



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 20, 2023 – 09:44 AM EDT

PDB ID : 2HZS
Title : Structure of the Mediator head submodule Med8C/18/20
Authors : Lariviere, L.; Geiger, S.; Hoepfner, S.; Rother, S.; Straesser, K.; Cramer, P.
Deposited on : 2006-08-09
Resolution : 2.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ 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 : 2.35
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) : 2.35

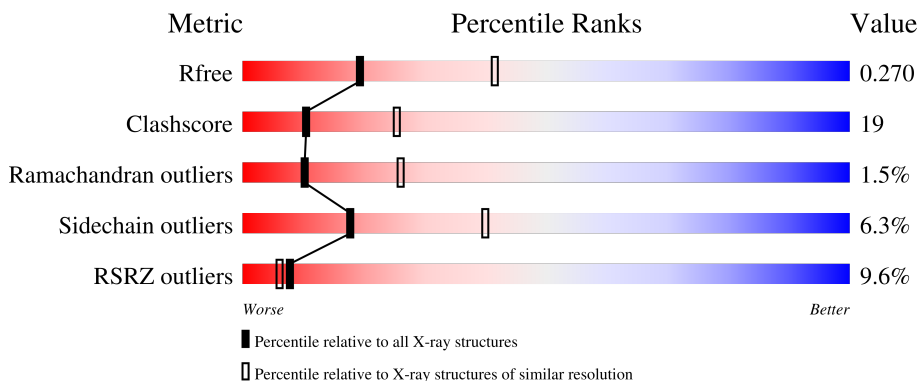
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	209	
1	C	209	
1	E	209	
1	G	209	
2	B	306	

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Mol	Chain	Length	Quality of chain
2	D	306	<p>5% 49% 19% 30%</p>
2	F	306	<p>4% 46% 28% 23%</p>
2	H	306	<p>4% 50% 20% 5% 25%</p>
3	I	27	<p>4% 63% 19% 19%</p>
3	J	27	<p>56% 15% 30%</p>
3	K	27	<p>52% 7% 41%</p>
3	L	27	<p>56% 7% 37%</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 14086 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 RNA polymerase II mediator complex subunit 20.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	203	1560	987	263	305	5	0	0	0
1	C	202	1554	984	262	303	5	0	0	0
1	E	203	1560	987	263	305	5	0	0	0
1	G	203	1560	987	263	305	5	0	0	0

- Molecule 2 is a protein called RNA polymerase II mediator complex subunit 18.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	235	1844	1175	302	358	9	0	0	0
2	D	214	1671	1065	273	326	7	0	0	0
2	F	235	1829	1156	298	367	8	0	0	0
2	H	230	1803	1146	297	351	9	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	274	VAL	ALA	engineered mutation	UNP P32585
D	274	VAL	ALA	engineered mutation	UNP P32585
F	274	VAL	ALA	engineered mutation	UNP P32585
H	274	VAL	ALA	engineered mutation	UNP P32585

- Molecule 3 is a protein called RNA polymerase II mediator complex subunit 8.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	22	Total	C	N	O	0	0	0
			192	123	37	32			
3	J	19	Total	C	N	O	0	0	0
			156	102	25	29			
3	K	16	Total	C	N	O	0	0	0
			131	87	19	25			
3	L	17	Total	C	N	O	0	0	0
			141	93	22	26			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	211	HIS	-	expression tag	UNP P38304
I	212	HIS	-	expression tag	UNP P38304
I	213	HIS	-	expression tag	UNP P38304
I	214	HIS	-	expression tag	UNP P38304
I	215	HIS	-	expression tag	UNP P38304
I	216	HIS	-	expression tag	UNP P38304
J	211	HIS	-	expression tag	UNP P38304
J	212	HIS	-	expression tag	UNP P38304
J	213	HIS	-	expression tag	UNP P38304
J	214	HIS	-	expression tag	UNP P38304
J	215	HIS	-	expression tag	UNP P38304
J	216	HIS	-	expression tag	UNP P38304
K	211	HIS	-	expression tag	UNP P38304
K	212	HIS	-	expression tag	UNP P38304
K	213	HIS	-	expression tag	UNP P38304
K	214	HIS	-	expression tag	UNP P38304
K	215	HIS	-	expression tag	UNP P38304
K	216	HIS	-	expression tag	UNP P38304
L	211	HIS	-	expression tag	UNP P38304
L	212	HIS	-	expression tag	UNP P38304
L	213	HIS	-	expression tag	UNP P38304
L	214	HIS	-	expression tag	UNP P38304
L	215	HIS	-	expression tag	UNP P38304
L	216	HIS	-	expression tag	UNP P38304

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	O	0	0
			3	3		
4	B	34	Total	O	0	0
			34	34		

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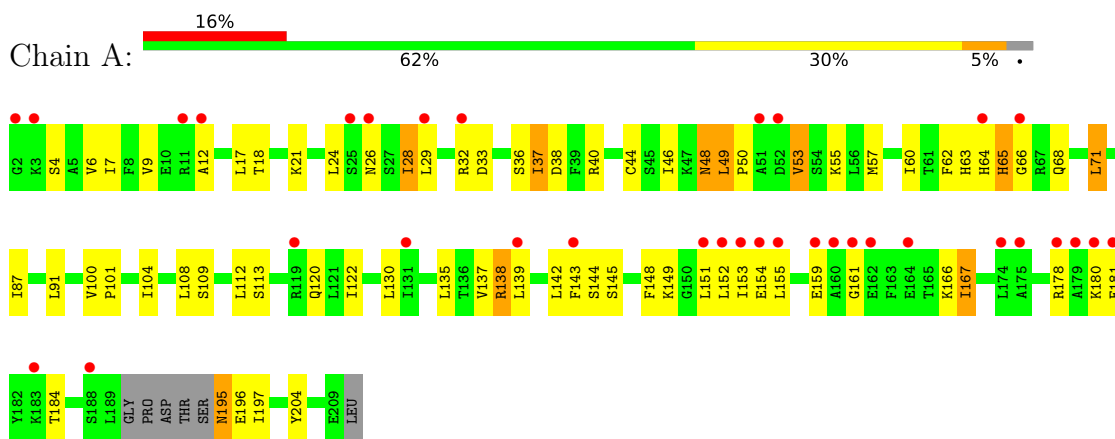
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	C	2	Total O 2 2	0	0
4	D	12	Total O 12 12	0	0
4	E	2	Total O 2 2	0	0
4	F	13	Total O 13 13	0	0
4	H	15	Total O 15 15	0	0
4	I	4	Total O 4 4	0	0

