77
1:B:184:ASP:HB2	1:B:205:LEU:HB3	1.65	0.76
1:D:196:VAL:HG13	1:D:201:LEU:HD12	1.66	0.76
1:C:133:PRO:HB3	1:C:164:THR:HG21	1.67	0.76
1:C:187:LEU:HD22	1:C:192:HIS:HB3	1.65	0.76
1:A:239:MET:CE	1:B:159:GLY:HA3	2.15	0.76
1:D:90:THR:CG2	1:D:92:GLU:H	2.00	0.75
1:B:120:LEU:O	1:B:125:PHE:HB2	1.86	0.75
1:C:94:TRP:HA	1:C:126:LEU:HB2	1.69	0.74
1:C:40:VAL:HG23	1:C:64:VAL:HG11	1.70	0.74
1:C:120:LEU:O	1:C:125:PHE:HB2	1.88	0.73
1:A:148:THR:HG22	1:A:149:VAL:N	2.02	0.73
1:C:164:THR:HG22	1:C:168:LEU:HG	1.69	0.73
1:A:156:ILE:HG12	1:A:185:ALA:CB	2.19	0.71
1:C:38:GLU:O	1:C:64:VAL:HG13	1.89	0.71
1:C:85:LEU:HD11	2:G:33:LEU:HD11	1.73	0.71
1:B:41:THR:HA	1:B:67:LEU:O	1.89	0.71
1:C:28:MET:HE2	1:C:61:LEU:HD21	1.73	0.71
1:A:41:THR:HG22	1:A:67:LEU:HB3	1.73	0.71
1:C:140:ARG:NH1	3:C:356:HOH:O	2.24	0.71
1:A:109:ASP:HB3	1:A:112:GLU:HB2	1.73	0.70
1:C:28:MET:HE3	1:C:61:LEU:HD21	1.72	0.70
1:A:184:ASP:HB3	1:A:205:LEU:HB3	1.74	0.70
1:C:49:LEU:HG	2:G:23:MSE:HE3	1.74	0.69
1:C:69:ASN:C	1:C:69:ASN:HD22	1.96	0.69
1:A:239:MET:HE1	1:B:159:GLY:HA3	1.74	0.68
1:D:184:ASP:HB2	1:D:205:LEU:HB3	1.75	0.68
1:C:156:ILE:HG12	1:C:185:ALA:HB1	1.76	0.68
1:B:38:GLU:O	1:B:64:VAL:HG13	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:LEU:HD12	1:C:114:LEU:HD23	1.74	0.68
1:D:150:MET:HG2	1:D:182:VAL:HB	1.75	0.68
2:F:35:ASN:O	2:F:36:GLU:HB2	1.93	0.67
1:B:94:TRP:HD1	1:B:94:TRP:O	1.76	0.67
1:D:156:ILE:HG12	1:D:185:ALA:HB1	1.77	0.67
1:A:99:VAL:HG11	1:A:112:GLU:HB3	1.75	0.67
1:D:90:THR:HG23	1:D:92:GLU:H	1.60	0.67
1:C:196:VAL:HG13	1:C:201:LEU:HD12	1.77	0.66
1:D:187:LEU:CD1	1:D:204:VAL:HG13	2.25	0.66
1:C:133:PRO:HB3	1:C:164:THR:CG2	2.25	0.66
2:H:33:LEU:HB3	2:H:56:GLU:HB2	1.78	0.66
1:C:20:GLY:O	1:C:21:LYS:HB2	1.95	0.65
1:A:4:TRP:HD1	1:A:4:TRP:H	1.45	0.65
1:C:6:VAL:HG13	1:C:9:VAL:HB	1.78	0.65
1:D:103:PRO:HA	1:D:106:LEU:HD23	1.79	0.65
1:B:41:THR:HG22	1:B:67:LEU:HD23	1.79	0.64
1:D:187:LEU:HD12	1:D:204:VAL:HG13	1.80	0.64
1:C:152:LEU:HA	1:C:184:ASP:O	1.96	0.64
1:C:182:VAL:HG22	1:C:203:ALA:HB3	1.78	0.64
1:A:223:PHE:O	1:A:227:VAL:HG23	1.99	0.63
2:G:26:GLU:HG2	3:G:68:HOH:O	1.97	0.63
1:A:184:ASP:OD1	1:A:184:ASP:N	2.31	0.63
1:C:28:MET:HE1	1:C:57:LEU:HD12	1.81	0.63
2:F:47:ARG:O	2:F:47:ARG:HG2	1.99	0.63
1:B:187:LEU:HD22	1:B:192:HIS:HB3	1.80	0.63
1:D:128:LEU:HB3	1:D:148:THR:HG21	1.81	0.63
1:C:148:THR:HG22	1:C:149:VAL:N	2.14	0.62
1:C:156:ILE:HG12	1:C:185:ALA:CB	2.29	0.62
1:C:225:LEU:HD22	1:D:225:LEU:HD22	1.80	0.62
1:A:103:PRO:HA	1:A:106:LEU:HD23	1.81	0.62
1:A:4:TRP:N	1:A:4:TRP:CD1	2.67	0.62
1:B:158:SER:HB2	1:B:160:TRP:CD1	2.34	0.62
1:C:148:THR:HG23	1:C:180:PRO:O	1.99	0.61
1:C:43:SER:CB	2:G:63:GLY:HA3	2.30	0.61
