Full wwPDB X-ray Structure Validation Report ⓘ

Oct 18, 2023 – 12:18 AM EDT

PDB ID	:	1WX0
Title	:	Crystal structure of transaldolase from Thermus thermophilus HB8
Authors	:	Asada, Y.; Kunishima, N.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2005-01-19
Resolution	:	2.27 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 ⓘ 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:

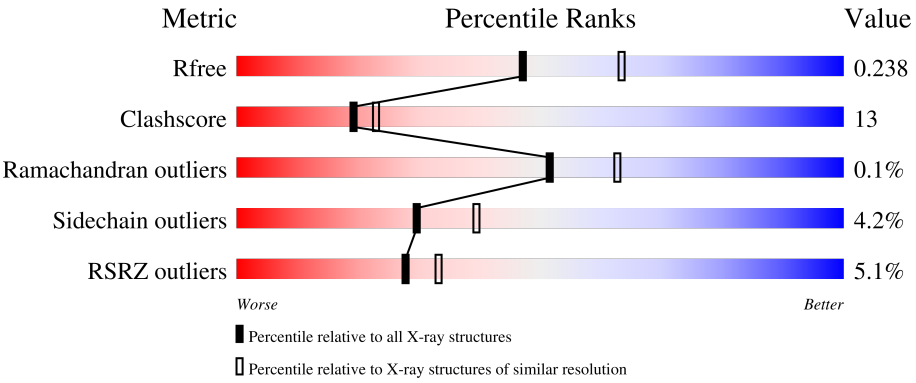
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.27 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	6980 (2.30-2.26)
Clashscore	141614	7711 (2.30-2.26)
Ramachandran outliers	138981	7597 (2.30-2.26)
Sidechain outliers	138945	7598 (2.30-2.26)
RSRZ outliers	127900	6849 (2.30-2.26)

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	223	8% 69% 24% • 5%
1	B	223	4% 76% 17% • 5%
1	C	223	3% 74% 19% • 5%
1	D	223	5% 68% 26% • 5%
1	E	223	11% 61% 32% • 5%

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Mol	Chain	Length	Quality of chain
1	F	223	6% 65% 27% • 5%
1	G	223	3% 68% 23% • 5%
1	H	223	4% 74% 18% • 5%
1	I	223	4% 73% 20% • 5%
1	J	223	% 74% 18% • 5%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 17083 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 transaldolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	211	Total	C	N	O	S	13	0	0
			1577	1003	272	295	7			
1	B	211	Total	C	N	O	S	9	0	0
			1577	1003	272	295	7			
1	C	211	Total	C	N	O	S	4	0	0
			1577	1003	272	295	7			
1	D	211	Total	C	N	O	S	8	0	0
			1577	1003	272	295	7			
1	E	211	Total	C	N	O	S	12	0	0
			1577	1003	272	295	7			
1	F	211	Total	C	N	O	S	10	0	0
			1577	1003	272	295	7			
1	G	211	Total	C	N	O	S	12	0	0
			1577	1003	272	295	7			
1	H	211	Total	C	N	O	S	3	0	0
			1577	1003	272	295	7			
1	I	211	Total	C	N	O	S	1	0	0
			1577	1003	272	295	7			
1	J	211	Total	C	N	O	S	3	0	0
			1577	1003	272	295	7			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	107	Total	O	0	0
			107	107		
2	B	147	Total	O	0	0
			147	147		
2	C	135	Total	O	0	0
			135	135		
2	D	107	Total	O	0	0
			107	107		

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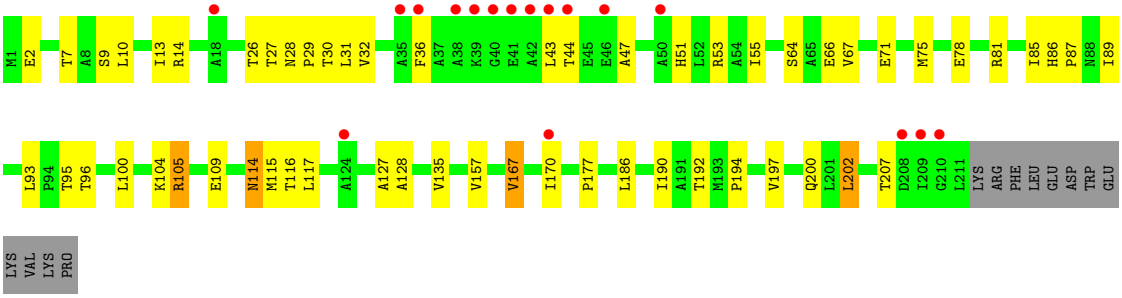
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	E	108	Total O 108 108	0	0
2	F	108	Total O 108 108	0	0
2	G	130	Total O 130 130	0	0
2	H	139	Total O 139 139	0	0
2	I	159	Total O 159 159	0	0
2	J	173	Total O 173 173	0	0

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.

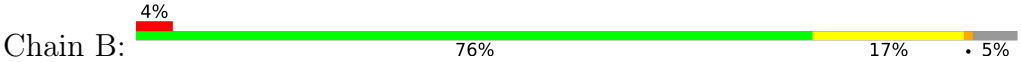
• Molecule 1: transaldolase

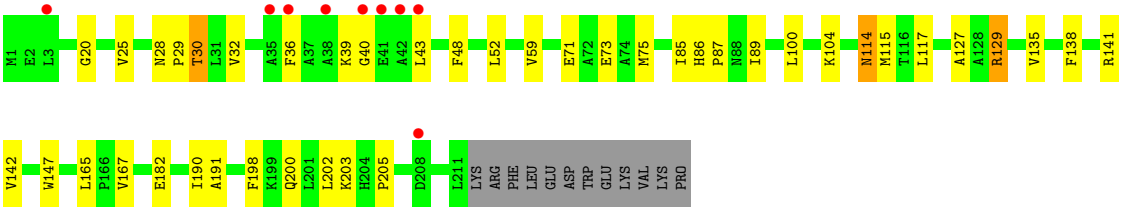
Chain A:



• Molecule 1: transaldolase

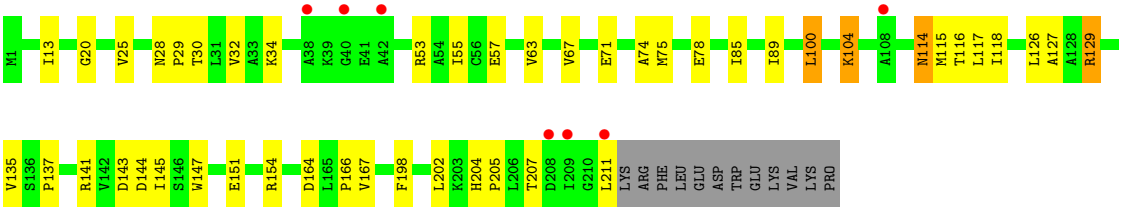
Chain B:





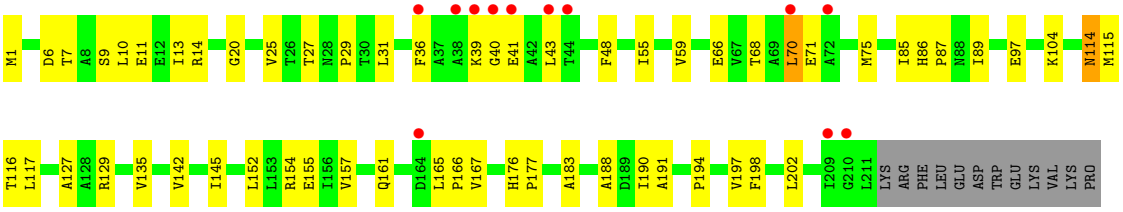
• Molecule 1: transaldolase

Chain C:

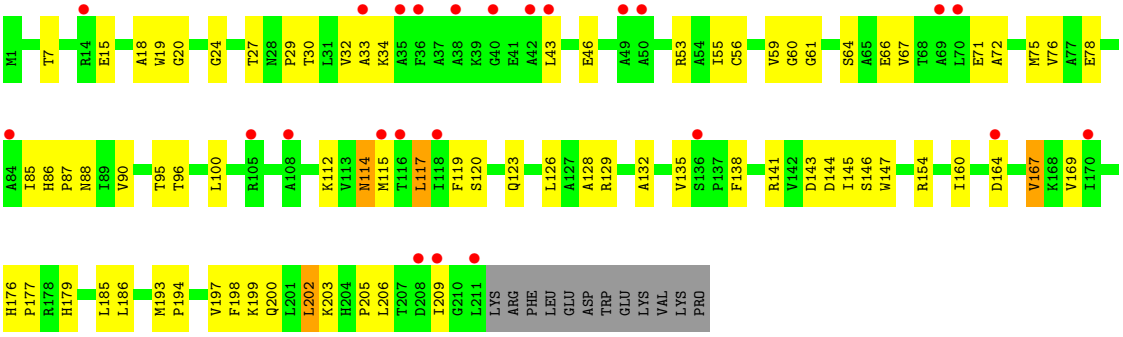


• Molecule 1: transaldolase

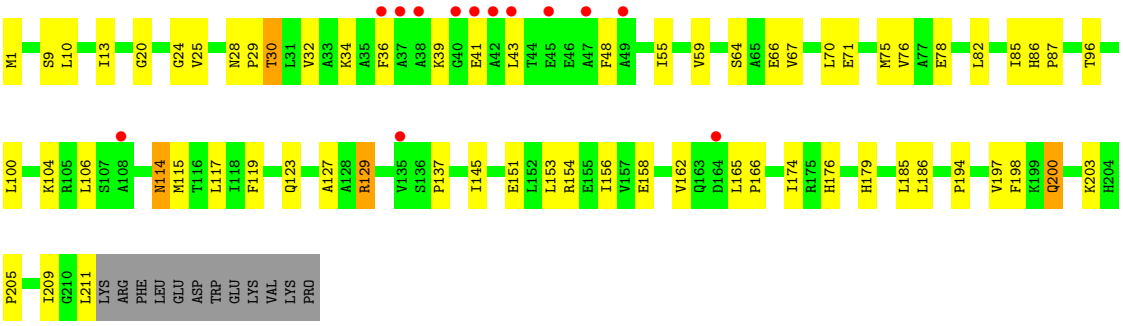
Chain D:



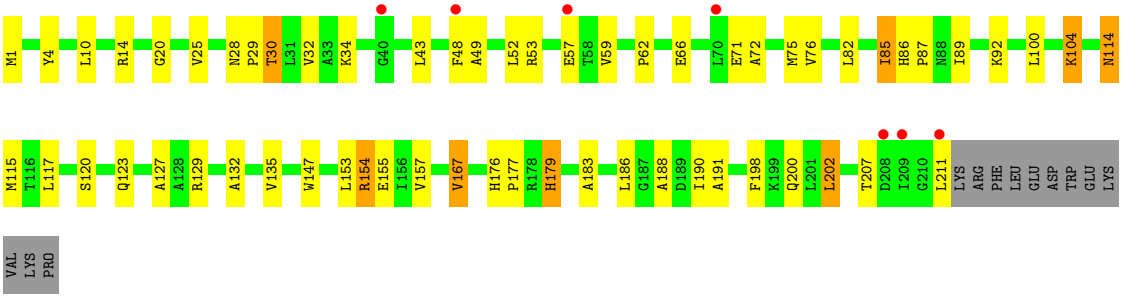
• Molecule 1: transaldolase



• Molecule 1: transaldolase

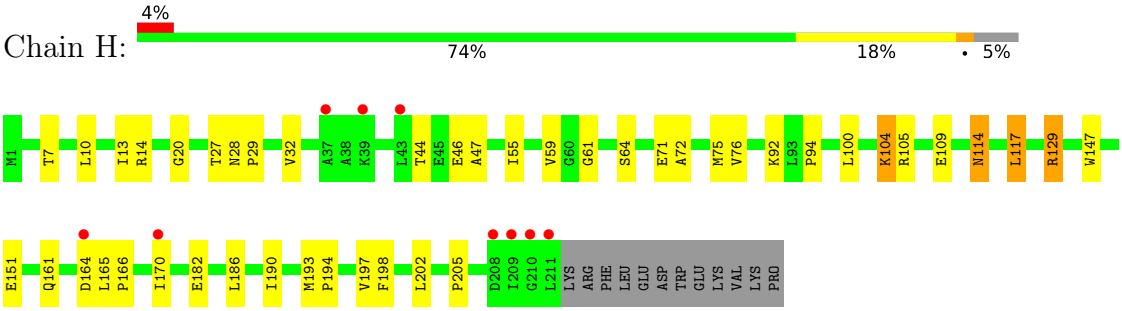


• Molecule 1: transaldolase



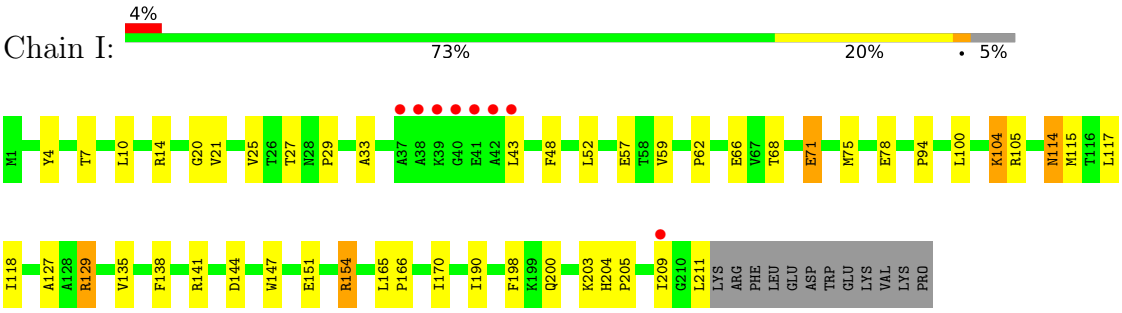
• Molecule 1: transaldolase

Chain H:



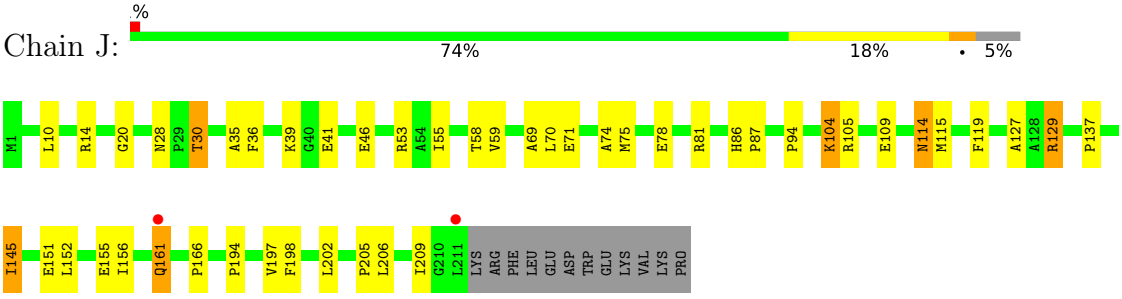
• Molecule 1: transaldolase

Chain I:



• Molecule 1: transaldolase

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	93.69Å 142.70Å 96.59Å 90.00° 114.46° 90.00°	Depositor
Resolution (Å)	29.60 – 2.27 29.60 – 2.27	Depositor EDS
% Data completeness (in resolution range)	98.8 (29.60-2.27) 98.9 (29.60-2.27)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) >$ [1]	3.76 (at 2.26Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.196 , 0.239 0.196 , 0.238	Depositor DCC
R_{free} test set	5198 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å^2)	34.6	Xtriage
Anisotropy	0.508	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 64.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	17083	wwPDB-VP
Average B, all atoms (Å^2)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.20% of the height of the origin peak. No significant pseudotranslation is detected.*

[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

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>5$	RMSZ	#$\|Z\|>5$
1	A	0.32	0/1602	0.59	0/2178
1	B	0.38	0/1602	0.61	0/2178
1	C	0.37	0/1602	0.61	0/2178
1	D	0.33	0/1602	0.58	0/2178
1	E	0.33	0/1602	0.57	0/2178
1	F	0.34	0/1602	0.58	0/2178
1	G	0.34	0/1602	0.59	0/2178
1	H	0.35	0/1602	0.58	0/2178
1	I	0.37	0/1602	0.63	0/2178
1	J	0.38	0/1602	0.62	0/2178
All	All	0.35	0/16020	0.60	0/21780

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1577	0	1629	46	0
1	B	1577	0	1629	36	0
1	C	1577	0	1629	39	0
1	D	1577	0	1629	53	0
1	E	1577	0	1629	55	0
1	F	1577	0	1629	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1577	0	1629	53	0
1	H	1577	0	1629	36	0
1	I	1577	0	1629	39	0
1	J	1577	0	1629	48	0
2	A	107	0	0	0	0
2	B	147	0	0	2	0
2	C	135	0	0	2	0
2	D	107	0	0	1	0
2	E	108	0	0	3	0
2	F	108	0	0	2	0
2	G	130	0	0	2	0
2	H	139	0	0	2	0
2	I	159	0	0	4	0
2	J	173	0	0	3	0
All	All	17083	0	16290	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 13.

