Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 05:27 AM GMT

PDB ID	:	2QQ4
Title	:	Crystal structure of Iron-sulfur cluster biosynthesis protein IscU (TTHA1736) from thermus thermophilus HB8
Authors	:	Jeyakanthan, J.; Kanaujia, S.P.; Sekar, K.; Agari, Y.; Ebihara, A.; Shinkai, A.; Kuramitsu, S.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2007-07-26
Resolution	:	1.85 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

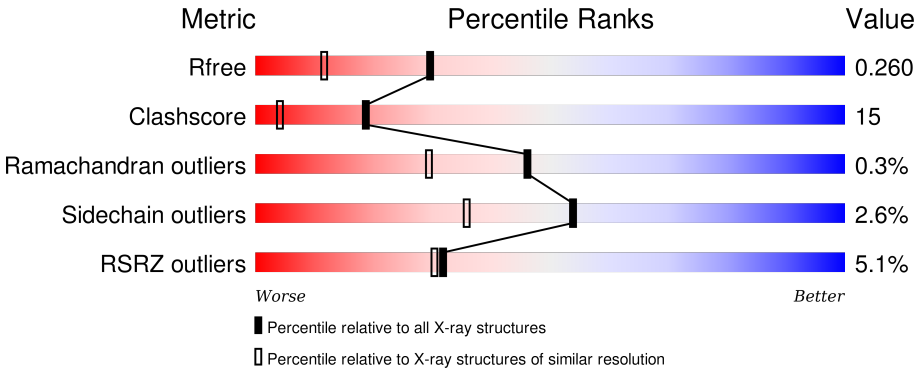
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 1.85 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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 <=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	138	4% 78% 20%
1	B	138	% 83% 17%
1	C	138	% 78% 20%
1	D	138	% 74% 23%
1	E	138	4% 75% 24%

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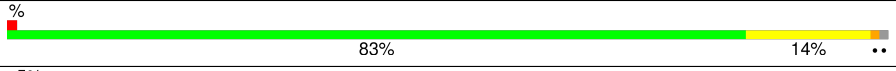
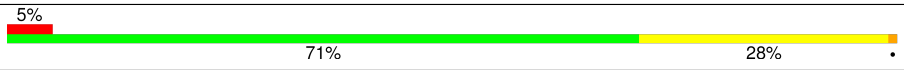
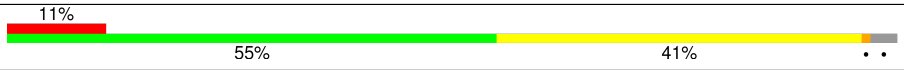
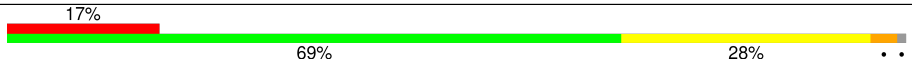
Mol	Chain	Length	Quality of chain
1	F	138	
1	G	138	
1	H	138	
1	I	138	
1	J	138	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ZN	I	139	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11013 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 Iron-sulfur cluster biosynthesis protein IscU.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	138	Total	C	N	O	S	0	0	0
			1032	649	178	197	8			
1	B	137	Total	C	N	O	S	0	0	0
			1024	644	177	196	7			
1	C	138	Total	C	N	O	S	0	0	0
			1032	649	178	197	8			
1	D	137	Total	C	N	O	S	0	0	0
			1024	644	177	196	7			
1	E	137	Total	C	N	O	S	0	0	0
			1024	644	177	196	7			
1	F	136	Total	C	N	O	S	0	0	0
			1018	641	176	194	7			
1	G	137	Total	C	N	O	S	0	0	0
			1024	644	177	196	7			
1	H	138	Total	C	N	O	S	0	0	0
			1032	649	178	197	8			
1	I	134	Total	C	N	O	S	0	0	0
			1003	630	174	192	7			
1	J	137	Total	C	N	O	S	0	0	0
			1024	644	177	196	7			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	G	1	Total	Zn	0	0
			1	1		
2	J	1	Total	Zn	0	0
			1	1		
2	D	1	Total	Zn	0	0
			1	1		
2	E	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	H	1	Total Zn 1 1	0	0
2	B	1	Total Zn 1 1	0	0
2	I	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0
2	F	1	Total Zn 1 1	0	0

- Molecule 3 is water.

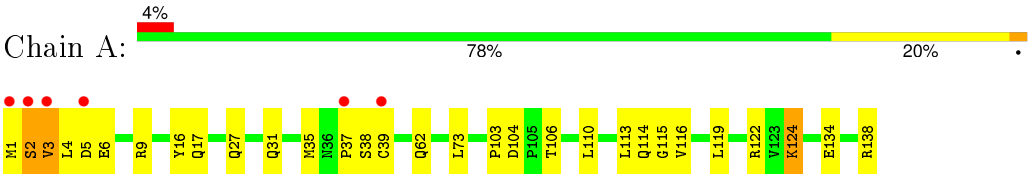
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	108	Total O 108 108	0	0
3	B	84	Total O 84 84	0	0
3	C	97	Total O 97 97	0	0
3	D	99	Total O 99 99	0	0
3	E	77	Total O 77 77	0	0
3	F	49	Total O 49 49	0	0
3	G	87	Total O 87 87	0	0
3	H	57	Total O 57 57	0	0
3	I	48	Total O 48 48	0	0
3	J	60	Total O 60 60	0	0

3 Residue-property plots (i)

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.