1:C:103:PRO:HA	1:C:106:LEU:HD23	1.81	0.61
1:B:184:ASP:O	1:B:185:ALA:HB3	2.01	0.61
1:A:105:TYR:O	1:A:106:LEU:HB2	1.99	0.61
1:C:54:HIS:NE2	1:C:55:VAL:HG23	2.15	0.61
1:D:41:THR:CG2	2:H:64:GLY:HA2	2.31	0.60
1:D:141:LEU:O	1:D:146:THR:HG23	2.01	0.60
1:B:69:ASN:HD22	1:B:69:ASN:C	2.03	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:164:THR:CG2	1:C:164:THR:O	2.48	0.60
1:D:29:ARG:HG3	1:D:60:ALA:HB1	1.82	0.60
1:D:61:LEU:HD13	1:D:66:LEU:HD22	1.84	0.60
1:A:58:LEU:HD21	2:E:60:LEU:HD12	1.83	0.60
1:D:88:LEU:C	1:D:88:LEU:HD12	2.21	0.60
1:C:94:TRP:CA	1:C:126:LEU:HB2	2.30	0.60
1:A:152:LEU:HA	1:A:184:ASP:O	2.02	0.59
1:B:14:ARG:HG2	1:B:14:ARG:NH1	2.17	0.59
1:C:135:LEU:HD22	1:C:170:LEU:HB3	1.83	0.59
1:B:100:ILE:HG21	1:B:106:LEU:HA	1.84	0.59
1:B:87:ARG:NH2	1:B:123:GLU:O	2.36	0.59
1:B:175:LYS:NZ	1:B:200:GLY:O	2.28	0.59
1:C:78:GLU:O	1:C:81:ARG:HB3	2.03	0.59
2:E:40:LEU:HD12	2:E:43:GLU:OE1	2.03	0.59
1:C:25:PHE:HB3	1:C:60:ALA:CB	2.33	0.59
1:D:85:LEU:HD13	2:H:58:VAL:HG21	1.84	0.58
1:A:20:GLY:O	1:A:21:LYS:HB2	2.02	0.58
2:H:62:GLN:HG2	3:H:66:HOH:O	2.03	0.58
2:E:16:LEU:HD12	2:E:45:PRO:HD2	1.85	0.58
2:E:47:ARG:HG3	2:E:47:ARG:O	1.99	0.58
1:C:236:ALA:O	1:D:214:GLN:HB2	2.03	0.58
1:A:45:ARG:NH1	1:A:45:ARG:HG2	2.06	0.57
1:B:94:TRP:HA	1:B:126:LEU:HB2	1.85	0.57
1:C:25:PHE:HB3	1:C:60:ALA:HB2	1.87	0.57
1:C:225:LEU:HD22	1:D:225:LEU:CD2	2.33	0.57
1:B:148:THR:HA	1:B:179:PRO:HB2	1.86	0.57
1:D:128:LEU:HA	1:D:148:THR:HG22	1.84	0.57
1:A:23:GLU:O	1:A:24:ASP:HB3	2.05	0.57
2:H:47:ARG:HD3	2:H:48:PRO:O	2.03	0.57
1:D:77:GLU:HG3	3:D:275:HOH:O	2.02	0.57
1:D:120:LEU:O	1:D:125:PHE:HB2	2.04	0.57
1:A:142:ALA:HA	1:A:146:THR:HG22	1.87	0.57
1:A:148:THR:CG2	1:A:149:VAL:N	2.67	0.57
1:C:43:SER:HB2	2:G:63:GLY:HA3	1.85	0.57
1:A:94:TRP:HD1	1:A:94:TRP:O	1.88	0.57
1:B:197:MET:SD	1:B:227:VAL:HG13	2.45	0.56
1:D:184:ASP:CB	1:D:205:LEU:HB3	2.35	0.56
1:D:90:THR:HG22	1:D:92:GLU:H	1.70	0.56
2:E:2:VAL:HB	2:E:11:LEU:HB2	1.88	0.56
1:B:14:ARG:HG2	1:B:14:ARG:HH11	1.69	0.56
1:D:19:SER:O	1:D:22:TYR:HD2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:49:LEU:C	1:C:49:LEU:HD23	2.26	0.56
1:A:19:SER:O	2:E:62:GLN:NE2	2.39	0.56
1:B:85:LEU:HD13	2:F:58:VAL:HG21	1.87	0.56
1:C:87:ARG:HD3	3:C:309:HOH:O	2.05	0.56
2:F:33:LEU:HB3	2:F:56:GLU:HB2	1.86	0.56
1:B:94:TRP:CD1	1:B:94:TRP:O	2.58	0.56
1:D:119:ARG:HH11	1:D:119:ARG:HG3	1.70	0.56
1:A:90:THR:HG22	2:E:60:LEU:HD11	1.88	0.56
1:C:188:GLY:HA2	1:C:209:ALA:HB2	1.86	0.55
1:D:100:ILE:CG2	1:D:106:LEU:HA	2.35	0.55
1:A:239:MET:HE2	1:B:159:GLY:HA3	1.86	0.55
1:A:133:PRO:HG3	1:A:164:THR:HG21	1.89	0.55
1:B:128:LEU:HG	1:B:148:THR:HG22	1.88	0.55
1:B:19:SER:O	1:B:22:TYR:HD2	1.89	0.55