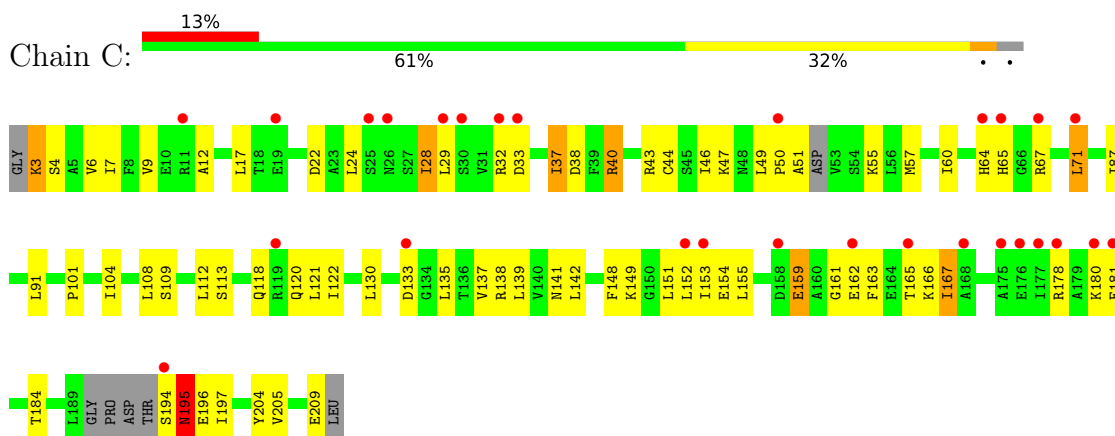
3 Residue-property plots [i](#)

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.

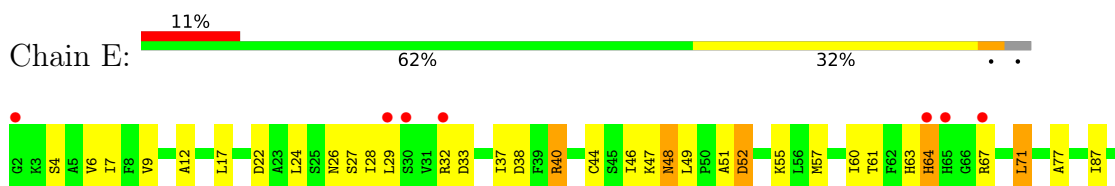
- Molecule 1: RNA polymerase II mediator complex subunit 20

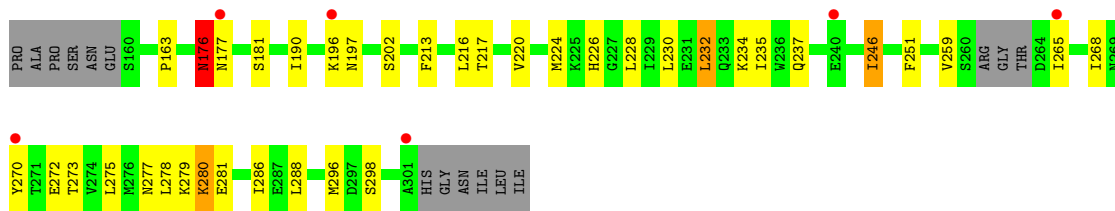


- Molecule 1: RNA polymerase II mediator complex subunit 20

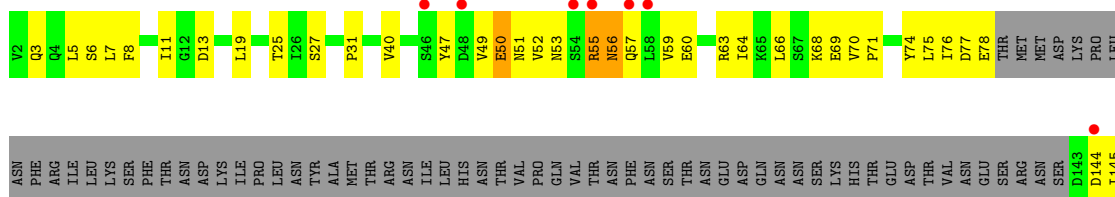


- Molecule 1: RNA polymerase II mediator complex subunit 20

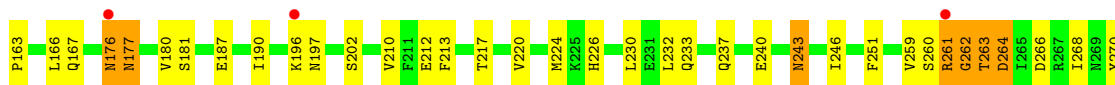
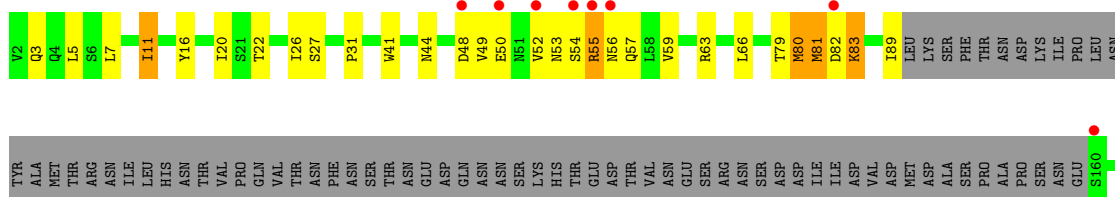




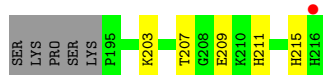
• Molecule 2: RNA polymerase II mediator complex subunit 18



• Molecule 2: RNA polymerase II mediator complex subunit 18



• Molecule 3: RNA polymerase II mediator complex subunit 8



- Molecule 3: RNA polymerase II mediator complex subunit 8

Chain J:  56% 15% 30%



- Molecule 3: RNA polymerase II mediator complex subunit 8

Chain K:  52% 7% 41%



- Molecule 3: RNA polymerase II mediator complex subunit 8

Chain L:  56% 7% 37%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	75.36Å 115.76Å 129.16Å 90.00° 98.49° 90.00°	Depositor
Resolution (Å)	20.00 – 2.70 19.79 – 2.67	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.70) 99.1 (19.79-2.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.26 (at 2.67Å)	Xtrriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.236 , 0.272 0.232 , 0.270	Depositor DCC
R_{free} test set	3117 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	57.6	Xtrriage
Anisotropy	0.191	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	14086	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.38	0/1584	0.87	8/2145 (0.4%)
1	C	0.38	0/1577	0.63	1/2134 (0.0%)
1	E	0.35	0/1584	0.64	1/2145 (0.0%)
1	G	0.36	0/1584	0.59	0/2145
2	B	0.46	0/1876	0.73	2/2541 (0.1%)
2	D	0.44	0/1700	0.68	1/2304 (0.0%)
2	F	0.45	0/1861	0.70	0/2526
2	H	0.45	0/1835	0.70	0/2486
3	I	0.45	0/201	0.60	0/269
3	J	0.49	0/160	0.59	0/214
3	K	0.55	0/134	0.65	0/179
3	L	0.52	0/145	0.59	0/194
All	All	0.42	0/14241	0.69	13/19282 (0.1%)