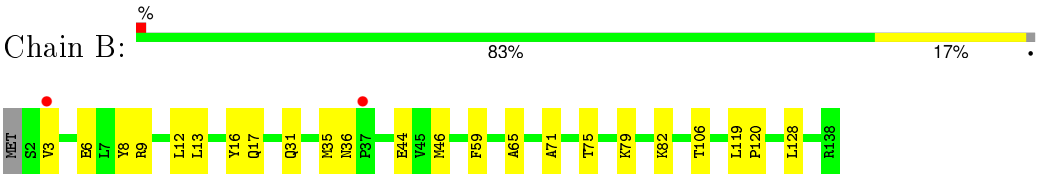
- Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain A:



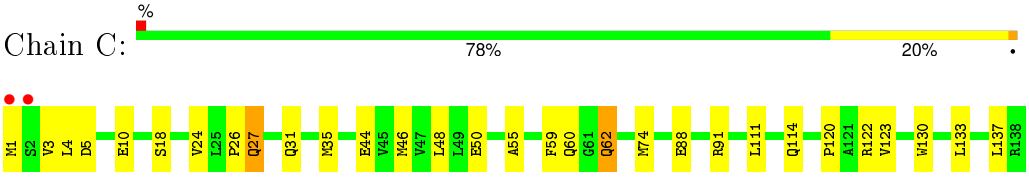
- Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain B:



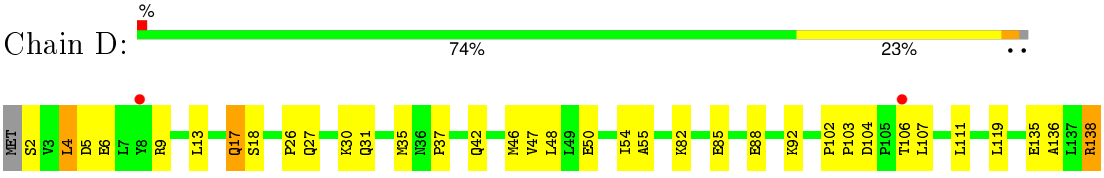
- Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain C:



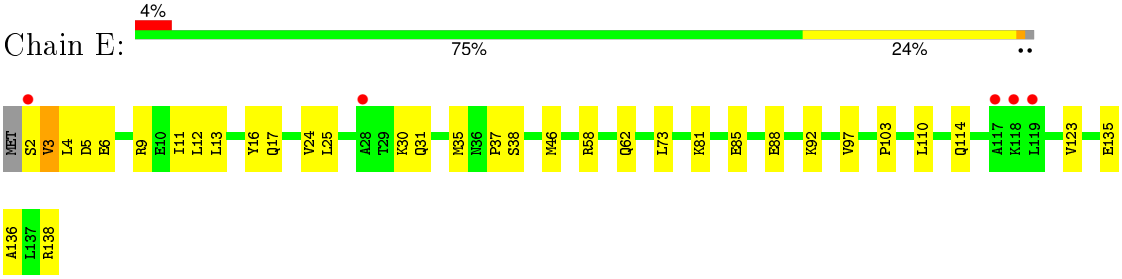
- Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain D:



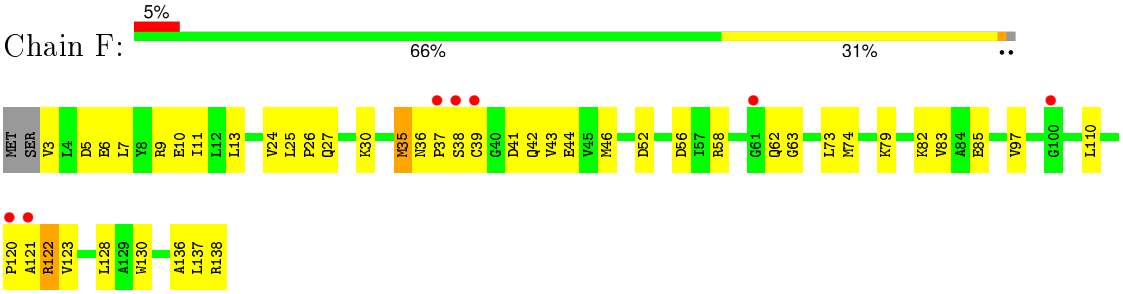
- Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain E:



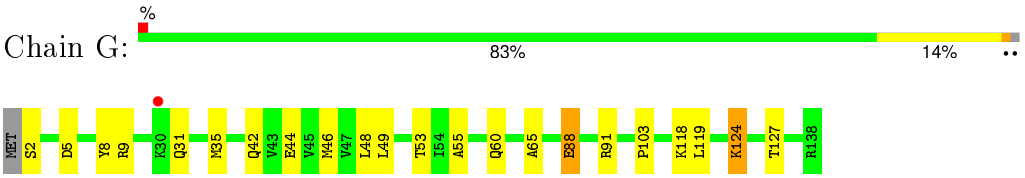
• Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain F:



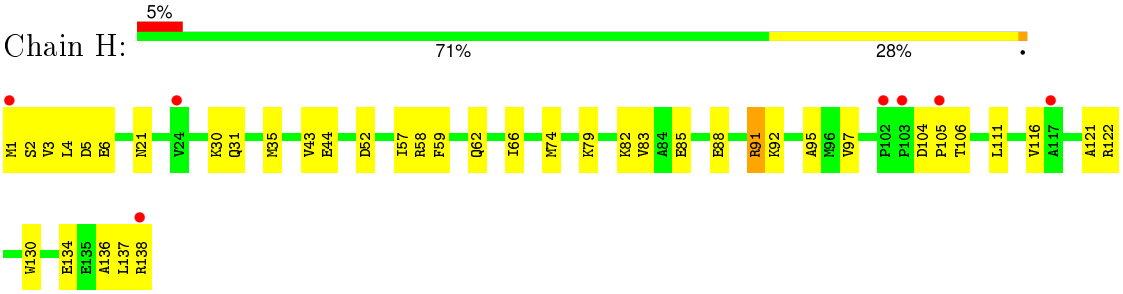
• Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain G:



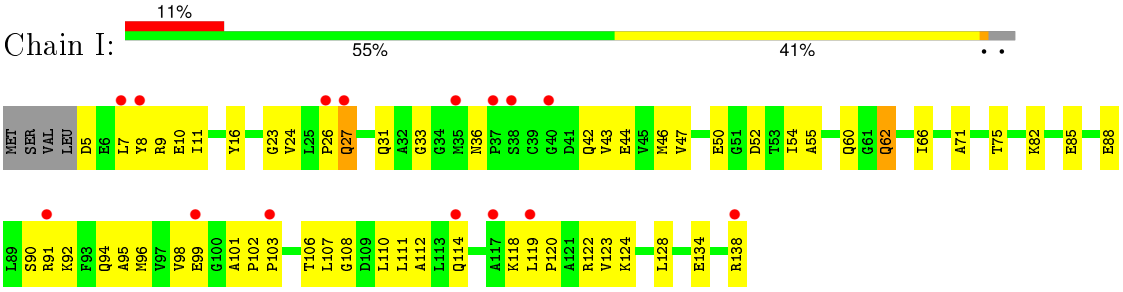
• Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain H:



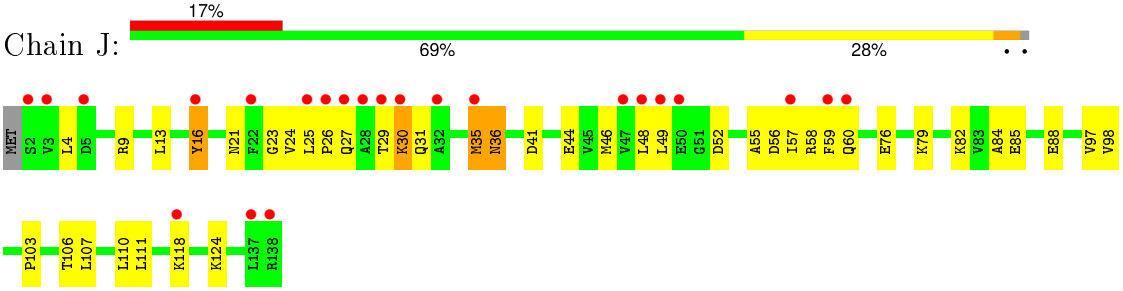
• Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain I:



• Molecule 1: Iron-sulfur cluster biosynthesis protein IscU

Chain J:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	58.89Å 64.87Å 96.26Å 71.18° 78.96° 79.02°	Depositor
Resolution (Å)	38.85 – 1.85 39.06 – 1.85	Depositor EDS
% Data completeness (in resolution range)	92.6 (38.85-1.85) 84.0 (39.06-1.85)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	0.04	Depositor
$< I/\sigma(I) >$ [1]	2.83 (at 1.85Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.225 , 0.260 0.225 , 0.260	Depositor DCC
R_{free} test set	10320 reflections (10.02%)	DCC
Wilson B-factor (Å^2)	27.5	Xtriage
Anisotropy	0.153	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 54.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 105591 reflections	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	11013	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 5.60% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.37	0/1047	0.60	0/1417
1	B	0.35	0/1039	0.56	0/1407
1	C	0.35	0/1047	0.61	0/1417
1	D	0.32	0/1039	0.56	0/1407
1	E	0.32	0/1039	0.57	0/1407
1	F	0.27	0/1033	0.55	0/1399
1	G	0.29	0/1039	0.53	0/1407
1	H	0.28	0/1047	0.51	0/1417
1	I	0.34	0/1018	0.61	0/1378
1	J	0.28	0/1039	0.50	0/1407
All	All	0.32	0/10387	0.56	0/14063

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	1032	0	1051	34	0
1	B	1024	0	1039	19	0
1	C	1032	0	1051	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	1024	0	1039	33	0
1	E	1024	0	1039	29	0
1	F	1018	0	1034	40	0
1	G	1024	0	1039	16	0
1	H	1032	0	1051	43	0
1	I	1003	0	1014	61	0
1	J	1024	0	1039	52	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
2	E	1	0	0	0	0
2	F	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
2	I	1	0	0	0	0
2	J	1	0	0	0	0
3	A	108	0	0	3	0
3	B	84	0	0	2	0
3	C	97	0	0	5	0
3	D	99	0	0	3	0
3	E	77	0	0	2	0
3	F	49	0	0	1	0
3	G	87	0	0	2	0
3	H	57	0	0	0	0
3	I	48	0	0	3	0
3	J	60	0	0	3	0
All	All	11013	0	10396	317	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 15.