1:C:16:ILE:O	1:C:17:LEU:HD23	2.06	0.55
1:A:101:PRO:O	1:A:103:PRO:HD3	2.06	0.55
1:C:184:ASP:HB2	1:C:205:LEU:HB3	1.89	0.55
1:A:65:ARG:NH2	3:A:297:HOH:O	2.27	0.55
1:C:100:ILE:HG21	1:C:106:LEU:HA	1.87	0.55
1:A:41:THR:HG22	1:A:67:LEU:HD23	1.89	0.54
1:A:134:ASP:HB3	1:A:137:LEU:HB3	1.88	0.54
1:A:100:ILE:HG21	1:A:106:LEU:HA	1.90	0.54
1:D:152:LEU:O	1:D:152:LEU:HD12	2.07	0.54
1:B:205:LEU:C	1:B:205:LEU:HD23	2.28	0.54
1:D:129:PRO:HD2	1:D:148:THR:O	2.06	0.54
1:C:6:VAL:O	1:C:6:VAL:HG22	2.06	0.54
1:A:189:LEU:O	1:A:192:HIS:HB2	2.07	0.54
1:D:119:ARG:NH1	1:D:119:ARG:HG3	2.23	0.54
1:A:6:VAL:HG12	1:A:6:VAL:O	2.08	0.54
1:B:216:PRO:HB2	1:B:217:PRO:HD3	1.89	0.54
1:A:214:GLN:HG3	1:B:237:GLY:HA3	1.90	0.54
1:A:149:VAL:HG13	1:A:179:PRO:HG2	1.88	0.54
1:C:129:PRO:HD2	1:C:148:THR:O	2.08	0.54
1:C:214:GLN:HG3	1:D:237:GLY:HA3	1.90	0.53
2:E:33:LEU:HB3	2:E:56:GLU:HB2	1.89	0.53
1:B:58:LEU:HD21	2:F:60:LEU:HD12	1.89	0.53
1:C:19:SER:O	2:G:62:GLN:HB2	2.08	0.53
2:G:62:GLN:HG3	2:G:62:GLN:O	2.08	0.53
1:C:43:SER:HA	1:C:69:ASN:ND2	2.23	0.53
1:C:184:ASP:O	1:C:185:ALA:HB3	2.09	0.53
1:B:20:GLY:O	1:B:21:LYS:HB2	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:35:ALA:O	1:B:36:LYS:HB2	2.08	0.53
1:A:69:ASN:C	1:A:69:ASN:HD22	2.10	0.53
1:C:207:ASN:HD22	1:C:207:ASN:C	2.10	0.53
1:A:165:ARG:HG2	1:A:165:ARG:HH11	1.72	0.53
1:B:4:TRP:CD1	1:B:4:TRP:N	2.77	0.53
1:B:153:ALA:HB3	1:B:186:GLY:HA3	1.90	0.52
1:D:128:LEU:HB3	1:D:148:THR:CG2	2.39	0.52
1:A:17:LEU:CD2	1:A:210:ILE:HD12	2.39	0.52
1:D:61:LEU:HB3	1:D:66:LEU:HD21	1.91	0.52
1:B:208:THR:HG23	1:B:212:GLU:HG3	1.90	0.52
1:A:121:ILE:HG13	1:A:127:VAL:HG23	1.91	0.52
1:A:164:THR:O	1:A:164:THR:CG2	2.54	0.52
1:C:92:GLU:HG2	3:C:274:HOH:O	2.08	0.52
1:C:35:ALA:O	1:C:224:ARG:HG3	2.10	0.52
2:G:4:LEU:HD21	2:G:23:MSE:SE	2.60	0.52
2:E:15:THR:HG22	2:E:16:LEU:N	2.25	0.52
1:A:41:THR:HA	1:A:67:LEU:O	2.09	0.51
1:C:59:GLU:O	1:C:59:GLU:HG2	2.09	0.51
1:A:133:PRO:HB3	1:A:164:THR:HG21	1.93	0.51
1:D:8:PRO:HD2	1:D:126:LEU:HD11	1.93	0.51
1:B:94:TRP:CD1	1:B:94:TRP:C	2.83	0.51
1:A:165:ARG:HG2	1:A:165:ARG:NH1	2.26	0.51
1:A:123:GLU:O	1:A:124:ASP:HB3	2.11	0.51
1:D:184:ASP:O	1:D:185:ALA:HB3	2.11	0.51
2:F:26:GLU:N	2:F:26:GLU:OE1	2.43	0.51
2:G:12:GLU:HG3	2:G:50:ARG:HA	1.92	0.51
1:A:133:PRO:HG3	1:A:164:THR:CG2	2.41	0.50
1:C:43:SER:HA	1:C:69:ASN:HD21	1.77	0.50
1:D:187:LEU:HD12	1:D:204:VAL:CG1	2.41	0.50
1:B:148:THR:HG23	1:B:149:VAL:N	2.25	0.50
1:C:119:ARG:O	1:C:122:GLU:HG2	2.12	0.50
2:F:1:MSE:N	2:F:12:GLU:OE1	2.43	0.50
1:D:223:PHE:O	1:D:227:VAL:HG23	2.11	0.50
2:F:2:VAL:HB	2:F:11:LEU:HB2	1.93	0.50
1:B:107:LEU:HD11	1:C:170:LEU:HD12	1.94	0.50
1:C:134:ASP:HB3	1:C:137:LEU:HB3	1.94	0.50
1:D:148:THR:CG2	1:D:150:MET:HG3	2.42	0.50