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	138	ARG	NE-CZ-NH1	-14.18	113.21	120.30
1	A	40	ARG	NE-CZ-NH2	-13.12	113.74	120.30
1	A	138	ARG	NE-CZ-NH2	12.83	126.72	120.30
1	A	40	ARG	NE-CZ-NH1	9.33	124.97	120.30
2	B	303	GLY	N-CA-C	-7.56	94.19	113.10
1	A	65	HIS	N-CA-C	-7.17	91.64	111.00
1	A	138	ARG	CD-NE-CZ	6.71	133.00	123.60
1	A	53	VAL	N-CA-C	-6.66	93.02	111.00
1	C	40	ARG	NE-CZ-NH1	-6.18	117.21	120.30
1	E	40	ARG	NE-CZ-NH1	-5.65	117.48	120.30
2	D	176	ASN	N-CA-C	-5.54	96.05	111.00
2	B	301	ALA	N-CA-C	5.31	125.34	111.00
1	A	40	ARG	CD-NE-CZ	5.30	131.02	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	1560	0	1576	70	0
1	C	1554	0	1573	66	0
1	E	1560	0	1576	61	0
1	G	1560	0	1576	52	0
2	B	1844	0	1851	79	0
2	D	1671	0	1676	53	1
2	F	1829	0	1811	87	1
2	H	1803	0	1809	67	0
3	I	192	0	168	5	0
3	J	156	0	150	5	0
3	K	131	0	126	2	0
3	L	141	0	133	2	0
4	A	3	0	0	0	0
4	B	34	0	0	2	0
4	C	2	0	0	0	0
4	D	12	0	0	0	0
4	E	2	0	0	0	0
4	F	13	0	0	1	0
4	H	15	0	0	0	0
4	I	4	0	0	0	0
All	All	14086	0	14025	522	1

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 19.