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:F:123:GLN:HE22	1:G:207:THR:HG21	1.18	1.05
1:J:166:PRO:HD2	2:J:382:HOH:O	1.59	1.02
1:G:202:LEU:HD23	1:G:202:LEU:H	1.26	0.99
1:H:104:LYS:HG3	1:I:20:GLY:HA3	1.49	0.94
1:D:70:LEU:H	1:D:70:LEU:HD23	1.32	0.92
1:F:154:ARG:HH11	1:F:154:ARG:HB3	1.37	0.88
1:J:70:LEU:HA	1:J:75:MET:HE2	1.57	0.87
1:E:202:LEU:HD23	1:E:202:LEU:H	1.43	0.83
1:A:105:ARG:HB2	1:A:105:ARG:HH11	1.42	0.82
1:H:44:THR:HG23	1:H:47:ALA:H	1.43	0.81
1:D:39:LYS:HD3	1:D:40:GLY:N	1.96	0.80
1:G:52:LEU:HB2	1:G:85:ILE:HD11	1.67	0.77
1:F:117:LEU:O	1:G:207:THR:HG22	1.87	0.75
1:F:154:ARG:HB3	1:F:154:ARG:NH1	2.00	0.74
1:G:1:MET:CE	1:G:188:ALA:HB3	2.18	0.74
1:B:104:LYS:HG3	1:C:20:GLY:HA3	1.68	0.74
1:G:82:LEU:O	1:G:85:ILE:HG23	1.87	0.74
1:J:70:LEU:HA	1:J:75:MET:CE	2.18	0.73
1:H:202:LEU:HD23	1:H:202:LEU:H	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:PRO:HG2	1:A:200:GLN:HG2	1.71	0.73
1:D:1:MET:CE	1:D:188:ALA:HB3	2.18	0.73
1:G:53:ARG:O	1:G:57:GLU:HG2	1.88	0.73
1:E:135:VAL:HG13	1:E:167:VAL:HG11	1.71	0.71
1:F:32:VAL:HG21	1:F:48:PHE:HE1	1.55	0.71
1:F:29:PRO:HD3	1:F:66:GLU:HB3	1.72	0.70
1:H:194:PRO:HG2	1:H:197:VAL:HG23	1.75	0.69
1:C:154:ARG:HH11	1:C:154:ARG:HB3	1.56	0.69
1:C:100:LEU:HD22	1:D:202:LEU:HD11	1.73	0.69
1:H:44:THR:CG2	1:H:47:ALA:H	2.05	0.69
1:A:202:LEU:HD13	1:E:126:LEU:HD12	1.74	0.68
1:G:202:LEU:HD23	1:G:202:LEU:N	2.06	0.68
1:E:71:GLU:O	1:E:75:MET:HG3	1.93	0.68
1:F:123:GLN:NE2	1:G:207:THR:HG21	2.01	0.68
1:J:28:ASN:OD1	1:J:30:THR:HG23	1.93	0.68
1:F:200:GLN:OE1	1:F:203:LYS:HD2	1.93	0.68
1:E:205:PRO:O	1:E:209:ILE:HG23	1.95	0.67
1:F:36:PHE:HD1	1:F:41:GLU:HB3	1.58	0.67
1:G:28:ASN:OD1	1:G:30:THR:HG23	1.94	0.67
1:I:10:LEU:O	1:I:14:ARG:HG3	1.94	0.67
1:A:71:GLU:O	1:A:75:MET:HG3	1.94	0.67
1:I:104:LYS:HG3	1:J:20:GLY:HA3	1.77	0.67
1:B:200:GLN:OE1	1:B:203:LYS:HD2	1.94	0.67
1:D:1:MET:HE1	1:D:183:ALA:HB1	1.76	0.66
1:C:71:GLU:O	1:C:75:MET:HG3	1.95	0.66
1:C:114:ASN:C	1:C:114:ASN:HD22	1.98	0.66
1:A:67:VAL:HG21	1:A:93:LEU:HD23	1.77	0.66
1:B:104:LYS:CG	1:C:20:GLY:HA3	2.26	0.66
1:J:114:ASN:HD22	1:J:114:ASN:C	1.98	0.66
1:I:104:LYS:CG	1:J:20:GLY:HA3	2.26	0.66
1:C:116:THR:HG23	1:C:117:LEU:HD22	1.78	0.66
1:A:202:LEU:HD13	1:E:126:LEU:CD1	2.26	0.64
1:G:202:LEU:H	1:G:202:LEU:CD2	2.07	0.64
1:B:86:HIS:CG	1:B:87:PRO:HD2	2.33	0.64
1:E:194:PRO:HG2	1:E:197:VAL:HG23	1.80	0.64
1:E:59:VAL:HG13	1:E:61:GLY:H	1.63	0.64
1:G:71:GLU:O	1:G:75:MET:HG3	1.98	0.63
1:I:118:ILE:CD1	1:I:135:VAL:HG13	2.29	0.63
1:A:194:PRO:HG2	1:A:197:VAL:HG23	1.81	0.63
1:E:141:ARG:O	1:E:144:ASP:HB2	1.99	0.63
1:J:105:ARG:O	1:J:109:GLU:HG3	1.97	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:129:ARG:HB3	1:I:21:VAL:HG12	1.81	0.63
1:I:154:ARG:HB3	1:I:154:ARG:HH11	1.64	0.62
1:E:114:ASN:C	1:E:114:ASN:HD22	2.03	0.62
1:G:32:VAL:HG11	1:G:48:PHE:CE1	2.35	0.62
1:I:71:GLU:HB3	2:I:371:HOH:O	1.99	0.61
1:A:10:LEU:O	1:A:14:ARG:HG3	1.99	0.61
1:H:71:GLU:O	1:H:75:MET:HG3	2.00	0.61
1:B:36:PHE:CD2	1:B:43:LEU:HD13	2.35	0.61
1:B:100:LEU:HD12	1:C:202:LEU:HD11	1.82	0.61
1:B:25:VAL:CG2	1:B:59:VAL:HG21	2.30	0.61
1:G:52:LEU:HB2	1:G:85:ILE:CD1	2.30	0.61
1:A:85:ILE:HB	1:A:89:ILE:HD12	1.81	0.60
1:I:151:GLU:OE2	1:I:154:ARG:HD3	2.00	0.60
1:A:114:ASN:C	1:A:114:ASN:HD22	2.05	0.60
1:F:10:LEU:CD2	1:F:55:ILE:HD13	2.31	0.60
1:G:1:MET:HE2	1:G:188:ALA:HB3	1.83	0.60
1:G:135:VAL:HG13	1:G:167:VAL:HG21	1.84	0.60
1:B:29:PRO:O	1:B:32:VAL:HG22	2.02	0.60
1:F:154:ARG:O	1:F:158:GLU:HG3	2.02	0.60
1:C:71:GLU:HG3	1:C:74:ALA:HB3	1.84	0.59
1:D:154:ARG:HB3	1:D:154:ARG:HH11	1.67	0.59
1:F:20:GLY:HA3	1:J:104:LYS:HG2	1.85	0.59
1:G:104:LYS:HG3	1:H:20:GLY:HA3	1.84	0.59
1:C:104:LYS:CG	1:D:20:GLY:HA3	2.32	0.59
1:J:10:LEU:HB3	1:J:14:ARG:NH1	2.18	0.59
1:G:176:HIS:O	1:G:179:HIS:HB2	2.02	0.59
1:I:118:ILE:HD13	1:I:135:VAL:HG13	1.84	0.59
1:B:85:ILE:HB	1:B:89:ILE:HD12	1.85	0.59
1:D:25:VAL:CG2	1:D:59:VAL:HG21	2.33	0.59
1:E:202:LEU:H	1:E:202:LEU:CD2	2.15	0.58
1:H:13:ILE:HD13	1:H:55:ILE:HG23	1.84	0.58
1:J:30:THR:HG22	2:J:364:HOH:O	2.03	0.58
1:A:86:HIS:CG	1:A:87:PRO:HD2	2.38	0.58
1:B:205:PRO:HD3	1:J:145:ILE:HG13	1.85	0.58
1:B:28:ASN:OD1	1:B:30:THR:HG23	2.03	0.58
1:C:145:ILE:HD11	1:H:147:TRP:HH2	1.68	0.58
1:D:25:VAL:HG23	1:D:59:VAL:HG21	1.85	0.58
1:G:153:LEU:HD23	1:G:186:LEU:HD12	1.84	0.58
1:I:25:VAL:HG23	1:I:59:VAL:HG21	1.85	0.58
1:E:200:GLN:HG2	2:G:294:HOH:O	2.03	0.57
1:F:185:LEU:HD11	1:J:155:GLU:HG3	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:207:THR:O	1:C:211:LEU:HG	2.04	0.57
1:H:166:PRO:HD2	2:H:287:HOH:O	2.04	0.57
1:F:29:PRO:O	1:F:32:VAL:HG22	2.05	0.57
1:D:155:GLU:HG3	1:E:185:LEU:HD11	1.85	0.57
1:C:116:THR:HG23	1:C:117:LEU:CD2	2.34	0.56
1:D:39:LYS:HD3	1:D:40:GLY:H	1.71	0.56
1:E:199:LYS:O	1:E:203:LYS:HE2	2.06	0.56
1:I:29:PRO:HD3	1:I:66:GLU:HB3	1.87	0.56
1:C:104:LYS:HG3	1:D:20:GLY:HA3	1.86	0.56
1:F:104:LYS:HG3	1:G:20:GLY:HA3	1.87	0.56
1:D:43:LEU:HD21	1:D:48:PHE:HB2	1.88	0.56
1:G:32:VAL:HG11	1:G:48:PHE:HE1	1.71	0.56
1:F:205:PRO:O	1:F:209:ILE:HG13	2.06	0.55
1:D:39:LYS:HD2	1:D:41:GLU:HG3	1.87	0.55
1:H:105:ARG:O	1:H:109:GLU:HG3	2.06	0.55
1:I:200:GLN:OE1	1:I:203:LYS:HD2	2.07	0.55
1:E:114:ASN:C	1:E:114:ASN:ND2	2.60	0.55
1:C:53:ARG:O	1:C:57:GLU:HG2	2.07	0.55
1:G:154:ARG:HH12	1:G:155:GLU:CG	2.20	0.54
1:F:153:LEU:HD23	1:F:186:LEU:HD12	1.89	0.54
1:B:39:LYS:HG3	1:B:40:GLY:N	2.22	0.54
1:F:104:LYS:CG	1:G:20:GLY:HA3	2.37	0.54
1:I:25:VAL:CG2	1:I:59:VAL:HG21	2.37	0.54
1:E:128:ALA:CB	1:E:167:VAL:HG21	2.38	0.54
1:E:59:VAL:HG13	1:E:60:GLY:N	2.23	0.54
1:G:49:ALA:HA	1:G:85:ILE:HD12	1.90	0.54
1:F:29:PRO:HD2	1:F:66:GLU:OE1	2.07	0.54
1:D:70:LEU:H	1:D:70:LEU:CD2	2.11	0.54
1:F:43:LEU:HD22	1:F:43:LEU:H	1.72	0.54
1:J:205:PRO:O	1:J:209:ILE:HG23	2.08	0.54
1:J:206:LEU:HA	1:J:209:ILE:HG12	1.90	0.54
1:A:53:ARG:HD3	1:A:85:ILE:O	2.08	0.54
1:C:166:PRO:HD2	2:C:321:HOH:O	2.08	0.54
1:J:114:ASN:C	1:J:114:ASN:ND2	2.61	0.54
1:F:28:ASN:OD1	1:F:30:THR:HG23	2.07	0.53
1:A:44:THR:H	1:A:47:ALA:HB3	1.74	0.53
2:E:319:HOH:O	1:G:177:PRO:HB2	2.08	0.53
1:D:104:LYS:HD3	1:E:20:GLY:HA3	1.90	0.53
1:C:145:ILE:HD11	1:H:147:TRP:CH2	2.44	0.53
1:E:72:ALA:O	1:E:76:VAL:HG23	2.08	0.53