1:D:20:GLY:HA2	2:H:62:GLN:HB2	1.93	0.49
1:B:99:VAL:HG11	1:B:112:GLU:HB3	1.93	0.49
1:A:150:MET:HA	1:A:182:VAL:O	2.12	0.49
1:C:43:SER:OG	2:G:63:GLY:HA3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:LEU:HD23	1:B:111:LEU:C	2.31	0.49
1:C:184:ASP:CB	1:C:205:LEU:HB3	2.42	0.49
1:A:73:ALA:HB2	1:A:82:LEU:HD12	1.94	0.49
1:D:148:THR:HG23	1:D:150:MET:HG3	1.93	0.49
1:C:148:THR:CG2	1:C:149:VAL:N	2.75	0.49
1:C:164:THR:CG2	1:C:168:LEU:HG	2.39	0.49
1:C:28:MET:HE1	1:C:57:LEU:CD1	2.43	0.49
2:H:11:LEU:O	2:H:14:LYS:HB2	2.13	0.49
1:C:28:MET:CE	1:C:57:LEU:HD12	2.42	0.49
1:C:94:TRP:CB	1:C:126:LEU:HB2	2.43	0.49
1:D:25:PHE:N	1:D:25:PHE:CD1	2.80	0.49
1:C:49:LEU:O	1:C:49:LEU:HD23	2.13	0.48
1:C:216:PRO:HB2	1:C:217:PRO:HD3	1.95	0.48
1:D:41:THR:HG23	2:H:64:GLY:HA2	1.94	0.48
2:G:47:ARG:NH2	2:G:53:ASP:OD2	2.46	0.48
1:D:101:PRO:HG3	1:D:109:ASP:HB2	1.94	0.48
1:C:156:ILE:CG1	1:C:185:ALA:HB1	2.41	0.48
1:A:90:THR:HG22	2:E:60:LEU:CD1	2.43	0.48
1:D:4:TRP:CD1	1:D:4:TRP:N	2.81	0.48
1:A:148:THR:HG22	1:A:149:VAL:H	1.75	0.48
1:A:102:ASP:HB3	3:A:355:HOH:O	2.13	0.48
1:B:65:ARG:HD3	1:B:92:GLU:OE2	2.13	0.48
1:C:99:VAL:HG11	1:C:112:GLU:HB3	1.95	0.48
1:D:85:LEU:O	1:D:89:LEU:HB2	2.12	0.48
1:A:41:THR:HG22	1:A:67:LEU:CB	2.42	0.48
1:B:105:TYR:O	1:B:106:LEU:HB2	2.12	0.48
1:A:57:LEU:HG	1:A:61:LEU:HD12	1.95	0.48
2:E:35:ASN:O	2:E:36:GLU:HB2	2.13	0.48
1:A:43:SER:HA	1:A:69:ASN:ND2	2.28	0.48
1:D:94:TRP:HD1	1:D:94:TRP:O	1.96	0.48
1:A:160:TRP:HB3	1:A:163:ARG:HE	1.79	0.48
2:F:27:LEU:O	2:F:41:GLY:HA3	2.12	0.48
1:D:86:GLY:O	1:D:90:THR:HB	2.13	0.47
1:C:78:GLU:HB3	3:C:314:HOH:O	2.14	0.47
2:H:35:ASN:O	2:H:36:GLU:HB2	2.14	0.47
1:A:12:LYS:N	1:A:12:LYS:HD2	2.28	0.47
1:D:190:PRO:HB3	1:D:226:ALA:HB2	1.96	0.47
1:D:97:LEU:HD21	1:D:116:ALA:HB3	1.96	0.47
1:A:36:LYS:HG3	1:A:224:ARG:HD2	1.96	0.47
1:B:150:MET:HA	1:B:182:VAL:O	2.14	0.47
2:F:34:LEU:HD12	2:F:55:VAL:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:102:ASP:HB3	3:C:327:HOH:O	2.13	0.47
1:D:41:THR:HG21	2:H:64:GLY:HA2	1.96	0.47
1:D:88:LEU:C	1:D:88:LEU:CD1	2.83	0.47
1:C:54:HIS:NE2	1:C:55:VAL:CG2	2.78	0.47
1:D:90:THR:CG2	1:D:92:GLU:HB2	2.44	0.47
1:C:94:TRP:HB3	1:C:126:LEU:HB2	1.97	0.47
1:A:41:THR:OG1	2:E:64:GLY:HA3	2.14	0.47
1:C:233:ALA:HB2	1:D:190:PRO:HG2	1.96	0.47
1:A:151:PRO:HB2	1:A:168:LEU:HD21	1.97	0.47
1:C:135:LEU:O	1:C:138:ALA:HB3	2.15	0.47
1:C:239:MET:HG3	1:C:239:MET:O	2.13	0.47
1:A:225:LEU:HB2	1:B:229:ALA:HB2	1.96	0.47
2:F:36:GLU:CA	2:F:36:GLU:OE1	2.44	0.46
1:D:102:ASP:HA	1:D:103:PRO:HD3	1.74	0.46
1:C:176:ALA:HA	3:C:312:HOH:O	2.15	0.46
2:G:50:ARG:HG2	2:G:53:ASP:OD2	2.14	0.46
1:D:216:PRO:HB2	1:D:217:PRO:HD3	1.97	0.46