All (522) 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:A:142:LEU:HD11	1:A:152:LEU:HD12	1.35	1.06
1:G:142:LEU:HD11	1:G:152:LEU:HD12	1.36	1.05
2:F:265:ILE:HD12	2:F:265:ILE:H	1.25	1.02
1:C:142:LEU:HD11	1:C:152:LEU:HD12	1.37	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:142:LEU:HD11	1:E:152:LEU:HD12	1.37	1.00
1:C:71:LEU:HD11	1:C:104:ILE:HG12	1.54	0.90
2:B:53:ASN:HD22	2:B:57:GLN:HB2	1.35	0.89
1:A:66:GLY:HA3	1:A:68:GLN:HG3	1.54	0.89
2:B:83:LYS:O	2:B:84:PRO:C	2.10	0.88
1:E:40:ARG:HD3	1:E:118:GLN:NE2	1.90	0.87
1:A:100:VAL:HB	2:B:2:VAL:HG21	1.55	0.86
1:A:100:VAL:HB	2:B:2:VAL:CG2	2.05	0.86
1:E:27:SER:O	1:E:132:LEU:HD22	1.77	0.84
2:H:11:ILE:HD11	2:H:251:PHE:HB2	1.60	0.83
1:G:71:LEU:HD11	1:G:104:ILE:HG12	1.60	0.82
2:D:75:LEU:HD22	2:D:216:LEU:HD21	1.61	0.82
2:H:263:THR:HG22	2:H:264:ASP:H	1.45	0.82
2:B:53:ASN:HB2	2:B:57:GLN:H	1.44	0.82
2:B:232:LEU:HD13	2:B:253:LEU:HD13	1.62	0.82
1:C:130:LEU:HB2	1:C:137:VAL:HG13	1.60	0.82
1:A:130:LEU:HB2	1:A:137:VAL:HG13	1.61	0.82
1:A:62:PHE:HB3	1:A:65:HIS:HB2	1.62	0.81
1:G:40:ARG:HD3	1:G:118:GLN:NE2	1.96	0.80
1:E:130:LEU:HB2	1:E:137:VAL:HG13	1.63	0.80
1:E:178:ARG:HA	1:E:180:LYS:HE2	1.64	0.79
1:A:57:MET:SD	1:A:71:LEU:HD23	2.22	0.79
1:G:130:LEU:HB2	1:G:137:VAL:HG13	1.64	0.79
2:H:83:LYS:H	2:H:83:LYS:HE2	1.46	0.79
1:C:135:LEU:HD22	1:C:166:LYS:HB3	1.64	0.79
1:G:178:ARG:HA	1:G:180:LYS:HE2	1.65	0.78
1:A:49:LEU:HD23	1:A:55:LYS:HD2	1.63	0.78
2:F:224:MET:HE3	2:F:230:LEU:HD12	1.63	0.78
1:C:178:ARG:HA	1:C:180:LYS:HE2	1.66	0.77
1:C:40:ARG:HD3	1:C:118:GLN:NE2	1.99	0.77
2:F:259:VAL:HG21	2:F:268:ILE:HD11	1.67	0.77
1:A:135:LEU:HD22	1:A:166:LYS:HB3	1.67	0.77
1:C:49:LEU:HD23	1:C:55:LYS:HD2	1.66	0.76
2:H:279:LYS:HE2	2:H:288:LEU:O	1.85	0.76
1:E:57:MET:SD	1:E:71:LEU:HD23	2.25	0.76
2:F:71:PRO:HG2	2:F:74:TYR:HD2	1.49	0.76
2:F:50:GLU:CD	2:F:50:GLU:H	1.90	0.75
1:E:134:GLY:O	1:E:166:LYS:NZ	2.15	0.75
1:E:135:LEU:HD22	1:E:166:LYS:HB3	1.69	0.75
2:F:228:LEU:HD21	2:F:278:LEU:HD22	1.68	0.75
3:I:209:GLU:OE1	3:I:211:HIS:HE1	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:145:ILE:HG13	2:F:146:ILE:HD12	1.69	0.74
2:H:176:ASN:O	2:H:177:ASN:HB2	1.88	0.74
2:F:52:VAL:CG2	2:F:56:ASN:HA	2.17	0.73
1:G:135:LEU:HD22	1:G:166:LYS:HB3	1.71	0.73
1:A:139:LEU:CD2	1:A:153:ILE:HD12	2.18	0.73
2:F:64:ILE:HD13	2:F:209:TYR:CE2	2.24	0.73
2:H:53:ASN:ND2	2:H:55:ARG:HD3	2.05	0.72
2:F:259:VAL:HG21	2:F:268:ILE:CD1	2.21	0.71
1:G:49:LEU:HD12	1:G:55:LYS:HE2	1.71	0.71
1:A:178:ARG:HA	1:A:180:LYS:HE2	1.71	0.70
2:F:224:MET:CE	2:F:230:LEU:HD12	2.22	0.70
1:C:49:LEU:CD2	1:C:55:LYS:HD2	2.21	0.69
2:H:49:VAL:HG22	2:H:50:GLU:H	1.56	0.69
2:B:83:LYS:O	2:B:85:LEU:N	2.25	0.69
2:D:11:ILE:HD11	2:D:232:LEU:HD11	1.75	0.68
2:B:53:ASN:HB3	2:B:55:ARG:H	1.57	0.68
2:H:49:VAL:HG22	2:H:50:GLU:N	2.09	0.68
2:B:83:LYS:HB3	2:B:84:PRO:HD3	1.76	0.68
1:E:71:LEU:HD11	1:E:104:ILE:HG12	1.75	0.68
2:B:90:LEU:N	2:B:90:LEU:HD12	2.08	0.67
2:F:77:ASP:O	2:F:78:GLU:HG3	1.94	0.67
2:D:176:ASN:O	2:D:177:ASN:HB3	1.93	0.67
2:D:259:VAL:HG21	2:D:268:ILE:CD1	2.25	0.67
2:B:171:ILE:HG13	2:B:297:ASP:HB2	1.78	0.66
1:G:142:LEU:HD11	1:G:152:LEU:CD1	2.20	0.66
2:H:55:ARG:H	2:H:55:ARG:HD2	1.59	0.66
2:H:11:ILE:HD13	2:H:11:ILE:N	2.10	0.66
1:E:142:LEU:HD11	1:E:152:LEU:CD1	2.23	0.65
2:F:31:PRO:HB2	2:F:220:VAL:HB	1.78	0.65
1:C:142:LEU:HD11	1:C:152:LEU:CD1	2.22	0.65
2:D:53:ASN:HD21	2:D:57:GLN:HB2	1.60	0.65
1:E:44:CYS:SG	1:E:46:ILE:HG12	2.36	0.65
2:F:27:SER:HB3	2:F:224:MET:HE2	1.79	0.65
2:D:259:VAL:HG21	2:D:268:ILE:HD11	1.80	0.64
2:H:11:ILE:HD13	2:H:11:ILE:H	1.62	0.64
2:B:83:LYS:HB3	2:B:84:PRO:CD	2.28	0.64
2:B:83:LYS:CB	2:B:84:PRO:CD	2.75	0.63
1:A:142:LEU:HD11	1:A:152:LEU:CD1	2.19	0.63
1:C:138:ARG:HB2	1:C:154:GLU:HB3	1.81	0.62
1:G:71:LEU:CD1	1:G:104:ILE:HG12	2.28	0.62
1:G:205:VAL:O	1:G:209:GLU:HG3	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:LEU:HD11	1:A:104:ILE:HG12	1.81	0.62