1:D:11:GLU:HB2	2:D:322:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:158:GLU:HG2	2:F:324:HOH:O	2.08	0.53
1:I:205:PRO:O	1:I:209:ILE:HG23	2.09	0.53
1:H:105:ARG:HB3	2:H:256:HOH:O	2.08	0.52
1:B:25:VAL:HG23	1:B:59:VAL:HG21	1.90	0.52
1:B:205:PRO:HD3	1:J:145:ILE:CG1	2.40	0.52
1:E:120:SER:OG	1:E:123:GLN:HG3	2.09	0.52
1:D:1:MET:HE1	1:D:183:ALA:CB	2.39	0.52
1:A:9:SER:O	1:A:13:ILE:HG13	2.10	0.52
1:G:85:ILE:HG12	1:G:89:ILE:CD1	2.40	0.52
1:J:46:GLU:CD	1:J:46:GLU:H	2.13	0.52
1:A:105:ARG:HB2	1:A:105:ARG:NH1	2.19	0.52
1:E:55:ILE:O	1:E:59:VAL:HG12	2.10	0.52
1:F:43:LEU:HD22	1:F:43:LEU:N	2.24	0.52
1:F:70:LEU:HD11	2:G:261:HOH:O	2.09	0.52
1:A:128:ALA:CB	1:A:167:VAL:HG21	2.40	0.52
1:D:154:ARG:HB3	1:D:154:ARG:NH1	2.23	0.52
1:E:117:LEU:H	1:E:138:PHE:HE1	1.58	0.52
1:F:211:LEU:HD22	1:J:70:LEU:HD21	1.92	0.52
1:H:114:ASN:C	1:H:114:ASN:HD22	2.11	0.52
1:I:105:ARG:HG2	2:I:269:HOH:O	2.10	0.52
1:E:86:HIS:CG	1:E:87:PRO:HD2	2.45	0.52
1:G:104:LYS:CG	1:H:20:GLY:HA3	2.39	0.52
1:C:29:PRO:HA	1:C:32:VAL:HG22	1.92	0.51
1:D:10:LEU:O	1:D:14:ARG:HB2	2.10	0.51
1:C:67:VAL:HA	1:C:78:GLU:OE2	2.10	0.51
1:F:10:LEU:HD21	1:F:55:ILE:HD13	1.91	0.51
1:G:114:ASN:C	1:G:114:ASN:HD22	2.14	0.51
1:A:115:MET:HG3	1:A:127:ALA:HB1	1.93	0.51
1:J:145:ILE:HG23	1:J:145:ILE:O	2.11	0.51
1:A:177:PRO:CG	1:A:200:GLN:HG2	2.41	0.51
1:E:53:ARG:HD3	1:E:85:ILE:O	2.10	0.51
1:G:72:ALA:O	1:G:76:VAL:HG23	2.10	0.51
1:C:71:GLU:HG2	2:C:239:HOH:O	2.11	0.51
1:C:85:ILE:HB	1:C:89:ILE:HD12	1.92	0.51
1:E:203:LYS:NZ	2:E:325:HOH:O	2.42	0.51
1:F:71:GLU:O	1:F:75:MET:HG3	2.09	0.51
1:F:114:ASN:C	1:F:114:ASN:HD22	2.13	0.51
1:I:75:MET:HE1	1:I:94:PRO:HD2	1.92	0.51
1:A:7:THR:HA	1:A:31:LEU:HD13	1.91	0.51
1:A:36:PHE:CD2	1:A:43:LEU:HB3	2.46	0.51
1:B:135:VAL:HG13	1:B:167:VAL:HG21	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:LEU:CD2	1:D:202:LEU:HD11	2.41	0.51
1:D:71:GLU:O	1:D:75:MET:HG3	2.12	0.50
1:H:29:PRO:O	1:H:32:VAL:HG22	2.10	0.50
1:D:115:MET:HG3	1:D:127:ALA:HB1	1.93	0.50
1:C:154:ARG:HB3	1:C:154:ARG:NH1	2.26	0.50
1:F:30:THR:O	1:F:34:LYS:HG3	2.10	0.50
1:B:71:GLU:HG3	1:B:71:GLU:O	2.10	0.50
1:A:67:VAL:CG2	1:A:93:LEU:HD23	2.40	0.50
1:I:115:MET:HG3	1:I:127:ALA:HB1	1.93	0.50
1:D:142:VAL:HG21	1:D:152:LEU:HD22	1.93	0.50
1:D:70:LEU:HD23	1:D:70:LEU:N	2.15	0.50
1:E:46:GLU:HG2	2:E:256:HOH:O	2.12	0.50
1:A:29:PRO:HD3	1:A:66:GLU:HB3	1.94	0.49
1:A:114:ASN:HD22	1:A:115:MET:N	2.10	0.49
1:F:96:THR:O	1:F:100:LEU:HD13	2.12	0.49
1:E:205:PRO:HB2	1:H:205:PRO:HB3	1.94	0.49
1:D:114:ASN:C	1:D:114:ASN:HD22	2.15	0.49
1:F:158:GLU:O	1:F:162:VAL:HG23	2.12	0.49
1:J:55:ILE:O	1:J:59:VAL:HG12	2.13	0.49
1:B:147:TRP:CE3	1:I:147:TRP:CE3	3.00	0.49
1:C:114:ASN:HD22	1:C:115:MET:N	2.11	0.49
1:J:115:MET:HG3	1:J:127:ALA:HB1	1.95	0.49
1:B:25:VAL:HG21	1:B:59:VAL:HG21	1.94	0.49
1:E:176:HIS:O	1:E:179:HIS:HB2	2.13	0.49
1:B:85:ILE:HB	1:B:89:ILE:CD1	2.42	0.49
1:C:13:ILE:HD13	1:C:55:ILE:HG23	1.95	0.49
1:E:176:HIS:HB2	1:E:177:PRO:HD2	1.95	0.49
1:F:71:GLU:HG3	2:F:286:HOH:O	2.12	0.49
1:C:115:MET:HG3	1:C:127:ALA:HB1	1.94	0.49
1:A:116:THR:HG23	1:A:117:LEU:HD13	1.95	0.48
1:I:170:ILE:HG12	1:I:190:ILE:HB	1.95	0.48
1:E:96:THR:O	1:E:100:LEU:HD13	2.13	0.48
1:H:55:ILE:O	1:H:59:VAL:HG12	2.14	0.48
1:I:75:MET:CE	1:I:94:PRO:HD2	2.44	0.48
1:J:71:GLU:HG3	1:J:74:ALA:HB3	1.95	0.48
1:C:114:ASN:C	1:C:114:ASN:ND2	2.66	0.48
1:D:29:PRO:HD3	1:D:66:GLU:HB3	1.95	0.48
1:E:115:MET:HG2	1:E:132:ALA:HB2	1.95	0.48
1:I:4:TYR:OH	1:I:62:PRO:HG2	2.12	0.48
1:I:71:GLU:O	1:I:75:MET:HG3	2.14	0.48
1:B:115:MET:HG3	1:B:127:ALA:HB1	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:4:TYR:OH	1:G:62:PRO:HG2	2.13	0.48
1:A:51:HIS:O	1:A:55:ILE:HG13	2.14	0.48
1:B:182:GLU:HG3	2:B:368:HOH:O	2.13	0.48
1:E:24:GLY:HA2	1:E:59:VAL:HG21	1.96	0.48
1:F:115:MET:HG3	1:F:127:ALA:HB1	1.95	0.48
1:C:104:LYS:HG2	1:D:20:GLY:HA3	1.95	0.48
1:C:143:ASP:HA	1:C:147:TRP:O	2.14	0.48
1:I:7:THR:O	1:I:27:THR:HG22	2.13	0.48
1:G:154:ARG:HH11	1:G:154:ARG:HB3	1.79	0.47
1:J:53:ARG:NH1	2:J:360:HOH:O	2.41	0.47
1:D:116:THR:HG23	1:D:117:LEU:HD13	1.97	0.47
1:G:43:LEU:HD11	1:G:48:PHE:HD1	1.80	0.47
1:J:69:ALA:O	1:J:75:MET:HE2	2.13	0.47
1:H:28:ASN:O	1:H:32:VAL:HG13	2.15	0.47
1:F:119:PHE:HD1	1:G:207:THR:HG23	1.78	0.47
1:G:1:MET:HE1	1:G:183:ALA:HB1	1.95	0.47
1:I:114:ASN:C	1:I:114:ASN:HD22	2.17	0.47
1:F:176:HIS:O	1:F:179:HIS:HB2	2.13	0.47
1:C:29:PRO:O	1:C:32:VAL:HG22	2.15	0.47
1:C:126:LEU:HD13	1:D:202:LEU:HG	1.96	0.47
1:D:135:VAL:HG13	1:D:167:VAL:HG21	1.96	0.47
1:G:25:VAL:CG2	1:G:59:VAL:HG21	2.45	0.47
1:A:105:ARG:O	1:A:109:GLU:HG3	2.14	0.47
1:B:129:ARG:HA	1:B:129:ARG:HD3	1.46	0.47
1:I:129:ARG:HD3	1:I:129:ARG:HA	1.62	0.47
1:G:115:MET:HG3	1:G:127:ALA:HB1	1.96	0.47
1:I:48:PHE:CZ	1:I:52:LEU:HD11	2.50	0.46
1:D:157:VAL:O	1:D:161:GLN:HG3	2.14	0.46
1:F:36:PHE:CD1	1:F:41:GLU:HB3	2.44	0.46
1:H:114:ASN:C	1:H:114:ASN:ND2	2.68	0.46
1:D:85:ILE:HB	1:D:89:ILE:HD12	1.96	0.46
1:E:206:LEU:HA	1:E:209:ILE:HG12	1.98	0.46
1:F:129:ARG:HA	1:F:129:ARG:HD3	1.67	0.46
1:F:1:MET:N	1:J:129:ARG:HH21	2.13	0.46
1:D:114:ASN:C	1:D:114:ASN:ND2	2.69	0.46
1:B:190:ILE:HG22	1:B:191:ALA:N	2.31	0.46
1:F:39:LYS:O	1:F:39:LYS:HG3	2.15	0.46
1:F:151:GLU:HG3	1:F:154:ARG:NH1	2.31	0.46
1:A:28:ASN:OD1	1:A:30:THR:HB	2.15	0.46
1:D:1:MET:HE1	1:D:188:ALA:HB3	1.94	0.46
1:H:182:GLU:O	1:H:186:LEU:HG	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:ILE:HG12	1:A:190:ILE:HB	1.98	0.46
1:F:9:SER:O	1:F:13:ILE:HG13	2.16	0.46
1:F:86:HIS:CG	1:F:87:PRO:HD2	2.50	0.46
1:A:114:ASN:C	1:A:114:ASN:ND2	2.69	0.46
1:A:135:VAL:HG13	1:A:167:VAL:HG11	1.98	0.46
1:J:39:LYS:HE2	1:J:41:GLU:CD	2.37	0.46
1:H:129:ARG:HD3	1:H:129:ARG:HA	1.51	0.46
1:G:25:VAL:HG23	1:G:59:VAL:HG21	1.97	0.45
1:I:104:LYS:HG2	1:J:20:GLY:HA3	1.96	0.45
1:G:29:PRO:HD3	1:G:66:GLU:HB3	1.98	0.45
1:A:207:THR:HG1	1:E:119:PHE:HD1	1.64	0.45
1:B:71:GLU:OE1	1:B:73:GLU:HB3	2.15	0.45
1:C:129:ARG:HA	1:C:129:ARG:HD3	1.50	0.45
1:D:9:SER:O	1:D:13:ILE:HG13	2.16	0.45
1:G:157:VAL:HG11	1:G:186:LEU:O	2.16	0.45
1:G:190:ILE:HG22	1:G:191:ALA:N	2.32	0.45
1:I:57:GLU:CD	2:I:254:HOH:O	2.54	0.45
1:J:206:LEU:HD22	1:J:209:ILE:HD11	1.98	0.45
1:A:192:THR:HG23	1:A:192:THR:O	2.15	0.45