All (317) 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:35:MET:HG2	1:G:42:GLN:HG2	1.46	0.95
1:C:1:MET:HB3	3:C:258:HOH:O	1.72	0.90
1:A:104:ASP:OD1	1:A:106:THR:HG22	1.70	0.90
1:B:3:VAL:HG11	1:E:12:LEU:HD12	1.54	0.88
1:I:36:ASN:HD21	1:I:124:LYS:HB3	1.40	0.86
1:D:88:GLU:HG3	1:D:92:LYS:NZ	1.94	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:36:ASN:HD21	1:J:41:ASP:HB2	1.42	0.83
1:A:39:CYS:HA	1:H:106:THR:HA	1.59	0.82
1:A:134:GLU:O	1:A:138:ARG:HG2	1.80	0.82
1:D:104:ASP:OD1	1:D:106:THR:HG22	1.81	0.81
1:H:1:MET:HE3	1:H:3:VAL:HB	1.64	0.80
1:C:1:MET:HG2	1:D:119:LEU:HD21	1.62	0.79
1:E:103:PRO:HG2	1:E:114:GLN:HE21	1.47	0.79
1:J:29:THR:HG21	1:J:49:LEU:HB2	1.65	0.79
1:E:135:GLU:HA	1:E:138:ARG:HH11	1.48	0.78
1:C:50:GLU:HG3	1:C:55:ALA:HB2	1.67	0.77
1:F:36:ASN:HB3	1:F:41:ASP:H	1.49	0.77
1:C:10:GLU:HG3	1:D:13:LEU:HD22	1.66	0.76
1:J:36:ASN:HD22	1:J:36:ASN:H	1.32	0.76
1:D:30:LYS:HD3	1:D:136:ALA:O	1.86	0.76
1:D:88:GLU:HG3	1:D:92:LYS:HZ2	1.50	0.75
1:H:1:MET:CE	1:H:3:VAL:HB	2.18	0.74
1:A:4:LEU:HD21	1:I:66:ILE:HD11	1.69	0.74
1:I:36:ASN:ND2	1:I:124:LYS:HB3	2.02	0.73
1:E:31:GLN:CG	1:E:46:MET:HG2	2.19	0.72
1:I:119:LEU:N	1:I:120:PRO:HD3	2.04	0.72
1:E:103:PRO:HG2	1:E:114:GLN:NE2	2.05	0.72
1:F:97:VAL:HG12	1:F:123:VAL:HG13	1.71	0.71
1:I:134:GLU:O	1:I:138:ARG:HG3	1.90	0.71
1:A:2:SER:HA	1:A:5:ASP:HB3	1.73	0.71
1:A:124:LYS:HE2	1:H:105:PRO:HG3	1.71	0.71
1:J:25:LEU:HD21	1:J:58:ARG:HG3	1.71	0.71
1:F:82:LYS:HB2	1:F:85:GLU:HG3	1.72	0.69
1:J:82:LYS:HB2	1:J:85:GLU:HG3	1.74	0.69
1:E:88:GLU:HG3	1:E:92:LYS:HE2	1.73	0.69
1:C:27:GLN:OE1	1:C:48:LEU:HD22	1.91	0.69
1:F:43:VAL:HG22	3:F:303:HOH:O	1.91	0.69
1:F:3:VAL:HB	1:F:6:GLU:HG3	1.76	0.68
1:A:2:SER:HB3	1:I:9:ARG:NH2	2.09	0.68
1:I:122:ARG:HH11	1:I:122:ARG:HG2	1.59	0.67
1:J:25:LEU:HD13	1:J:48:LEU:HD13	1.76	0.67
1:I:66:ILE:HD12	1:I:122:ARG:HE	1.59	0.67
1:E:30:LYS:HD3	1:E:136:ALA:O	1.95	0.67
1:F:36:ASN:HD22	1:F:39:CYS:HB3	1.60	0.67
1:J:48:LEU:HD22	1:J:56:ASP:HB3	1.77	0.67
1:I:66:ILE:CD1	1:I:122:ARG:HE	2.08	0.66
1:I:24:VAL:HG22	1:I:60:GLN:OE1	1.96	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:36:ASN:ND2	1:J:41:ASP:HB2	2.11	0.65
1:J:44:GLU:HB2	1:J:60:GLN:HB2	1.77	0.65
1:C:111:LEU:O	1:C:114:GLN:HB2	1.97	0.65
1:H:1:MET:HE2	1:H:4:LEU:HG	1.79	0.64
1:J:58:ARG:HG2	1:J:58:ARG:HH11	1.63	0.64
1:D:17:GLN:NE2	1:D:18:SER:OG	2.31	0.64
1:C:26:PRO:HB2	1:C:27:GLN:HE21	1.63	0.64
1:I:50:GLU:HG3	1:I:55:ALA:HB2	1.79	0.63
1:A:115:GLY:HA3	1:H:1:MET:HG3	1.81	0.63
1:J:21:ASN:HD21	1:J:79:LYS:NZ	1.97	0.63
1:A:115:GLY:HA3	1:H:1:MET:CE	2.28	0.62
1:I:94:GLN:O	1:I:98:VAL:HB	1.99	0.62
1:H:134:GLU:O	1:H:138:ARG:HG3	1.99	0.62
1:F:35:MET:HG3	1:F:42:GLN:HG3	1.81	0.62
1:C:27:GLN:H	1:C:27:GLN:NE2	1.97	0.62
1:A:35:MET:O	1:A:37:PRO:HD3	2.00	0.62
1:I:8:TYR:HD1	1:I:11:ILE:HD12	1.64	0.61
1:C:31:GLN:HG2	1:C:44:GLU:OE2	1.99	0.61
1:F:5:ASP:O	1:F:9:ARG:HG3	2.01	0.61
1:F:74:MET:HG3	1:F:130:TRP:CE2	2.36	0.61
1:H:21:ASN:HD21	1:H:79:LYS:NZ	1.98	0.61
1:F:9:ARG:O	1:F:13:LEU:HG	2.01	0.61
1:I:27:GLN:HG2	1:I:27:GLN:O	1.99	0.61
1:A:115:GLY:CA	1:H:1:MET:HG3	2.31	0.61
1:I:96:MET:SD	1:I:114:GLN:HG2	2.41	0.60
1:I:120:PRO:HA	1:I:123:VAL:HG23	1.83	0.60
1:I:36:ASN:HD21	1:I:124:LYS:CB	2.14	0.60
1:D:50:GLU:HG3	1:D:55:ALA:HB2	1.82	0.60
1:A:4:LEU:HD12	1:I:119:LEU:HD22	1.83	0.59
1:C:24:VAL:HG12	1:C:60:GLN:NE2	2.17	0.59
1:I:66:ILE:HD12	1:I:122:ARG:HH21	1.68	0.59
1:H:66:ILE:HD12	1:H:122:ARG:CZ	2.33	0.58
1:J:30:LYS:HD3	1:J:49:LEU:HD12	1.84	0.58
1:C:3:VAL:HG22	1:D:9:ARG:NH1	2.17	0.58
1:H:88:GLU:HG3	1:H:92:LYS:HE3	1.85	0.58
1:C:27:GLN:H	1:C:27:GLN:CD	2.06	0.58
1:D:27:GLN:O	1:D:48:LEU:HD13	2.02	0.58
1:I:66:ILE:HD12	1:I:122:ARG:NE	2.18	0.58
1:F:56:ASP:OD1	1:F:79:LYS:HE2	2.04	0.58
1:F:137:LEU:O	1:F:138:ARG:HB2	2.03	0.58
1:J:25:LEU:CD2	1:J:58:ARG:HG3	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MET:HG2	1:D:119:LEU:CD2	2.34	0.57
1:D:47:VAL:HG13	1:D:54:ILE:HG23	1.85	0.57
1:C:122:ARG:NH1	1:G:8:TYR:OH	2.29	0.57
1:J:35:MET:HE2	1:J:35:MET:H	1.69	0.57
1:A:5:ASP:OD1	1:H:3:VAL:HG22	2.05	0.57
1:E:135:GLU:HA	1:E:138:ARG:NH1	2.18	0.57
1:A:103:PRO:HG2	1:A:114:GLN:NE2	2.20	0.57
1:H:82:LYS:HB2	1:H:85:GLU:HG3	1.86	0.57
1:H:30:LYS:HD3	1:H:136:ALA:O	2.05	0.57
1:H:74:MET:HG3	1:H:130:TRP:CE2	2.40	0.56
1:E:6:GLU:OE1	1:G:9:ARG:HG2	2.05	0.56
1:F:25:LEU:HD21	1:F:56:ASP:OD2	2.05	0.56
1:H:58:ARG:HG2	1:H:58:ARG:HH11	1.70	0.56
1:H:1:MET:CE	1:H:4:LEU:HG	2.35	0.56
1:J:48:LEU:HD22	1:J:56:ASP:CB	2.36	0.56
1:E:2:SER:HB2	1:E:5:ASP:HB3	1.86	0.56
1:E:58:ARG:HG3	1:E:58:ARG:HH11	1.71	0.56
1:B:31:GLN:HB3	1:B:46:MET:HG2	1.89	0.55
1:J:9:ARG:O	1:J:13:LEU:HG	2.05	0.55
1:E:5:ASP:O	1:E:9:ARG:HG3	2.06	0.55
1:I:43:VAL:HG12	1:I:128:LEU:HG	1.89	0.55