1:G:138:ARG:HB2	1:G:154:GLU:HB3	1.82	0.62
1:E:51:ALA:O	1:E:52:ASP:HB2	1.99	0.62
2:F:7:LEU:HG	2:F:180:VAL:HG23	1.81	0.62
1:E:57:MET:SD	1:E:71:LEU:CD2	2.87	0.62
1:E:63:HIS:ND1	1:E:67:ARG:NH2	2.48	0.62
2:B:48:ASP:HB3	4:B:339:HOH:O	1.99	0.62
2:B:31:PRO:HB2	2:B:220:VAL:HB	1.81	0.61
2:D:19:LEU:HD13	2:D:286:ILE:HD12	1.82	0.61
2:B:27:SER:HB3	2:B:224:MET:HE2	1.82	0.61
2:F:55:ARG:O	2:F:57:GLN:HG3	2.00	0.61
2:D:53:ASN:HD21	2:D:57:GLN:HE21	1.48	0.61
1:E:138:ARG:HB2	1:E:154:GLU:HB3	1.83	0.61
2:H:3:GLN:HB2	2:H:259:VAL:HG22	1.82	0.61
2:H:31:PRO:HB2	2:H:220:VAL:HB	1.83	0.61
2:D:27:SER:HB3	2:D:224:MET:HE2	1.82	0.60
1:C:71:LEU:CD1	1:C:104:ILE:HG12	2.30	0.60
2:B:84:PRO:HB2	2:B:87:PHE:HB3	1.84	0.60
2:F:71:PRO:HG2	2:F:74:TYR:CD2	2.34	0.60
2:H:286:ILE:HD13	2:H:286:ILE:C	2.22	0.60
1:C:24:LEU:O	1:C:28:ILE:HG12	2.01	0.60
2:D:197:ASN:HB3	2:D:202:SER:HB3	1.82	0.60
1:C:60:ILE:HD12	1:C:60:ILE:N	2.16	0.59
2:B:167:GLN:HG2	2:B:187:GLU:HB2	1.84	0.59
1:C:162:GLU:O	1:C:166:LYS:HE3	2.03	0.59
1:A:49:LEU:HD23	1:A:55:LYS:CD	2.32	0.59
1:A:91:LEU:CD2	2:B:68:LYS:HA	2.33	0.59
1:E:32:ARG:HG2	1:E:33:ASP:H	1.67	0.59
2:B:53:ASN:ND2	2:B:57:GLN:HB2	2.14	0.59
1:C:135:LEU:HB2	1:C:166:LYS:HD3	1.84	0.59
2:D:224:MET:CE	2:D:230:LEU:HD12	2.33	0.59
2:H:79:THR:HG22	2:H:80:MET:N	2.17	0.59
1:A:32:ARG:HG2	1:A:33:ASP:H	1.68	0.58
1:A:135:LEU:HB2	1:A:166:LYS:HD3	1.85	0.58
2:D:75:LEU:O	2:D:76:ILE:HB	2.03	0.58
2:F:60:GLU:CD	2:F:299:ARG:HH21	2.07	0.58
1:G:37:ILE:HG12	1:G:38:ASP:N	2.18	0.58
2:H:259:VAL:HG21	2:H:268:ILE:HD11	1.84	0.58
2:F:52:VAL:HA	2:F:57:GLN:O	2.03	0.58
2:F:265:ILE:H	2:F:265:ILE:CD1	2.04	0.58
1:C:180:LYS:HD2	1:C:180:LYS:N	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:224:MET:HE3	2:B:230:LEU:HD13	1.86	0.58
1:C:167:ILE:HD11	1:C:184:THR:HG21	1.86	0.58
2:D:75:LEU:HD22	2:D:216:LEU:CD2	2.33	0.58
1:C:32:ARG:HG2	1:C:33:ASP:H	1.68	0.57
2:F:68:LYS:HE2	2:F:164:TRP:CH2	2.39	0.57
1:G:180:LYS:N	1:G:180:LYS:HD2	2.18	0.57
1:A:46:ILE:HD13	2:B:49:VAL:HB	1.85	0.57
2:D:273:THR:HG22	2:D:277:ASN:HD21	1.69	0.57
2:H:180:VAL:HG21	2:H:275:LEU:HD23	1.86	0.57
1:E:37:ILE:HG12	1:E:38:ASP:N	2.20	0.57
2:F:253:LEU:HD22	2:F:286:ILE:CD1	2.35	0.57
1:E:167:ILE:HD11	1:E:184:THR:HG21	1.87	0.57
1:A:66:GLY:CA	1:A:68:GLN:HG3	2.31	0.57
1:E:60:ILE:N	1:E:60:ILE:HD12	2.20	0.57
2:D:232:LEU:HD12	2:D:251:PHE:HB3	1.87	0.57
1:G:178:ARG:HA	1:G:180:LYS:CE	2.34	0.57
2:H:27:SER:HB3	2:H:224:MET:HE2	1.86	0.57
2:H:53:ASN:HD22	2:H:55:ARG:HD3	1.68	0.57
2:H:55:ARG:O	2:H:57:GLN:N	2.34	0.57
1:A:57:MET:SD	1:A:71:LEU:CD2	2.93	0.56
1:C:178:ARG:HA	1:C:180:LYS:CE	2.35	0.56
1:E:4:SER:HA	1:E:155:LEU:O	2.06	0.56
1:E:49:LEU:HD12	1:E:55:LYS:HG2	1.87	0.56
1:A:62:PHE:CB	1:A:65:HIS:HB2	2.35	0.56
2:F:64:ILE:HD13	2:F:209:TYR:CZ	2.41	0.56
2:F:60:GLU:OE2	2:F:299:ARG:NH2	2.37	0.56
1:G:32:ARG:HG2	1:G:33:ASP:H	1.70	0.56
1:E:178:ARG:HA	1:E:180:LYS:CE	2.34	0.56
1:G:139:LEU:CD2	1:G:153:ILE:HD12	2.35	0.56
2:F:279:LYS:HE2	2:F:288:LEU:O	2.05	0.56
2:H:82:ASP:OD2	2:H:83:LYS:HD3	2.05	0.56
1:C:64:HIS:O	1:C:65:HIS:HB2	2.06	0.56
2:F:68:LYS:HE2	2:F:164:TRP:CZ2	2.41	0.56
2:F:69:GLU:OE2	2:F:69:GLU:N	2.36	0.56
1:A:143:PHE:CD2	1:A:148:PHE:HA	2.41	0.55
2:H:197:ASN:HB3	2:H:202:SER:CB	2.36	0.55
2:F:3:GLN:HB2	2:F:259:VAL:HG22	1.87	0.55
2:F:51:ASN:HB3	2:F:59:VAL:O	2.07	0.55
1:A:180:LYS:HD2	1:A:180:LYS:N	2.21	0.55
2:B:68:LYS:HG2	2:B:164:TRP:CZ3	2.42	0.55
2:D:232:LEU:HD12	2:D:251:PHE:CB	2.37	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ILE:HD12	1:A:204:TYR:CE1	2.42	0.55
2:B:53:ASN:HD22	2:B:57:GLN:HE21	1.55	0.55
1:C:91:LEU:CD2	2:D:68:LYS:HA	2.38	0.54
1:E:40:ARG:HD3	1:E:118:GLN:HE22	1.70	0.54
1:E:71:LEU:CD1	1:E:104:ILE:HG12	2.36	0.54
1:E:27:SER:O	1:E:132:LEU:CD2	2.54	0.54
1:E:90:ALA:O	1:E:94:ASN:OD1	2.26	0.54
2:H:7:LEU:HG	2:H:180:VAL:HG23	1.88	0.54
2:B:232:LEU:CD1	2:B:253:LEU:HD13	2.35	0.54
1:E:100:VAL:HG11	2:F:260:SER:HB3	1.88	0.54