1:G:85:ILE:HG12	1:G:89:ILE:HD11	1.97	0.45
1:H:170:ILE:HG12	1:H:190:ILE:HB	1.98	0.45
1:D:7:THR:O	1:D:27:THR:HG22	2.17	0.45
1:D:36:PHE:CE2	1:D:43:LEU:HG	2.52	0.45
1:E:86:HIS:ND1	1:E:88:ASN:HB2	2.31	0.45
1:G:86:HIS:CG	1:G:87:PRO:HD2	2.51	0.45
1:J:71:GLU:CG	1:J:74:ALA:HB3	2.45	0.45
1:A:13:ILE:HD13	1:A:55:ILE:HG23	1.98	0.45
1:H:59:VAL:HG13	1:H:61:GLY:H	1.81	0.45
1:A:7:THR:O	1:A:27:THR:HG22	2.16	0.45
1:D:104:LYS:CD	1:E:20:GLY:HA3	2.47	0.45
1:F:24:GLY:HA2	1:F:59:VAL:HG11	1.99	0.45
1:H:10:LEU:O	1:H:14:ARG:HG3	2.17	0.45
1:G:30:THR:O	1:G:34:LYS:HG3	2.17	0.44
1:H:165:LEU:HA	1:H:166:PRO:HD3	1.82	0.44
1:J:14:ARG:HG2	1:J:58:THR:HG21	1.98	0.44
1:J:36:PHE:HA	1:J:39:LYS:HG2	1.98	0.44
1:J:129:ARG:HA	1:J:129:ARG:HD3	1.62	0.44
1:C:28:ASN:OD1	1:C:30:THR:HB	2.18	0.44
1:J:119:PHE:HA	1:J:152:LEU:HD21	2.00	0.44
1:A:2:GLU:HB2	1:A:190:ILE:HG12	1.99	0.44
1:E:193:MET:HB2	1:E:194:PRO:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:10:LEU:O	1:J:14:ARG:HG3	2.18	0.44
1:A:157:VAL:HG11	1:A:186:LEU:O	2.18	0.44
1:E:29:PRO:O	1:E:32:VAL:HG22	2.18	0.44
1:F:174:ILE:HG23	1:F:179:HIS:HB3	1.98	0.44
1:H:117:LEU:HD12	1:H:117:LEU:HA	1.90	0.44
1:J:145:ILE:O	1:J:145:ILE:CG2	2.64	0.44
1:E:160:ILE:HD12	1:E:169:VAL:CG2	2.48	0.44
1:H:72:ALA:O	1:H:76:VAL:HG23	2.17	0.44
1:I:33:ALA:HA	1:I:43:LEU:HD12	1.98	0.44
1:A:95:THR:HG22	1:B:202:LEU:HD11	1.99	0.44
1:D:97:GLU:HG2	1:E:19:TRP:CZ2	2.53	0.43
1:D:129:ARG:HA	1:D:129:ARG:HD3	1.74	0.43
1:H:7:THR:O	1:H:27:THR:HG22	2.18	0.43
1:J:194:PRO:HG2	1:J:197:VAL:HG23	2.00	0.43
1:B:48:PHE:CZ	1:B:52:LEU:HD11	2.53	0.43
1:F:194:PRO:HG2	1:F:197:VAL:HG23	2.01	0.43
1:I:165:LEU:HA	1:I:166:PRO:HD3	1.88	0.43
1:E:7:THR:O	1:E:27:THR:HG22	2.18	0.43
1:E:143:ASP:HA	1:E:147:TRP:O	2.19	0.43
1:J:161:GLN:HE21	1:J:161:GLN:HB3	1.68	0.43
1:B:114:ASN:C	1:B:114:ASN:HD22	2.21	0.43
1:E:67:VAL:HA	1:E:78:GLU:OE2	2.18	0.43
1:F:119:PHE:HD1	1:G:207:THR:CG2	2.32	0.43
1:H:44:THR:HG22	1:H:47:ALA:CB	2.49	0.43
1:J:71:GLU:O	1:J:75:MET:HG3	2.18	0.43
1:H:202:LEU:H	1:H:202:LEU:CD2	2.28	0.43
1:E:43:LEU:C	1:E:43:LEU:HD13	2.39	0.43
1:E:147:TRP:HH2	1:F:145:ILE:HD11	1.84	0.43
1:F:25:VAL:CG2	1:F:59:VAL:HG21	2.49	0.43
1:I:100:LEU:HD22	1:J:202:LEU:HD11	2.00	0.43
1:J:78:GLU:HG3	1:J:81:ARG:HH12	1.84	0.43
1:C:30:THR:O	1:C:34:LYS:HG3	2.19	0.43
1:D:13:ILE:HD13	1:D:55:ILE:HG23	2.00	0.43
1:D:86:HIS:ND1	1:D:87:PRO:HD2	2.34	0.43
1:F:25:VAL:HG23	1:F:59:VAL:HG21	2.00	0.43
1:D:68:THR:O	1:D:68:THR:HG22	2.18	0.43
1:E:64:SER:HA	1:E:90:VAL:O	2.18	0.43
1:E:202:LEU:CD2	1:E:202:LEU:N	2.82	0.43
1:A:96:THR:C	1:B:202:LEU:HD21	2.40	0.42
1:B:71:GLU:O	1:B:75:MET:HG3	2.18	0.42
1:C:25:VAL:O	1:C:63:VAL:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:190:ILE:HG22	1:D:191:ALA:N	2.33	0.42
1:H:64:SER:HB3	1:H:92:LYS:HD3	2.01	0.42
1:D:145:ILE:HD11	1:G:147:TRP:HH2	1.83	0.42
1:E:95:THR:HG21	1:E:123:GLN:HB3	2.01	0.42
1:F:114:ASN:C	1:F:114:ASN:ND2	2.72	0.42
1:G:120:SER:OG	1:G:123:GLN:HG3	2.19	0.42
1:G:202:LEU:N	1:G:202:LEU:CD2	2.75	0.42
1:I:141:ARG:O	1:I:144:ASP:HB2	2.19	0.42
1:A:200:GLN:O	1:A:200:GLN:HG3	2.18	0.42
1:E:154:ARG:HG3	1:E:186:LEU:HD22	2.01	0.42
1:E:30:THR:O	1:E:33:ALA:HB3	2.18	0.42
1:B:165:LEU:HB3	2:B:330:HOH:O	2.19	0.42
1:D:165:LEU:HA	1:D:166:PRO:HD3	1.86	0.42
1:J:86:HIS:CG	1:J:87:PRO:HD2	2.53	0.42
1:A:26:THR:HA	1:A:64:SER:HB2	2.00	0.42
1:A:28:ASN:O	1:A:32:VAL:HG23	2.20	0.42
1:A:32:VAL:HG12	1:A:43:LEU:HD22	2.01	0.42
1:A:78:GLU:HA	1:A:81:ARG:HE	1.84	0.42
1:I:68:THR:H	1:I:78:GLU:CD	2.22	0.42
1:I:118:ILE:HD12	1:I:135:VAL:HG13	1.98	0.42
1:J:53:ARG:HH11	1:J:53:ARG:HD3	1.61	0.42
1:F:67:VAL:HG22	1:F:78:GLU:HG2	2.01	0.42
1:F:76:VAL:HA	1:F:106:LEU:HD21	2.00	0.42
1:I:204:HIS:HA	1:I:205:PRO:HD3	1.88	0.42
1:D:6:ASP:OD1	1:D:31:LEU:HD11	2.20	0.42
1:H:193:MET:HB2	1:H:194:PRO:HD2	2.02	0.41
1:D:194:PRO:HG2	1:D:197:VAL:HG23	2.02	0.41
1:E:56:CYS:HB3	1:E:86:HIS:CE1	2.55	0.41
1:G:207:THR:O	1:G:211:LEU:HG	2.20	0.41
1:G:154:ARG:HH12	1:G:155:GLU:HG3	1.85	0.41
1:D:43:LEU:CD2	1:D:48:PHE:HB2	2.49	0.41
1:D:36:PHE:CD2	1:D:43:LEU:HG	2.55	0.41
1:E:15:GLU:O	1:E:18:ALA:HB3	2.20	0.41
1:G:66:GLU:OE2	1:G:92:LYS:HE3	2.20	0.41
1:B:138:PHE:O	1:B:142:VAL:HG23	2.20	0.41
1:C:204:HIS:HA	1:C:205:PRO:HD3	1.88	0.41
1:F:165:LEU:HA	1:F:166:PRO:HD3	1.85	0.41
1:J:35:ALA:O	1:J:39:LYS:HG2	2.21	0.41
1:B:100:LEU:HD23	1:B:100:LEU:HA	1.90	0.41
1:H:94:PRO:HB3	1:I:211:LEU:HD21	2.02	0.41
1:B:52:LEU:HD12	1:B:85:ILE:CD1	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:138:PHE:HD2	1:B:141:ARG:HD2	1.85	0.41
1:C:118:ILE:O	1:C:137:PRO:HA	2.21	0.41
1:F:82:LEU:HD23	1:F:85:ILE:HD11	2.02	0.41
1:F:137:PRO:HB3	1:F:156:ILE:CD1	2.50	0.41
1:A:67:VAL:HG21	1:A:93:LEU:CD2	2.47	0.41
1:A:202:LEU:HD13	1:E:126:LEU:HD13	2.03	0.41
1:B:29:PRO:HA	1:B:32:VAL:HG22	2.03	0.41
1:E:66:GLU:HG2	1:E:67:VAL:O	2.21	0.40
1:F:13:ILE:CD1	1:F:55:ILE:HD12	2.52	0.40
1:F:211:LEU:HD21	1:J:94:PRO:HB3	2.04	0.40
1:J:114:ASN:HD22	1:J:115:MET:N	2.17	0.40
1:H:44:THR:HG23	1:H:46:GLU:H	1.86	0.40
1:I:138:PHE:N	1:I:138:PHE:CD1	2.90	0.40
1:I:200:GLN:HG3	2:I:340:HOH:O	2.21	0.40
1:C:135:VAL:HG13	1:C:167:VAL:HG21	2.04	0.40
1:G:10:LEU:O	1:G:14:ARG:HB2	2.22	0.40
1:G:49:ALA:CA	1:G:85:ILE:HD12	2.52	0.40
1:J:137:PRO:HB3	1:J:156:ILE:CD1	2.51	0.40
1:A:104:LYS:HG2	1:B:20:GLY:HA3	2.04	0.40
1:C:141:ARG:O	1:C:144:ASP:HB2	2.22	0.40
1:D:39:LYS:CD	1:D:41:GLU:HG3	2.50	0.40
1:D:176:HIS:HB2	1:D:177:PRO:CD	2.51	0.40
1:E:145:ILE:O	1:E:146:SER:HB2	2.22	0.40
1:F:20:GLY:HA3	1:J:104:LYS:CG	2.51	0.40
1:G:115:MET:HG2	1:G:132:ALA:HB2	2.04	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	209/223 (94%)	203 (97%)	5 (2%)	1 (0%)	29 34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	209/223 (94%)	206 (99%)	3 (1%)	0	100	100
1	C	209/223 (94%)	204 (98%)	5 (2%)	0	100	100
1	D	209/223 (94%)	205 (98%)	4 (2%)	0	100	100
1	E	209/223 (94%)	203 (97%)	5 (2%)	1 (0%)	29	34
1	F	209/223 (94%)	201 (96%)	8 (4%)	0	100	100
1	G	209/223 (94%)	204 (98%)	4 (2%)	1 (0%)	29	34
1	H	209/223 (94%)	206 (99%)	3 (1%)	0	100	100
1	I	209/223 (94%)	203 (97%)	6 (3%)	0	100	100
1	J	209/223 (94%)	208 (100%)	1 (0%)	0	100	100
All	All	2090/2230 (94%)	2043 (98%)	44 (2%)	3 (0%)	51	63