1:C:95:VAL:HG11	1:C:120:LEU:HD13	1.97	0.46
1:B:27:VAL:HG11	1:B:216:PRO:HG2	1.97	0.46
1:C:163:ARG:NH2	3:C:280:HOH:O	2.48	0.46
1:A:74:ARG:HE	1:A:74:ARG:HB2	1.63	0.46
2:G:15:THR:O	2:G:19:VAL:HG23	2.15	0.46
1:B:96:LYS:HA	1:B:128:LEU:O	2.15	0.46
1:D:14:ARG:HG2	1:D:14:ARG:HH11	1.80	0.46
1:C:42:VAL:HG11	1:C:66:LEU:HD22	1.97	0.46
1:C:87:ARG:NH1	1:C:124:ASP:O	2.45	0.46
1:B:196:VAL:HG13	1:B:201:LEU:HD12	1.97	0.46
1:D:36:LYS:NZ	3:D:301:HOH:O	2.46	0.46
1:A:43:SER:HA	1:A:69:ASN:HD21	1.80	0.46
1:C:93:ARG:HH11	1:C:93:ARG:HD3	1.62	0.46
1:A:87:ARG:O	1:A:91:GLY:N	2.45	0.46
1:A:135:LEU:HD21	1:A:174:GLU:HG3	1.97	0.46
2:F:16:LEU:HD13	2:F:44:VAL:HB	1.98	0.46
1:B:148:THR:O	1:B:149:VAL:HG13	2.16	0.45
1:A:85:LEU:HD21	2:E:33:LEU:HB2	1.98	0.45
1:D:208:THR:CG2	1:D:212:GLU:HG3	2.46	0.45
1:B:40:VAL:HG23	1:B:64:VAL:CG1	2.27	0.45
1:D:128:LEU:HD22	1:D:148:THR:HB	1.99	0.45
1:D:187:LEU:CD1	1:D:204:VAL:CG1	2.93	0.45
1:D:153:ALA:O	1:D:164:THR:HG23	2.17	0.45
1:A:89:LEU:HG	2:E:31:ALA:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:MET:HE1	1:B:159:GLY:CA	2.46	0.45
1:C:69:ASN:C	1:C:69:ASN:ND2	2.67	0.45
1:B:221:GLU:O	1:B:224:ARG:HB3	2.16	0.45
1:C:240:ARG:HH11	1:C:240:ARG:HD3	1.64	0.45
1:B:152:LEU:HG	1:B:152:LEU:H	1.63	0.45
1:B:47:VAL:HG13	2:F:57:VAL:O	2.17	0.45
2:H:17:LYS:O	2:H:21:GLU:HB2	2.17	0.45
1:A:59:GLU:HG2	3:A:333:HOH:O	2.16	0.45
1:C:240:ARG:H	1:C:240:ARG:HG2	1.60	0.44
1:C:225:LEU:CD2	1:D:225:LEU:HD22	2.47	0.44
1:B:150:MET:HB3	1:B:182:VAL:O	2.17	0.44
1:C:190:PRO:HB3	1:C:226:ALA:HB2	1.98	0.44
1:C:193:ALA:HB2	1:C:223:PHE:HE1	1.81	0.44
1:B:128:LEU:HA	1:B:148:THR:HG22	1.99	0.44
1:A:45:ARG:CG	1:A:45:ARG:NH1	2.72	0.44
1:C:214:GLN:HB2	1:D:236:ALA:O	2.17	0.44
1:A:233:ALA:HB2	1:B:190:PRO:HG2	2.00	0.44
1:A:175:LYS:HE3	1:A:175:LYS:HB2	1.80	0.44
1:C:43:SER:HB2	2:G:63:GLY:CA	2.48	0.44
1:B:108:PRO:HG2	1:B:131:MET:HA	1.99	0.44
1:C:208:THR:O	1:C:212:GLU:HB2	2.18	0.44
2:F:20:LEU:HD11	2:F:32:VAL:HG21	1.99	0.44
1:C:28:MET:CE	1:C:57:LEU:CD1	2.95	0.44
1:A:148:THR:CG2	1:A:149:VAL:H	2.31	0.44
1:A:154:ALA:HB1	1:A:155:PRO:HD2	1.98	0.44
1:D:106:LEU:HD12	1:D:156:ILE:HB	1.99	0.44
1:C:96:LYS:NZ	3:C:272:HOH:O	2.50	0.44
1:D:161:GLY:HA2	1:D:192:HIS:ND1	2.33	0.44
1:B:128:LEU:HG	1:B:148:THR:CG2	2.48	0.44
1:A:94:TRP:CD1	1:A:94:TRP:C	2.91	0.44
2:F:12:GLU:O	2:F:12:GLU:HG2	2.17	0.44
1:A:88:LEU:HD12	1:A:89:LEU:N	2.33	0.43
1:D:17:LEU:HD11	1:D:35:ALA:HB3	2.00	0.43
1:B:168:LEU:HA	1:B:168:LEU:HD23	1.89	0.43
1:D:33:ALA:HA	3:D:288:HOH:O	2.18	0.43
1:B:109:ASP:HB3	1:B:112:GLU:HB2	1.99	0.43
1:C:32:ILE:HG21	1:C:64:VAL:HG21	2.00	0.43
1:A:148:THR:HG23	1:A:180:PRO:O	2.19	0.43
1:C:5:LYS:O	3:C:290:HOH:O	2.21	0.43