1:G:60:ILE:N	1:G:60:ILE:HD12	2.23	0.54
2:H:63:ARG:HG3	2:H:298:SER:O	2.08	0.54
2:H:197:ASN:HB3	2:H:202:SER:HB3	1.90	0.54
2:D:75:LEU:O	2:D:76:ILE:CB	2.56	0.54
2:D:197:ASN:HB3	2:D:202:SER:CB	2.38	0.54
2:F:13:ASP:OD1	2:F:250:GLY:HA2	2.07	0.54
1:A:37:ILE:HG12	1:A:38:ASP:N	2.22	0.53
1:A:48:ASN:N	1:A:48:ASN:ND2	2.56	0.53
1:E:180:LYS:N	1:E:180:LYS:HD2	2.23	0.53
2:H:259:VAL:HG21	2:H:268:ILE:CD1	2.39	0.53
1:A:36:SER:HB3	1:A:63:HIS:HB2	1.89	0.53
2:B:280:LYS:HA	2:B:280:LYS:HE2	1.90	0.53
1:C:139:LEU:CD2	1:C:153:ILE:HD12	2.38	0.53
1:E:22:ASP:C	1:E:24:LEU:N	2.62	0.53
1:G:49:LEU:HD22	1:G:50:PRO:HD2	1.91	0.53
2:D:53:ASN:ND2	2:D:57:GLN:HE21	2.06	0.53
1:G:57:MET:SD	1:G:71:LEU:CD2	2.97	0.53
1:G:135:LEU:HB2	1:G:166:LYS:HD3	1.91	0.53
1:E:22:ASP:C	1:E:24:LEU:H	2.11	0.53
2:H:224:MET:CE	2:H:230:LEU:HD12	2.39	0.53
1:C:28:ILE:HG22	1:C:29:LEU:N	2.24	0.53
1:C:120:GLN:CD	1:C:122:ILE:HD11	2.29	0.53
2:F:224:MET:HE3	2:F:230:LEU:CD1	2.36	0.53
2:H:11:ILE:CD1	2:H:251:PHE:HB2	2.37	0.53
1:A:60:ILE:HD12	1:A:60:ILE:N	2.24	0.53
1:C:50:PRO:O	1:C:51:ALA:C	2.46	0.53
2:D:3:GLN:HB2	2:D:259:VAL:HG22	1.90	0.53
1:A:149:LYS:O	1:A:149:LYS:HD3	2.09	0.53
2:D:268:ILE:O	2:D:272:GLU:HG3	2.08	0.52
2:F:52:VAL:HG22	2:F:56:ASN:HA	1.91	0.52
2:F:226:HIS:CD2	2:F:270:TYR:OH	2.61	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:37:ILE:HD12	1:G:204:TYR:CE1	2.44	0.52
2:H:268:ILE:O	2:H:272:GLU:HG3	2.09	0.52
1:A:138:ARG:HB2	1:A:154:GLU:HB3	1.91	0.52
1:A:167:ILE:HD11	1:A:184:THR:HG21	1.91	0.52
2:D:31:PRO:HB2	2:D:220:VAL:HB	1.91	0.52
1:G:120:GLN:CD	1:G:122:ILE:HD11	2.29	0.52
2:B:224:MET:HE3	2:B:230:LEU:CD1	2.40	0.52
1:C:32:ARG:HH21	1:C:138:ARG:NH2	2.07	0.52
1:G:7:ILE:HG13	1:G:184:THR:OG1	2.10	0.52
1:A:120:GLN:CD	1:A:122:ILE:HD11	2.30	0.52
2:B:268:ILE:O	2:B:272:GLU:HG3	2.10	0.52
1:E:7:ILE:HG13	1:E:184:THR:OG1	2.10	0.52
2:B:40:VAL:HG21	2:B:213:PHE:CZ	2.45	0.52
1:C:37:ILE:HG12	1:C:38:ASP:N	2.23	0.52
1:E:28:ILE:HG22	1:E:29:LEU:N	2.25	0.52
1:E:139:LEU:CD2	1:E:153:ILE:HD12	2.40	0.52
2:H:261:ARG:HG2	2:H:262:GLY:N	2.25	0.52
2:D:49:VAL:HG22	2:D:50:GLU:N	2.25	0.51
1:A:71:LEU:CD1	1:A:104:ILE:HG12	2.40	0.51
1:A:100:VAL:CB	2:B:2:VAL:CG2	2.86	0.51
1:A:7:ILE:HG13	1:A:184:THR:OG1	2.10	0.51
1:G:167:ILE:HD11	1:G:184:THR:HG21	1.93	0.51
2:D:53:ASN:ND2	2:D:57:GLN:HB2	2.24	0.51
1:E:48:ASN:O	1:E:49:LEU:C	2.49	0.51
2:B:224:MET:CE	2:B:230:LEU:HD13	2.39	0.51
1:A:62:PHE:HB3	1:A:65:HIS:CB	2.36	0.51
1:E:32:ARG:HH21	1:E:138:ARG:NH2	2.09	0.51
1:C:37:ILE:HD12	1:C:204:TYR:CE1	2.46	0.51
2:F:176:ASN:O	2:F:177:ASN:HB3	2.10	0.51
1:G:36:SER:HB3	1:G:63:HIS:CD2	2.46	0.51
2:F:157:SER:O	2:F:158:ASN:HB2	2.11	0.51
1:G:28:ILE:HG22	1:G:29:LEU:N	2.26	0.51
1:A:178:ARG:HA	1:A:180:LYS:CE	2.38	0.51
2:B:203:LEU:O	2:B:207:LEU:HD13	2.10	0.51
1:G:27:SER:O	1:G:132:LEU:HD22	2.12	0.50
2:H:167:GLN:HG2	2:H:187:GLU:HB2	1.93	0.50
2:H:52:VAL:HG22	2:H:53:ASN:N	2.26	0.50
1:A:100:VAL:HB	2:B:2:VAL:HG23	1.88	0.50
2:B:83:LYS:HG3	2:B:240:GLU:HG3	1.93	0.50
1:C:7:ILE:HG13	1:C:184:THR:OG1	2.12	0.50
1:E:120:GLN:HG2	1:E:122:ILE:HD13	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:108:LEU:HD23	1:G:112:LEU:HD12	1.92	0.50
2:F:75:LEU:HD23	2:F:148:VAL:HG12	1.92	0.50
1:A:28:ILE:HG22	1:A:29:LEU:N	2.26	0.50
1:C:44:CYS:SG	1:C:46:ILE:HG12	2.52	0.50
3:I:209:GLU:OE1	3:I:211:HIS:CE1	2.58	0.50
1:A:44:CYS:SG	1:A:46:ILE:HG12	2.52	0.50
2:D:296:MET:HA	3:J:206:PHE:CD2	2.46	0.50
1:G:9:VAL:HB	1:G:151:LEU:HB3	1.93	0.50
1:A:48:ASN:O	1:A:49:LEU:C	2.51	0.50
2:B:197:ASN:HB3	2:B:202:SER:HB3	1.94	0.49
1:G:4:SER:HA	1:G:155:LEU:O	2.12	0.49
1:A:48:ASN:N	1:A:48:ASN:HD22	2.09	0.49
1:C:163:PHE:O	1:C:166:LYS:N	2.45	0.49
2:D:279:LYS:HE2	2:D:288:LEU:O	2.12	0.49
1:E:135:LEU:HB2	1:E:166:LYS:HD3	1.94	0.49
1:G:114:ASN:HB3	2:H:59:VAL:HB	1.94	0.49
2:H:49:VAL:CG2	2:H:50:GLU:H	2.24	0.49
1:E:162:GLU:HA	1:E:162:GLU:OE1	2.12	0.49
1:C:87:ILE:HD11	1:C:101:PRO:HD3	1.94	0.49
1:G:40:ARG:HD3	1:G:118:GLN:HE22	1.77	0.49