1:H:52:ASP:OD2	1:H:82:LYS:HD2	2.06	0.55
1:I:43:VAL:HB	3:I:614:HOH:O	2.07	0.54
1:J:48:LEU:HB2	1:J:56:ASP:H	1.71	0.54
1:E:13:LEU:HD11	1:E:17:GLN:OE1	2.07	0.54
1:E:31:GLN:HG2	1:E:46:MET:HG2	1.88	0.54
1:D:31:GLN:HG3	1:D:46:MET:HG2	1.88	0.54
1:E:35:MET:C	1:E:37:PRO:HD3	2.28	0.54
1:F:13:LEU:HD22	1:I:10:GLU:HG3	1.89	0.54
1:A:62:GLN:OE1	1:D:26:PRO:HG3	2.07	0.54
1:A:3:VAL:HG12	1:A:4:LEU:N	2.23	0.53
1:C:120:PRO:HA	1:C:123:VAL:HG23	1.90	0.53
1:J:30:LYS:HD3	1:J:49:LEU:CD1	2.38	0.53
1:D:92:LYS:HE2	1:D:106:THR:HG21	1.90	0.53
1:J:9:ARG:HE	1:J:13:LEU:HD11	1.74	0.53
1:F:43:VAL:HG12	1:F:44:GLU:N	2.24	0.53
1:H:121:ALA:O	1:H:122:ARG:HD2	2.09	0.53
1:H:116:VAL:HG23	1:J:4:LEU:HD11	1.90	0.53
1:C:74:MET:HG3	1:C:130:TRP:CZ2	2.44	0.53
1:A:39:CYS:HB2	3:A:943:HOH:O	2.09	0.52
1:B:119:LEU:HD12	1:D:4:LEU:HD23	1.89	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1:MET:O	1:A:5:ASP:HB2	2.08	0.52
1:I:66:ILE:HD12	1:I:122:ARG:NH2	2.23	0.52
1:A:17:GLN:NE2	3:A:533:HOH:O	2.43	0.52
1:F:13:LEU:HD22	1:I:10:GLU:CG	2.39	0.52
1:C:1:MET:HE2	3:C:892:HOH:O	2.09	0.52
1:E:3:VAL:HG12	1:E:4:LEU:N	2.25	0.52
1:E:35:MET:O	1:E:37:PRO:HD3	2.10	0.52
1:I:47:VAL:HG13	1:I:54:ILE:HG23	1.91	0.52
1:F:38:SER:O	1:I:106:THR:HG22	2.10	0.52
1:I:103:PRO:HG3	1:I:114:GLN:OE1	2.10	0.52
1:B:3:VAL:HG12	1:B:3:VAL:O	2.10	0.52
1:J:26:PRO:O	1:J:27:GLN:HB2	2.08	0.51
1:F:36:ASN:ND2	1:F:39:CYS:HB3	2.22	0.51
1:I:7:LEU:C	1:I:7:LEU:HD12	2.30	0.51
1:D:82:LYS:HB2	1:D:85:GLU:OE2	2.10	0.51
1:I:31:GLN:HG3	1:I:46:MET:HG2	1.91	0.51
1:I:33:GLY:HA2	1:I:44:GLU:HA	1.93	0.51
3:A:429:HOH:O	1:H:1:MET:HE1	2.11	0.51
1:D:26:PRO:HB2	3:D:961:HOH:O	2.10	0.51
1:J:21:ASN:HD21	1:J:79:LYS:CE	2.24	0.51
1:J:29:THR:HG22	1:J:30:LYS:HD2	1.92	0.51
1:D:104:ASP:CG	1:D:106:THR:HG22	2.31	0.51
1:J:76:GLU:HG2	3:J:395:HOH:O	2.10	0.51
1:F:120:PRO:C	1:F:122:ARG:H	2.13	0.50
1:B:9:ARG:HH11	1:B:9:ARG:HG2	1.77	0.50
1:I:88:GLU:HG2	3:I:628:HOH:O	2.10	0.50
1:I:122:ARG:NH1	1:I:122:ARG:HG2	2.26	0.50
1:B:106:THR:HB	3:E:963:HOH:O	2.10	0.50
1:I:92:LYS:O	1:I:95:ALA:HB3	2.12	0.50
1:J:84:ALA:O	1:J:88:GLU:HG2	2.12	0.50
1:H:1:MET:HB3	1:H:4:LEU:HB2	1.94	0.50
1:I:8:TYR:CD1	1:I:11:ILE:HD12	2.47	0.50
1:J:24:VAL:HG12	1:J:25:LEU:N	2.27	0.50
1:I:111:LEU:O	1:I:114:GLN:HG3	2.11	0.49
1:F:137:LEU:O	1:F:138:ARG:CB	2.60	0.49
1:I:91:ARG:HH21	1:I:91:ARG:HG2	1.77	0.49
1:A:2:SER:HB3	1:I:9:ARG:HH21	1.76	0.49
1:G:124:LYS:HE3	3:G:606:HOH:O	2.13	0.49
1:I:119:LEU:N	1:I:120:PRO:CD	2.73	0.49
1:F:120:PRO:O	1:F:121:ALA:HB3	2.12	0.49
1:D:35:MET:CE	1:D:37:PRO:HG3	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:6:GLU:HB3	1:J:9:ARG:NE	2.27	0.49
1:D:31:GLN:HG3	1:D:46:MET:CG	2.43	0.49
1:E:62:GLN:HG3	1:I:26:PRO:HB3	1.95	0.49
1:J:23:GLY:O	1:J:60:GLN:HG2	2.12	0.48
1:E:58:ARG:NE	3:E:541:HOH:O	2.46	0.48
1:G:118:LYS:O	1:G:119:LEU:HD23	2.13	0.48
1:J:35:MET:SD	1:J:35:MET:N	2.86	0.48
1:F:24:VAL:HG13	1:F:46:MET:SD	2.54	0.48
1:I:82:LYS:N	1:I:82:LYS:HD2	2.27	0.48
1:A:27:GLN:HB3	1:C:18:SER:HB3	1.95	0.48
1:D:135:GLU:O	1:D:138:ARG:HB2	2.13	0.48
1:I:90:SER:C	1:I:94:GLN:HE21	2.16	0.48
1:G:35:MET:HG3	3:G:862:HOH:O	2.14	0.48
1:H:1:MET:O	1:H:5:ASP:N	2.42	0.48
1:C:35:MET:HG3	3:C:925:HOH:O	2.13	0.48
1:A:113:LEU:O	1:A:116:VAL:HG12	2.12	0.48
1:F:62:GLN:HG2	1:F:63:GLY:N	2.28	0.48
1:F:52:ASP:O	1:F:83:VAL:HG23	2.14	0.48
1:C:24:VAL:HA	1:C:46:MET:HE1	1.96	0.47
1:D:35:MET:HG2	3:D:820:HOH:O	2.14	0.47
1:C:62:GLN:HB3	3:C:894:HOH:O	2.14	0.47
1:I:98:VAL:HG22	1:I:123:VAL:HG11	1.96	0.47
1:B:35:MET:N	1:B:128:LEU:HD11	2.29	0.47
1:E:4:LEU:HD12	1:G:119:LEU:HD13	1.95	0.47
1:J:36:ASN:N	1:J:36:ASN:HD22	1.98	0.47
1:F:30:LYS:HD3	1:F:136:ALA:O	2.15	0.47
1:F:26:PRO:HG2	1:F:27:GLN:H	1.79	0.47
1:E:31:GLN:HG3	1:E:46:MET:HG2	1.96	0.47
1:C:1:MET:O	1:C:5:ASP:N	2.44	0.47
1:J:57:ILE:O	1:J:58:ARG:HG2	2.14	0.47
1:J:27:GLN:OE1	1:J:27:GLN:HA	2.15	0.47
1:J:107:LEU:HB3	1:J:110:LEU:HB2	1.96	0.47
1:B:13:LEU:O	1:B:17:GLN:HG3	2.16	0.46
1:F:74:MET:HG3	1:F:130:TRP:CZ2	2.50	0.46
1:D:50:GLU:HG2	3:D:216:HOH:O	2.14	0.46
1:I:88:GLU:O	1:I:92:LYS:HG3	2.16	0.46
1:A:9:ARG:CD	1:H:6:GLU:HB3	2.45	0.46
1:I:119:LEU:H	1:I:120:PRO:HD3	1.79	0.46
1:C:74:MET:HG3	1:C:130:TRP:CE2	2.51	0.46
1:A:73:LEU:HB3	1:A:110:LEU:HD23	1.96	0.46
1:J:44:GLU:O	1:J:59:PHE:HA	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:101:ALA:HB1	1:I:102:PRO:HD2	1.97	0.46
1:F:7:LEU:O	1:F:11:ILE:HG13	2.16	0.46
1:J:48:LEU:HB3	1:J:55:ALA:HB3	1.98	0.46
1:B:9:ARG:CD	1:D:6:GLU:HB3	2.46	0.46
1:H:2:SER:O	1:H:6:GLU:HG3	2.16	0.46
1:G:88:GLU:OE1	1:G:91:ARG:NE	2.40	0.46
1:D:107:LEU:HB2	1:D:111:LEU:CD2	2.46	0.46
1:C:133:LEU:O	1:C:137:LEU:HG	2.16	0.46
1:H:104:ASP:HB2	1:H:105:PRO:HD2	1.98	0.46
1:B:82:LYS:NZ	3:B:786:HOH:O	2.49	0.46
1:H:21:ASN:HD21	1:H:79:LYS:HZ1	1.62	0.45