1:D:69:ASN:OD1	1:D:71:ALA:CB	2.67	0.43
1:A:88:LEU:C	1:A:88:LEU:HD12	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:LYS:HG2	1:C:178:LEU:HD21	2.00	0.43
2:E:47:ARG:HA	2:E:48:PRO:HD3	1.88	0.43
2:H:47:ARG:O	2:H:47:ARG:HD2	2.19	0.43
2:G:18:GLU:O	2:G:22:GLU:HB2	2.19	0.43
1:C:35:ALA:O	1:C:36:LYS:HB2	2.17	0.43
2:H:35:ASN:C	2:H:36:GLU:HG3	2.39	0.43
2:H:15:THR:O	2:H:19:VAL:HG23	2.19	0.43
1:C:150:MET:HA	1:C:182:VAL:O	2.18	0.43
1:A:106:LEU:HD12	1:A:156:ILE:HB	2.00	0.43
2:E:47:ARG:HD2	2:E:47:ARG:HH11	1.59	0.43
2:H:35:ASN:O	2:H:36:GLU:CB	2.67	0.43
1:B:135:LEU:HD21	1:B:174:GLU:HG3	2.00	0.42
1:B:45:ARG:HG2	1:B:45:ARG:HH11	1.83	0.42
1:A:94:TRP:CD1	1:A:94:TRP:O	2.69	0.42
1:A:88:LEU:HB2	2:E:40:LEU:HD21	2.01	0.42
1:A:123:GLU:O	1:A:124:ASP:CB	2.67	0.42
1:A:216:PRO:HB2	1:A:217:PRO:HD3	2.02	0.42
1:D:6:VAL:HG13	1:D:9:VAL:HB	2.02	0.42
1:A:69:ASN:ND2	1:A:69:ASN:C	2.73	0.42
1:D:208:THR:HG23	1:D:212:GLU:HG3	2.01	0.42
1:C:142:ALA:HA	1:C:146:THR:HG22	2.00	0.42
2:F:50:ARG:O	2:F:53:ASP:HB2	2.19	0.42
1:C:151:PRO:HB2	1:C:168:LEU:HD21	2.02	0.42
1:A:41:THR:CG2	1:A:67:LEU:HD23	2.50	0.42
1:D:14:ARG:HG2	1:D:14:ARG:NH1	2.35	0.42
1:D:181:VAL:HG11	1:D:201:LEU:HD22	2.02	0.42
1:B:14:ARG:CG	1:B:14:ARG:HH11	2.31	0.42
2:H:47:ARG:NH1	2:H:53:ASP:OD2	2.50	0.42
1:C:92:GLU:CG	3:C:274:HOH:O	2.68	0.42
1:A:5:LYS:HA	1:A:9:VAL:O	2.19	0.42
1:B:129:PRO:CG	1:B:141:LEU:HD13	2.50	0.42
1:C:36:LYS:HB2	1:C:224:ARG:HD2	2.01	0.41
1:D:87:ARG:NH2	1:D:124:ASP:O	2.53	0.41
1:A:59:GLU:OE2	3:A:281:HOH:O	2.21	0.41
2:H:25:VAL:HG21	2:H:30:VAL:HG11	2.02	0.41
1:A:184:ASP:O	1:A:185:ALA:HB3	2.20	0.41
1:A:156:ILE:HD13	3:A:277:HOH:O	2.20	0.41
1:B:94:TRP:CA	1:B:126:LEU:HB2	2.50	0.41
1:D:227:VAL:HB	3:D:293:HOH:O	2.21	0.41
1:D:175:LYS:HE3	1:D:175:LYS:HB2	1.67	0.41
1:B:81:ARG:HH11	1:B:81:ARG:HD2	1.63	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:PHE:N	1:A:25:PHE:CD1	2.87	0.41
1:D:152:LEU:C	1:D:152:LEU:HD12	2.41	0.41
1:D:4:TRP:CD1	1:D:11:LEU:O	2.74	0.41
1:B:108:PRO:HG3	1:B:130:TYR:CE2	2.56	0.41
1:D:145:GLY:O	3:D:309:HOH:O	2.22	0.41
1:A:152:LEU:HG	1:A:152:LEU:H	1.75	0.41
2:H:47:ARG:HH12	2:H:53:ASP:CG	2.23	0.41
2:E:35:ASN:O	2:E:36:GLU:CB	2.68	0.41
1:D:189:LEU:HB2	1:D:192:HIS:CE1	2.56	0.41
1:B:129:PRO:HG2	1:B:141:LEU:HD13	2.03	0.41
1:D:135:LEU:HD22	1:D:170:LEU:HB3	2.00	0.41
2:G:35:ASN:O	2:G:36:GLU:CB	2.69	0.41
1:C:154:ALA:HB1	1:C:155:PRO:HD2	2.03	0.41
1:B:167:LEU:HD23	1:B:170:LEU:HD12	2.01	0.41
1:D:128:LEU:CA	1:D:148:THR:HG22	2.51	0.41
1:D:182:VAL:HG22	1:D:203:ALA:HB3	2.03	0.41
2:G:35:ASN:O	2:G:36:GLU:HB2	2.21	0.41
2:E:50:ARG:HH11	2:E:50:ARG:HD2	1.64	0.41
1:D:89:LEU:HG	2:H:31:ALA:HB2	2.03	0.41
1:B:189:LEU:O	1:B:192:HIS:HB2	2.21	0.41