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	167	VAL
1	E	167	VAL
1	G	167	VAL

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	163/175 (93%)	159 (98%)	4 (2%)	47	62
1	B	163/175 (93%)	158 (97%)	5 (3%)	40	53
1	C	163/175 (93%)	156 (96%)	7 (4%)	29	38
1	D	163/175 (93%)	160 (98%)	3 (2%)	59	72
1	E	163/175 (93%)	155 (95%)	8 (5%)	25	33
1	F	163/175 (93%)	157 (96%)	6 (4%)	34	45
1	G	163/175 (93%)	151 (93%)	12 (7%)	13	16
1	H	163/175 (93%)	154 (94%)	9 (6%)	21	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	I	163/175 (93%)	156 (96%)	7 (4%)	29 38
1	J	163/175 (93%)	155 (95%)	8 (5%)	25 33
All	All	1630/1750 (93%)	1561 (96%)	69 (4%)	30 39

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	100	LEU
1	A	105	ARG
1	A	114	ASN
1	A	202	LEU
1	B	30	THR
1	B	114	ASN
1	B	117	LEU
1	B	129	ARG
1	B	198	PHE
1	C	100	LEU
1	C	104	LYS
1	C	114	ASN
1	C	129	ARG
1	C	151	GLU
1	C	164	ASP
1	C	198	PHE
1	D	70	LEU
1	D	114	ASN
1	D	198	PHE
1	E	34	LYS
1	E	112	LYS
1	E	114	ASN
1	E	117	LEU
1	E	129	ARG
1	E	164	ASP
1	E	198	PHE
1	E	202	LEU
1	F	30	THR
1	F	64	SER
1	F	114	ASN
1	F	129	ARG
1	F	198	PHE
1	F	200	GLN
1	G	30	THR