1:F:36:ASN:ND2	1:F:39:CYS:H	2.15	0.45
1:E:58:ARG:NH1	1:E:58:ARG:HG3	2.32	0.45
1:J:48:LEU:O	1:J:55:ALA:N	2.49	0.45
1:I:82:LYS:HB2	1:I:85:GLU:HG3	1.99	0.45
1:C:88:GLU:CD	1:C:91:ARG:HH11	2.20	0.45
1:B:3:VAL:HA	1:B:6:GLU:HB2	1.98	0.45
1:J:31:GLN:HG3	1:J:46:MET:HG2	1.97	0.45
1:F:25:LEU:HG	1:F:58:ARG:CG	2.47	0.45
1:B:120:PRO:HD2	3:B:381:HOH:O	2.16	0.45
1:J:124:LYS:HG3	3:J:539:HOH:O	2.16	0.45
1:C:74:MET:HG3	1:C:130:TRP:CH2	2.52	0.45
1:C:1:MET:CB	1:C:4:LEU:HB2	2.48	0.44
1:H:57:ILE:O	1:H:58:ARG:HG2	2.17	0.44
1:F:73:LEU:HB3	1:F:110:LEU:HD23	1.99	0.44
1:F:3:VAL:HB	1:F:6:GLU:CG	2.46	0.44
1:J:106:THR:HG22	1:J:106:THR:O	2.17	0.44
1:G:46:MET:HE1	1:G:60:GLN:HG3	1.98	0.44
1:F:10:GLU:HB2	1:J:13:LEU:HD22	1.98	0.44
1:B:9:ARG:HD3	1:D:6:GLU:CB	2.47	0.44
1:A:115:GLY:HA3	1:H:1:MET:HE1	1.99	0.44
1:A:6:GLU:HG2	1:I:9:ARG:HD3	2.00	0.44
1:I:23:GLY:O	1:I:60:GLN:HG3	2.18	0.44
1:E:97:VAL:HG12	1:E:123:VAL:HG13	1.98	0.44
1:J:52:ASP:HA	3:J:670:HOH:O	2.18	0.44
1:A:119:LEU:HD13	1:A:122:ARG:HD2	1.99	0.44
1:A:138:ARG:HH11	1:A:138:ARG:HG3	1.83	0.43
1:B:36:ASN:OD1	1:B:36:ASN:O	2.36	0.43
1:H:30:LYS:HG2	1:H:31:GLN:N	2.32	0.43
1:I:118:LYS:O	1:I:119:LEU:HB2	2.18	0.43
1:H:66:ILE:HD12	1:H:122:ARG:NH2	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:11:ILE:HD11	1:G:65:ALA:HB2	2.00	0.43
1:D:88:GLU:HG3	1:D:92:LYS:HZ3	1.78	0.43
1:G:46:MET:CE	1:G:60:GLN:HG3	2.49	0.43
1:H:74:MET:HG3	1:H:130:TRP:CD2	2.53	0.43
1:A:62:GLN:HE22	1:D:26:PRO:HA	1.83	0.43
1:I:52:ASP:O	1:I:82:LYS:HA	2.18	0.43
1:G:49:LEU:HD12	1:G:53:THR:O	2.18	0.43
1:I:71:ALA:O	1:I:75:THR:HG23	2.18	0.43
1:J:36:ASN:O	1:J:36:ASN:ND2	2.51	0.43
1:H:1:MET:SD	1:H:3:VAL:N	2.91	0.43
1:I:108:GLY:O	1:I:111:LEU:HG	2.19	0.43
1:E:81:LYS:HD2	1:E:85:GLU:CD	2.39	0.43
1:B:44:GLU:O	1:B:59:PHE:HA	2.19	0.43
1:D:2:SER:HA	1:D:5:ASP:HB2	1.99	0.43
1:A:38:SER:HB2	1:H:106:THR:HG22	2.00	0.43
1:I:118:LYS:C	1:I:119:LEU:HD12	2.39	0.43
1:J:25:LEU:HD13	1:J:48:LEU:CD1	2.47	0.43
1:F:6:GLU:OE2	1:J:9:ARG:HD2	2.19	0.43
1:A:9:ARG:HD3	1:H:6:GLU:HB3	2.00	0.43
1:C:44:GLU:O	1:C:59:PHE:HA	2.18	0.42
1:J:25:LEU:HD11	1:J:57:ILE:HA	2.01	0.42
1:G:2:SER:HA	1:G:5:ASP:HB2	2.02	0.42
1:F:74:MET:HG3	1:F:130:TRP:CD2	2.54	0.42
1:H:1:MET:HE3	1:H:4:LEU:N	2.34	0.42
1:I:66:ILE:HD12	1:I:122:ARG:CZ	2.49	0.42
1:E:4:LEU:HA	1:E:4:LEU:HD23	1.91	0.42
1:G:31:GLN:HE21	1:G:44:GLU:CG	2.32	0.42
1:I:102:PRO:HA	1:I:103:PRO:HD3	1.85	0.42
1:J:31:GLN:HG3	1:J:46:MET:CG	2.50	0.42
1:G:124:LYS:HA	1:G:127:THR:OG1	2.20	0.42
1:I:42:GLN:HB3	1:I:62:GLN:HE21	1.85	0.42
1:J:97:VAL:HG23	1:J:98:VAL:N	2.35	0.42
1:A:134:GLU:OE1	1:A:138:ARG:NH2	2.53	0.42
1:J:56:ASP:OD2	1:J:79:LYS:HE2	2.18	0.42
1:C:31:GLN:HG3	1:C:46:MET:HG2	2.02	0.42
1:H:43:VAL:HG22	1:H:44:GLU:N	2.35	0.42
1:B:16:TYR:CD1	1:B:65:ALA:HA	2.55	0.42
1:B:79:LYS:HE3	3:I:789:HOH:O	2.19	0.41
1:B:8:TYR:O	1:B:12:LEU:HG	2.20	0.41
1:J:103:PRO:HB2	1:J:111:LEU:CD2	2.49	0.41
1:F:43:VAL:HG23	1:F:128:LEU:CD2	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:48:LEU:HG	1:G:55:ALA:HB3	2.03	0.41
1:J:118:LYS:O	1:J:118:LYS:HG3	2.21	0.41
1:I:43:VAL:CG1	1:I:128:LEU:HG	2.49	0.41
1:I:43:VAL:HA	1:I:60:GLN:O	2.20	0.41
1:F:30:LYS:NZ	1:F:138:ARG:HA	2.36	0.41
1:D:135:GLU:HA	1:D:138:ARG:HD3	2.02	0.41
1:H:83:VAL:HG13	1:H:137:LEU:HD13	2.03	0.41
1:E:73:LEU:HB3	1:E:110:LEU:HD23	2.01	0.41
1:D:35:MET:HE3	1:D:37:PRO:HG3	2.02	0.41
1:I:99:GLU:OE1	1:I:99:GLU:HA	2.21	0.41
1:E:88:GLU:O	1:E:92:LYS:HG3	2.21	0.41
1:A:27:GLN:HB3	1:C:18:SER:CB	2.51	0.41
1:H:44:GLU:O	1:H:59:PHE:HA	2.21	0.41
1:I:107:LEU:HB3	1:I:110:LEU:HB2	2.01	0.41
1:F:83:VAL:HG13	1:F:137:LEU:HD13	2.03	0.41
1:B:71:ALA:O	1:B:75:THR:HG23	2.21	0.41
1:E:24:VAL:HG22	1:E:25:LEU:N	2.36	0.41
1:H:91:ARG:NH1	1:H:95:ALA:HB2	2.35	0.41
1:A:122:ARG:NE	1:H:111:LEU:HD13	2.37	0.40
1:J:103:PRO:HB2	1:J:111:LEU:HD22	2.03	0.40
1:H:97:VAL:HG13	1:H:116:VAL:CG1	2.51	0.40
1:D:102:PRO:HA	1:D:103:PRO:HD3	1.95	0.40
1:F:11:ILE:HG12	1:J:16:TYR:CZ	2.56	0.40
1:C:3:VAL:HG23	3:C:795:HOH:O	2.20	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	136/138 (99%)	133 (98%)	3 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	135/138 (98%)	133 (98%)	2 (2%)	0	100 100
1	C	136/138 (99%)	132 (97%)	4 (3%)	0	100 100
1	D	135/138 (98%)	131 (97%)	4 (3%)	0	100 100
1	E	135/138 (98%)	130 (96%)	4 (3%)	1 (1%)	26 11
1	F	134/138 (97%)	126 (94%)	7 (5%)	1 (1%)	26 11
1	G	135/138 (98%)	132 (98%)	2 (2%)	1 (1%)	26 11
1	H	136/138 (99%)	135 (99%)	1 (1%)	0	100 100
1	I	132/138 (96%)	122 (92%)	9 (7%)	1 (1%)	24 9
1	J	135/138 (98%)	129 (96%)	6 (4%)	0	100 100
All	All	1349/1380 (98%)	1303 (97%)	42 (3%)	4 (0%)	46 29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	I	112	ALA
1	E	3	VAL
1	G	103	PRO
1	F	37	PRO