1:C:225:LEU:HB2	1:D:229:ALA:HB2	2.02	0.41
2:G:47:ARG:NH2	2:G:53:ASP:CG	2.74	0.41
1:D:99:VAL:O	1:D:108:PRO:HA	2.21	0.41
2:G:16:LEU:HD12	2:G:44:VAL:HB	2.03	0.41
1:D:152:LEU:HG	1:D:152:LEU:H	1.67	0.40
1:A:17:LEU:HD22	1:A:210:ILE:HD12	2.03	0.40
1:A:108:PRO:HG2	1:A:131:MET:HA	2.03	0.40
1:B:123:GLU:O	1:B:124:ASP:CB	2.69	0.40
1:C:119:ARG:NH1	3:C:354:HOH:O	2.54	0.40
1:A:208:THR:O	1:A:212:GLU:HB2	2.21	0.40
1:A:90:THR:CG2	2:E:60:LEU:HD11	2.50	0.40
1:B:149:VAL:HG23	1:B:181:VAL:HG22	2.04	0.40
1:A:41:THR:HG22	1:A:67:LEU:CG	2.51	0.40
1:C:49:LEU:C	1:C:49:LEU:CD2	2.90	0.40
1:D:152:LEU:HA	1:D:184:ASP:O	2.22	0.40
1:D:77:GLU:CG	3:D:275:HOH:O	2.67	0.40
1:A:35:ALA:O	1:A:36:LYS:HB2	2.20	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 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	230/268 (86%)	217 (94%)	13 (6%)	0	100	100
1	B	229/268 (85%)	214 (93%)	14 (6%)	1 (0%)	39	48
1	C	239/268 (89%)	224 (94%)	15 (6%)	0	100	100
1	D	230/268 (86%)	213 (93%)	16 (7%)	1 (0%)	39	48
2	E	62/64 (97%)	60 (97%)	2 (3%)	0	100	100
2	F	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
2	G	62/64 (97%)	57 (92%)	5 (8%)	0	100	100
2	H	62/64 (97%)	61 (98%)	1 (2%)	0	100	100
All	All	1176/1328 (89%)	1107 (94%)	67 (6%)	2 (0%)	52	64

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	237	GLY
1	D	237	GLY

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	179/205 (87%)	164 (92%)	15 (8%)	14	16
1	B	178/205 (87%)	160 (90%)	18 (10%)	9	11
1	C	184/205 (90%)	170 (92%)	14 (8%)	16	20

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	179/205 (87%)	168 (94%)	11 (6%)	23	30
2	E	53/50 (106%)	51 (96%)	2 (4%)	40	54
2	F	53/50 (106%)	51 (96%)	2 (4%)	40	54
2	G	53/50 (106%)	50 (94%)	3 (6%)	25	34
2	H	53/50 (106%)	50 (94%)	3 (6%)	25	34
All	All	932/1020 (91%)	864 (93%)	68 (7%)	17	22

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	4	TRP
1	A	19	SER
1	A	29	ARG
1	A	43	SER
1	A	48	GLU
1	A	59	GLU
1	A	69	ASN
1	A	74	ARG
1	A	93	ARG
1	A	94	TRP
1	A	119	ARG
1	A	122	GLU
1	A	175	LYS
1	A	240	ARG
1	B	1	MET
1	B	45	ARG
1	B	65	ARG
1	B	69	ASN
1	B	92	GLU
1	B	94	TRP
1	B	115	LYS
1	B	119	ARG
1	B	121	ILE
1	B	140	ARG
1	B	150	MET
1	B	163	ARG
1	B	165	ARG
1	B	175	LYS
1	B	184	ASP

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Mol	Chain	Res	Type
1	B	197	MET
1	B	207	ASN
1	B	224	ARG
1	C	5	LYS
1	C	6	VAL
1	C	45	ARG
1	C	48	GLU
1	C	62	GLU
1	C	69	ASN
1	C	74	ARG
1	C	92	GLU
1	C	94	TRP
1	C	146	THR
1	C	207	ASN
1	C	214	GLN
1	C	223	PHE
1	C	240	ARG
1	D	1	MET
1	D	29	ARG
1	D	48	GLU
1	D	90	THR
1	D	93	ARG
1	D	94	TRP
1	D	148	THR
1	D	149	VAL
1	D	175	LYS
1	D	184	ASP
1	D	207	ASN
2	E	36	GLU
2	E	47	ARG
2	F	28	LYS
2	F	47	ARG