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Mol	Chain	Res	Type
1	G	85	ILE
1	G	100	LEU
1	G	104	LYS
1	G	114	ASN
1	G	117	LEU
1	G	129	ARG
1	G	154	ARG
1	G	179	HIS
1	G	198	PHE
1	G	200	GLN
1	G	202	LEU
1	H	100	LEU
1	H	104	LYS
1	H	114	ASN
1	H	117	LEU
1	H	129	ARG
1	H	151	GLU
1	H	161	GLN
1	H	164	ASP
1	H	198	PHE
1	I	71	GLU
1	I	104	LYS
1	I	114	ASN
1	I	117	LEU
1	I	129	ARG
1	I	154	ARG
1	I	198	PHE
1	J	30	THR
1	J	104	LYS
1	J	114	ASN
1	J	129	ARG
1	J	145	ILE
1	J	151	GLU
1	J	161	GLN
1	J	198	PHE

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	114	ASN
1	A	161	GLN
1	B	161	GLN

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Mol	Chain	Res	Type
1	C	114	ASN
1	C	161	GLN
1	D	114	ASN
1	D	200	GLN
1	E	114	ASN
1	E	161	GLN
1	E	200	GLN
1	F	114	ASN
1	F	161	GLN
1	G	114	ASN
1	G	161	GLN
1	H	114	ASN
1	H	200	GLN
1	I	161	GLN
1	J	114	ASN
1	J	161	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 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

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, 95^{th} 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	211/223 (94%)	0.32	17 (8%) 12 15	27, 45, 75, 81	4 (1%)
1	B	211/223 (94%)	-0.07	9 (4%) 35 40	19, 31, 64, 80	4 (1%)
1	C	211/223 (94%)	-0.12	7 (3%) 46 52	19, 31, 58, 80	1 (0%)
1	D	211/223 (94%)	0.10	12 (5%) 23 28	25, 38, 70, 89	3 (1%)
1	E	211/223 (94%)	0.57	24 (11%) 5 6	30, 47, 69, 85	4 (1%)
1	F	211/223 (94%)	0.21	13 (6%) 20 25	29, 41, 71, 87	4 (1%)
1	G	211/223 (94%)	0.04	7 (3%) 46 52	27, 40, 61, 74	3 (1%)
1	H	211/223 (94%)	0.09	9 (4%) 35 40	23, 33, 56, 70	1 (0%)
1	I	211/223 (94%)	-0.07	8 (3%) 40 45	19, 29, 62, 85	1 (0%)
1	J	211/223 (94%)	-0.33	2 (0%) 84 87	19, 29, 43, 60	1 (0%)
All	All	2110/2230 (94%)	0.07	108 (5%) 28 33	19, 37, 65, 89	26 (1%)

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	38	ALA	7.4
1	D	40	GLY	7.3
1	F	43	LEU	5.7
1	B	40	GLY	5.7
1	I	38	ALA	5.6
1	I	40	GLY	5.5
1	E	49	ALA	5.1
1	F	36	PHE	4.7
1	G	211	LEU	4.6
1	D	43	LEU	4.5
1	E	209	ILE	4.2
1	A	36	PHE	3.9
1	A	42	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	43	LEU	3.9
1	A	208	ASP	3.7
1	J	211	LEU	3.6
1	C	38	ALA	3.6
1	E	108	ALA	3.5
1	I	209	ILE	3.5
1	B	42	ALA	3.4
1	B	41	GLU	3.4
1	A	209	ILE	3.4
1	D	39	LYS	3.3
1	E	40	GLY	3.3
1	H	209	ILE	3.3
1	I	42	ALA	3.3
1	A	39	LYS	3.2
1	E	43	LEU	3.2
1	I	43	LEU	3.2
1	A	38	ALA	3.2
1	F	38	ALA	3.2
1	A	41	GLU	3.2
1	I	41	GLU	3.2
1	C	40	GLY	3.2
1	B	35	ALA	3.1
1	E	33	ALA	3.1
1	E	84	ALA	3.1
1	D	36	PHE	3.0
1	D	70	LEU	3.0
1	H	170	ILE	3.0
1	H	43	LEU	3.0
1	E	164	ASP	3.0
1	H	210	GLY	2.9
1	E	14	ARG	2.9
1	F	40	GLY	2.9
1	F	45	GLU	2.9
1	D	210	GLY	2.9
1	E	36	PHE	2.8
1	F	164	ASP	2.8
1	E	170	ILE	2.8
1	E	69	ALA	2.8
1	I	39	LYS	2.8
1	B	208	ASP	2.7
1	G	209	ILE	2.7
1	D	38	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	35	ALA	2.7
1	F	108	ALA	2.7
1	E	35	ALA	2.6
1	E	118	ILE	2.6
1	A	44	THR	2.6
1	E	208	ASP	2.6
1	E	42	ALA	2.6
1	F	47	ALA	2.5
1	C	42	ALA	2.5
1	A	40	GLY	2.5
1	H	39	LYS	2.5
1	H	208	ASP	2.4
1	E	70	LEU	2.4
1	H	211	LEU	2.4
1	D	44	THR	2.4
1	E	116	THR	2.4
1	G	40	GLY	2.4
1	J	161	GLN	2.4
1	E	50	ALA	2.4
1	E	136	SER	2.4
1	F	41	GLU	2.4
1	B	43	LEU	2.4
1	F	42	ALA	2.4
1	A	170	ILE	2.3
1	C	108	ALA	2.3
1	G	70	LEU	2.3
1	A	50	ALA	2.3
1	D	72	ALA	2.3
1	H	37	ALA	2.3
1	A	210	GLY	2.3
1	I	37	ALA	2.3
1	C	211	LEU	2.2
1	D	41	GLU	2.2
1	B	38	ALA	2.2
1	E	115	MET	2.2
1	D	164	ASP	2.2
1	C	208	ASP	2.1
1	C	209	ILE	2.1
1	B	36	PHE	2.1
1	A	46	GLU	2.1
1	H	164	ASP	2.1
1	A	124	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	105	ARG	2.1
1	E	211	LEU	2.1
1	F	37	ALA	2.1
1	A	18	ALA	2.1
1	F	49	ALA	2.1
1	G	48	PHE	2.1
1	F	135	VAL	2.0
1	B	3	LEU	2.0
1	D	209	ILE	2.0
1	G	57	GLU	2.0
1	G	208	ASP	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.