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	109/109 (100%)	104 (95%)	5 (5%)	33 14
1	B	108/109 (99%)	108 (100%)	0	100 100
1	C	109/109 (100%)	107 (98%)	2 (2%)	66 52
1	D	108/109 (99%)	104 (96%)	4 (4%)	41 20
1	E	108/109 (99%)	106 (98%)	2 (2%)	65 49
1	F	107/109 (98%)	105 (98%)	2 (2%)	65 49
1	G	108/109 (99%)	106 (98%)	2 (2%)	65 49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	H	109/109 (100%)	106 (97%)	3 (3%)	51 33
1	I	105/109 (96%)	101 (96%)	4 (4%)	40 19
1	J	108/109 (99%)	104 (96%)	4 (4%)	41 20
All	All	1079/1090 (99%)	1051 (97%)	28 (3%)	54 36

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
1	A	3	VAL
1	A	16	TYR
1	A	31	GLN
1	A	124	LYS
1	C	27	GLN
1	C	62	GLN
1	D	4	LEU
1	D	17	GLN
1	D	42	GLN
1	D	138	ARG
1	E	16	TYR
1	E	38	SER
1	F	35	MET
1	F	122	ARG
1	G	88	GLU
1	G	124	LYS
1	H	35	MET
1	H	62	GLN
1	H	91	ARG
1	I	5	ASP
1	I	16	TYR
1	I	27	GLN
1	I	62	GLN
1	J	16	TYR
1	J	30	LYS
1	J	35	MET
1	J	36	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	36	ASN
1	A	42	GLN
1	A	114	GLN
1	A	131	HIS
1	B	27	GLN
1	C	27	GLN
1	C	62	GLN
1	D	17	GLN
1	D	42	GLN
1	D	60	GLN
1	D	131	HIS
1	E	114	GLN
1	F	31	GLN
1	F	36	ASN
1	F	60	GLN
1	G	31	GLN
1	G	60	GLN
1	H	17	GLN
1	H	21	ASN
1	H	62	GLN
1	H	114	GLN
1	I	62	GLN
1	I	94	GLN
1	I	131	HIS
1	J	21	ASN
1	J	36	ASN
1	J	94	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 10 ligands modelled in this entry, 10 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	138/138 (100%)	0.07	6 (4%) 39 36	15, 27, 66, 97	0
1	B	137/138 (99%)	-0.05	2 (1%) 76 76	17, 30, 56, 67	0
1	C	138/138 (100%)	-0.05	2 (1%) 78 78	16, 29, 50, 74	0
1	D	137/138 (99%)	-0.11	2 (1%) 76 76	18, 33, 55, 76	0
1	E	137/138 (99%)	0.20	5 (3%) 46 44	20, 34, 59, 76	0
1	F	136/138 (98%)	0.50	7 (5%) 32 30	25, 43, 76, 88	0
1	G	137/138 (99%)	0.19	1 (0%) 89 88	20, 37, 61, 84	0
1	H	138/138 (100%)	0.35	7 (5%) 32 30	24, 44, 70, 85	0
1	I	134/138 (97%)	0.65	15 (11%) 7 6	20, 47, 78, 93	0
1	J	137/138 (99%)	0.96	23 (16%) 2 2	29, 49, 85, 98	0
All	All	1369/1380 (99%)	0.27	70 (5%) 32 30	15, 37, 70, 98	0