2	G	17	LYS
2	G	26	GLU
2	G	36	GLU
2	H	9	ARG
2	H	28	LYS
2	H	47	ARG

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

Mol	Chain	Res	Type
1	A	69	ASN
1	B	69	ASN
1	B	207	ASN
1	C	69	ASN
1	C	207	ASN
1	C	214	GLN
1	D	207	ASN
1	D	214	GLN
2	G	62	GLN
2	H	62	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 carbohydrates 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

6.1 Protein, DNA and RNA chains

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	234/268 (87%)	0.41	14 (5%) 25 33	24, 40, 59, 74	0
1	B	233/268 (86%)	0.48	13 (5%) 28 36	20, 39, 60, 73	0
1	C	241/268 (89%)	0.58	16 (6%) 22 29	32, 45, 66, 83	0
1	D	234/268 (87%)	0.54	15 (6%) 23 31	33, 44, 66, 82	0
2	E	61/64 (95%)	0.69	9 (14%) 3 5	35, 56, 69, 76	0
2	F	61/64 (95%)	0.77	5 (8%) 14 20	36, 57, 69, 75	0
2	G	61/64 (95%)	0.47	7 (11%) 6 10	39, 50, 67, 71	0
2	H	61/64 (95%)	0.94	10 (16%) 2 4	48, 68, 79, 90	0
All	All	1186/1328 (89%)	0.55	89 (7%) 17 24	20, 45, 69, 90	0

All (89) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	49	LEU	10.5
1	B	156	ILE	10.0
1	C	51	ALA	9.5
1	A	156	ILE	7.4
2	F	64	GLY	6.9
1	A	1	MET	5.8
1	D	156	ILE	5.7
1	C	55	VAL	5.6
1	B	240	ARG	4.5
1	D	1	MET	4.5
1	A	48	GLU	4.2
1	C	240	ARG	4.1
1	D	157	GLY	4.0
1	B	157	GLY	4.0
1	A	240	ARG	3.9
1	D	57	LEU	3.7

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Mol	Chain	Res	Type	RSRZ
2	E	50	ARG	3.7
2	E	46	ASP	3.6
1	B	1	MET	3.6
1	D	240	ARG	3.5
2	H	36	GLU	3.4
2	H	22	GLU	3.4
2	E	64	GLY	3.3
2	G	63	GLY	3.3
2	H	42	LEU	3.3
2	H	11	LEU	3.2
1	C	156	ILE	3.2
1	C	50	LYS	3.2
1	B	155	PRO	3.1
1	A	106	LEU	3.1
1	C	77	GLU	3.1
1	D	59	GLU	3.1
1	B	122	GLU	3.0
1	B	77	GLU	3.0
1	B	160	TRP	3.0
1	A	18	GLY	2.8
2	F	32	VAL	2.8
1	D	77	GLU	2.7
1	B	18	GLY	2.7
2	G	3	TRP	2.7
1	A	155	PRO	2.7
2	H	28	LYS	2.7
1	D	23	GLU	2.6
1	D	127	VAL	2.6
2	G	64	GLY	2.5
1	C	103	PRO	2.5
1	D	160	TRP	2.5
2	G	12	GLU	2.5
2	G	57	VAL	2.5
2	G	9	ARG	2.5
1	A	163	ARG	2.4
1	C	210	ILE	2.4
2	F	28	LYS	2.4
1	C	28	MET	2.4
1	A	157	GLY	2.4
1	C	230	GLY	2.4
1	A	122	GLU	2.4
1	C	176	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
2	H	3	TRP	2.3
1	A	111	LEU	2.3
1	D	226	ALA	2.3
1	B	74	ARG	2.3
1	A	77	GLU	2.3
2	H	7	GLU	2.3
2	E	51	ASP	2.3
2	E	28	LYS	2.3
1	B	185	ALA	2.3
1	C	1	MET	2.3
2	E	12	GLU	2.2
2	H	4	LEU	2.2
1	C	127	VAL	2.1
1	A	241	PRO	2.1
2	E	21	GLU	2.1
2	F	31	ALA	2.1
1	D	48	GLU	2.1
2	G	10	PRO	2.1
2	E	39	PHE	2.1
1	D	71	ALA	2.1
1	D	29	ARG	2.1
1	B	97	LEU	2.1
2	F	3	TRP	2.1
1	B	56	GLY	2.0
1	A	103	PRO	2.0
1	C	122	GLU	2.0
2	H	31	ALA	2.0
1	D	155	PRO	2.0
1	C	160	TRP	2.0
2	H	64	GLY	2.0
2	E	15	THR	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates 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.