1:A:144:SER:OG	1:A:145:SER:N	2.44	0.49
1:G:24:LEU:O	1:G:28:ILE:HG12	2.12	0.49
1:G:87:ILE:HD11	1:G:101:PRO:HD3	1.95	0.49
1:A:130:LEU:HB2	1:A:137:VAL:CG1	2.39	0.49
1:C:57:MET:SD	1:C:71:LEU:CD2	3.00	0.49
2:F:68:LYS:HG2	2:F:164:TRP:CZ3	2.47	0.49
1:C:130:LEU:HB2	1:C:137:VAL:CG1	2.38	0.49
1:E:87:ILE:HD11	1:E:101:PRO:HD3	1.93	0.49
2:H:83:LYS:HD2	2:H:240:GLU:OE1	2.13	0.49
2:F:40:VAL:HG21	2:F:213:PHE:CZ	2.48	0.49
2:H:50:GLU:HB2	2:H:52:VAL:HG12	1.95	0.49
2:D:24:THR:O	2:D:28:GLY:N	2.45	0.49
1:G:54:SER:O	1:G:73:LYS:NZ	2.46	0.49
1:G:50:PRO:HB2	1:G:53:VAL:HG23	1.96	0.48
2:D:40:VAL:HG11	2:D:63:ARG:HD3	1.94	0.48
2:F:253:LEU:HD22	2:F:286:ILE:HD13	1.96	0.48
2:F:261:ARG:HD3	2:F:267:ARG:HH21	1.78	0.48
2:D:226:HIS:CD2	2:D:270:TYR:OH	2.66	0.48
2:F:70:VAL:HB	2:F:75:LEU:HD11	1.95	0.48
1:G:32:ARG:HH21	1:G:138:ARG:NH2	2.12	0.48
2:H:3:GLN:HB2	2:H:259:VAL:CG2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:285:TYR:C	2:H:285:TYR:CD2	2.84	0.48
1:A:9:VAL:HB	1:A:151:LEU:HB3	1.96	0.48
2:D:259:VAL:HG21	2:D:268:ILE:HD13	1.95	0.48
2:F:3:GLN:HB2	2:F:259:VAL:CG2	2.44	0.48
2:H:55:ARG:H	2:H:55:ARG:CD	2.25	0.48
1:C:195:ASN:HD21	1:C:197:ILE:HG22	1.78	0.48
2:F:6:SER:O	2:F:180:VAL:HG22	2.13	0.48
2:H:224:MET:SD	2:H:230:LEU:HD12	2.54	0.48
1:E:46:ILE:HG23	2:F:47:TYR:HB3	1.96	0.48
2:H:49:VAL:CG2	2:H:50:GLU:N	2.77	0.48
1:G:57:MET:SD	1:G:71:LEU:HD23	2.54	0.48
1:G:64:HIS:C	1:G:66:GLY:H	2.18	0.48
2:B:83:LYS:HA	2:B:83:LYS:HD3	1.64	0.47
2:B:307:ILE:HG12	3:I:215:HIS:ND1	2.29	0.47
2:B:40:VAL:HG11	2:B:63:ARG:HD3	1.95	0.47
1:E:130:LEU:HB2	1:E:137:VAL:CG1	2.40	0.47
2:B:53:ASN:ND2	2:B:57:GLN:HE21	2.12	0.47
1:C:9:VAL:HB	1:C:151:LEU:HB3	1.97	0.47
2:F:11:ILE:HG12	2:F:19:LEU:CD2	2.43	0.47
2:H:5:LEU:HA	2:H:181:SER:O	2.14	0.47
2:B:49:VAL:HG22	2:B:50:GLU:O	2.13	0.47
2:D:26:ILE:HD12	2:D:281:GLU:OE1	2.15	0.47
1:A:87:ILE:HD11	1:A:101:PRO:HD3	1.97	0.47
1:C:108:LEU:HD23	1:C:112:LEU:HD12	1.95	0.47
1:E:109:SER:O	1:E:113:SER:HB3	2.14	0.47
1:E:134:GLY:O	1:E:135:LEU:HB2	2.15	0.47
1:A:139:LEU:HD22	1:A:153:ILE:HD12	1.92	0.47
1:C:6:VAL:HG13	1:C:152:LEU:HD21	1.94	0.47
2:F:76:ILE:HA	2:F:145:ILE:O	2.15	0.47
2:B:52:VAL:HG22	2:B:56:ASN:C	2.35	0.47
1:C:43:ARG:HH12	1:C:55:LYS:NZ	2.12	0.47
1:A:50:PRO:O	1:A:53:VAL:HG12	2.15	0.47
1:C:133:ASP:C	1:C:135:LEU:H	2.17	0.47
2:F:253:LEU:HD22	2:F:286:ILE:HD11	1.97	0.47
1:G:109:SER:O	1:G:113:SER:HB3	2.14	0.47
1:A:53:VAL:CG1	1:A:53:VAL:O	2.62	0.47
2:B:68:LYS:HE2	2:B:164:TRP:CH2	2.49	0.47
2:B:282:LEU:HB3	2:B:286:ILE:HG23	1.96	0.47
2:D:53:ASN:C	2:D:55:ARG:H	2.17	0.47
2:F:50:GLU:HB2	2:F:52:VAL:HG12	1.97	0.47
2:H:53:ASN:HD22	2:H:55:ARG:HH11	1.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:122:ILE:CG2	1:C:142:LEU:HB3	2.44	0.46
2:D:52:VAL:CG2	2:D:56:ASN:HA	2.44	0.46
2:H:163:PRO:HA	2:H:190:ILE:O	2.15	0.46
2:B:171:ILE:HG12	2:B:172:PRO:HD2	1.96	0.46
1:E:9:VAL:HB	1:E:151:LEU:HB3	1.97	0.46
2:D:273:THR:HG22	2:D:277:ASN:ND2	2.29	0.46
2:B:19:LEU:HD23	2:B:232:LEU:HD21	1.96	0.46
1:C:205:VAL:O	1:C:209:GLU:HG2	2.15	0.46
2:D:234:LYS:HE2	2:D:251:PHE:CZ	2.51	0.46
1:E:205:VAL:O	1:E:209:GLU:HG2	2.15	0.46
1:A:24:LEU:O	1:A:28:ILE:HG12	2.16	0.46
2:F:157:SER:HB2	2:F:196:LYS:O	2.16	0.46
2:H:226:HIS:CD2	2:H:270:TYR:OH	2.68	0.46
2:F:232:LEU:HD23	2:F:232:LEU:HA	1.80	0.46
1:G:122:ILE:CG2	1:G:142:LEU:HB3	2.45	0.46
2:H:237:GLN:O	2:H:243:ASN:HA	2.15	0.46
1:C:49:LEU:HA	1:C:50:PRO:HD3	1.75	0.46
2:F:167:GLN:HG2	2:F:187:GLU:HB2	1.98	0.46
1:A:46:ILE:HG23	2:B:47:TYR:HB3	1.98	0.46
2:B:84:PRO:HG2	2:H:251:PHE:CE1	2.51	0.46
2:B:197:ASN:HB3	2:B:202:SER:CB	2.46	0.46
2:D:63:ARG:HG3	2:D:298:SER:O	2.15	0.46
1:A:49:LEU:HD23	1:A:55:LYS:CE	2.45	0.46
2:B:237:GLN:O	2:B:243:ASN:HA	2.16	0.46
2:H:83:LYS:H	2:H:83:LYS:CE	2.23	0.46
1:C:141:ASN:HB3	1:C:148:PHE:HE1	1.80	0.45
2:D:19:LEU:HD13	2:D:286:ILE:CD1	2.46	0.45
2:D:280:LYS:HA	2:D:280:LYS:HE2	1.97	0.45
2:H:53:ASN:HD22	2:H:55:ARG:CD	2.29	0.45