All (70) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	39	CYS	6.0
1	F	121	ALA	5.7
1	J	26	PRO	5.7
1	I	119	LEU	5.5
1	I	37	PRO	5.2
1	C	1	MET	5.2
1	H	1	MET	5.0
1	J	2	SER	4.7
1	J	137	LEU	4.6
1	J	57	ILE	4.5
1	H	117	ALA	4.5
1	J	28	ALA	4.3
1	F	38	SER	4.2

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Mol	Chain	Res	Type	RSRZ
1	F	37	PRO	4.2
1	J	5	ASP	4.1
1	B	37	PRO	4.0
1	J	48	LEU	4.0
1	J	35	MET	3.9
1	I	8	TYR	3.8
1	I	138	ARG	3.8
1	A	5	ASP	3.8
1	J	50	GLU	3.8
1	J	16	TYR	3.7
1	J	47	VAL	3.5
1	I	117	ALA	3.4
1	J	25	LEU	3.4
1	E	117	ALA	3.3
1	J	3	VAL	3.2
1	I	7	LEU	3.2
1	A	1	MET	3.1
1	E	2	SER	3.0
1	H	24	VAL	3.0
1	J	30	LYS	3.0
1	J	22	PHE	3.0
1	H	138	ARG	2.7
1	J	138	ARG	2.6
1	C	2	SER	2.6
1	J	59	PHE	2.6
1	I	26	PRO	2.6
1	E	119	LEU	2.5
1	H	102	PRO	2.5
1	A	39	CYS	2.4
1	I	103	PRO	2.4
1	I	35	MET	2.4
1	A	3	VAL	2.3
1	D	106	THR	2.3
1	J	29	THR	2.3
1	E	28	ALA	2.3
1	A	2	SER	2.3
1	F	120	PRO	2.3
1	I	99	GLU	2.3
1	B	3	VAL	2.2
1	J	27	GLN	2.2
1	I	27	GLN	2.2
1	J	32	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	37	PRO	2.2
1	I	114	GLN	2.2
1	H	105	PRO	2.2
1	F	61	GLY	2.1
1	J	49	LEU	2.1
1	I	91	ARG	2.1
1	F	100	GLY	2.1
1	H	103	PRO	2.1
1	D	8	TYR	2.1
1	J	60	GLN	2.1
1	E	118	LYS	2.1
1	I	40	GLY	2.1
1	I	38	SER	2.0
1	G	30	LYS	2.0
1	J	118	LYS	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 carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	ZN	I	139	1/1	0.69	0.27	7.17	92,92,92,92	0
2	ZN	E	139	1/1	0.98	0.04	-1.37	28,28,28,28	0
2	ZN	G	139	1/1	1.00	0.05	-1.39	28,28,28,28	0
2	ZN	F	139	1/1	0.92	0.04	-1.46	59,59,59,59	0
2	ZN	A	139	1/1	1.00	0.02	-2.27	24,24,24,24	0
2	ZN	C	139	1/1	1.00	0.05	-2.31	26,26,26,26	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	ZN	J	139	1/1	0.98	0.03	-2.42	36,36,36,36	0
2	ZN	B	139	1/1	0.98	0.04	-2.44	29,29,29,29	0
2	ZN	D	139	1/1	1.00	0.03	-2.44	24,24,24,24	0
2	ZN	H	139	1/1	0.99	0.04	-3.17	35,35,35,35	0

6.5 Other polymers (i)

There are no such residues in this entry.