1:C:49:LEU:HD23	1:C:55:LYS:CD	2.41	0.45
1:E:121:LEU:HD22	1:E:123:LYS:HG3	1.98	0.45
2:F:268:ILE:O	2:F:272:GLU:HG3	2.16	0.45
1:G:120:GLN:HG2	1:G:122:ILE:HD12	1.99	0.45
1:A:46:ILE:HB	1:A:49:LEU:HD22	1.98	0.45
2:B:287:GLU:HG3	2:B:287:GLU:O	2.16	0.45
1:G:47:LYS:HD3	1:G:47:LYS:N	2.31	0.45
2:F:224:MET:SD	2:F:230:LEU:HD12	2.56	0.45
2:B:22:THR:HG22	2:B:26:ILE:HD12	1.99	0.45
1:C:49:LEU:HA	1:C:49:LEU:HD12	1.74	0.45
1:A:4:SER:HA	1:A:155:LEU:O	2.16	0.45
1:A:32:ARG:HH21	1:A:138:ARG:HH22	1.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:5:LEU:HA	2:F:181:SER:O	2.17	0.45
2:F:259:VAL:HG23	2:F:259:VAL:O	2.15	0.45
2:H:246:ILE:HG13	3:L:204:PHE:CD2	2.52	0.45
2:F:287:GLU:HA	4:F:319:HOH:O	2.17	0.45
2:B:224:MET:CE	2:B:230:LEU:CD1	2.95	0.45
2:B:295:SER:HA	3:I:203:LYS:HD3	1.98	0.45
2:D:246:ILE:CG2	3:J:201:VAL:HG13	2.46	0.45
2:H:79:THR:CG2	2:H:243:ASN:ND2	2.79	0.45
1:A:195:ASN:HD21	1:A:197:ILE:HG22	1.82	0.44
2:D:246:ILE:HG21	3:J:201:VAL:HG13	1.98	0.44
2:F:265:ILE:HD12	2:F:265:ILE:N	2.10	0.44
2:D:40:VAL:HG21	2:D:213:PHE:CZ	2.52	0.44
2:H:5:LEU:HD22	2:H:271:THR:CG2	2.47	0.44
2:B:73:SER:OG	2:D:28:GLY:HA2	2.18	0.44
1:C:22:ASP:C	1:C:24:LEU:H	2.20	0.44
2:H:232:LEU:HD23	2:H:232:LEU:HA	1.79	0.44
2:B:166:LEU:C	2:B:166:LEU:HD23	2.38	0.44
2:B:279:LYS:HE2	2:B:288:LEU:O	2.18	0.44
1:G:90:ALA:O	1:G:94:ASN:OD1	2.35	0.44
2:B:51:ASN:ND2	2:B:61:PRO:HD3	2.32	0.44
1:C:178:ARG:CA	1:C:180:LYS:HE2	2.42	0.44
2:F:60:GLU:H	2:F:60:GLU:HG2	1.59	0.44
2:B:89:ILE:HB	2:B:90:LEU:HD12	1.99	0.44
2:B:259:VAL:HG11	2:B:268:ILE:HD13	1.98	0.44
2:D:197:ASN:CB	2:D:202:SER:HB3	2.47	0.44
2:B:224:MET:SD	2:B:230:LEU:HD12	2.58	0.44
1:C:46:ILE:HG21	2:D:47:TYR:HB3	2.00	0.44
1:E:6:VAL:HG13	1:E:152:LEU:HD21	1.99	0.44
2:H:11:ILE:N	2:H:11:ILE:CD1	2.79	0.44
2:B:163:PRO:HA	2:B:190:ILE:O	2.18	0.44
2:D:5:LEU:HD12	2:D:5:LEU:N	2.32	0.44
3:J:194:LYS:HE2	3:J:194:LYS:HB3	1.75	0.44
2:F:296:MET:HA	3:K:206:PHE:CD2	2.52	0.43
2:D:163:PRO:HA	2:D:190:ILE:O	2.18	0.43
2:F:49:VAL:HG23	2:F:50:GLU:OE2	2.18	0.43
2:F:52:VAL:HG23	2:F:57:GLN:N	2.33	0.43
2:H:44:ASN:HB2	2:H:210:VAL:HG23	2.00	0.43
1:C:57:MET:SD	1:C:71:LEU:HD23	2.59	0.43
2:B:280:LYS:HE3	2:B:283:GLN:OE1	2.19	0.43
1:C:109:SER:O	1:C:113:SER:HB3	2.19	0.43
2:D:53:ASN:C	2:D:55:ARG:N	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:64:ILE:HG13	2:F:168:ILE:HD11	2.00	0.43
2:F:76:ILE:HG22	2:F:78:GLU:H	1.83	0.43
2:H:81:MET:SD	2:H:89:ILE:HG13	2.58	0.43
1:C:22:ASP:C	1:C:24:LEU:N	2.72	0.43
1:C:194:SER:O	1:C:195:ASN:HB2	2.17	0.43
2:D:40:VAL:CG1	2:D:63:ARG:HD3	2.49	0.43
1:E:9:VAL:HG12	1:E:12:ALA:HB2	2.01	0.43
2:B:259:VAL:HG11	2:B:268:ILE:CD1	2.48	0.43
2:D:50:GLU:H	2:D:50:GLU:HG3	1.66	0.43
2:F:11:ILE:HG12	2:F:19:LEU:HD23	2.00	0.43
1:A:9:VAL:HG12	1:A:12:ALA:HB2	2.00	0.43
1:A:122:ILE:CG2	1:A:142:LEU:HB3	2.49	0.43
2:B:228:LEU:HD21	2:B:278:LEU:HD22	2.01	0.43
1:C:149:LYS:O	1:C:149:LYS:HD3	2.17	0.43
1:C:195:ASN:C	1:C:195:ASN:HD22	2.21	0.43
2:F:261:ARG:HD3	2:F:267:ARG:NH2	2.32	0.43
2:F:264:ASP:OD1	2:F:266:ASP:HB2	2.19	0.43
1:A:108:LEU:HD23	1:A:112:LEU:HD12	2.00	0.43
2:B:27:SER:HB2	2:B:224:MET:HG2	2.01	0.43
2:D:19:LEU:CD1	2:D:286:ILE:HD12	2.49	0.43
1:E:37:ILE:CD1	1:E:204:TYR:CE1	3.01	0.43
2:H:22:THR:O	2:H:26:ILE:HG12	2.18	0.43
1:C:3:LYS:HE3	1:C:163:PHE:HB3	2.01	0.42
1:C:40:ARG:HD3	1:C:118:GLN:HE22	1.81	0.42
2:D:228:LEU:HD21	2:D:278:LEU:HD22	2.01	0.42
1:C:17:LEU:C	1:C:17:LEU:HD23	2.40	0.42
2:H:41:TRP:CD1	2:H:41:TRP:N	2.86	0.42
2:F:63:ARG:HG3	2:F:298:SER:O	2.18	0.42
2:F:157:SER:C	2:F:159:GLU:H	2.23	0.42
2:F:172:PRO:O	2:F:293:ARG:HD2	2.19	0.42
1:G:162:GLU:O	1:G:166:LYS:HE3	2.19	0.42
3:I:207:THR:OG1	3:I:209:GLU:HG2	2.19	0.42
1:C:4:SER:HA	1:C:155:LEU:O	2.18	0.42
1:E:108:LEU:HD23	1:E:112:LEU:HD12	2.00	0.42
2:F:145:ILE:CG1	2:F:146:ILE:HD12	2.43	0.42
2:F:146:ILE:HD12	2:F:146:ILE:N	2.35	0.42
1:A:139:LEU:HD23	1:A:153:ILE:HD12	1.98	0.42
2:B:44:ASN:OD1	2:B:46:SER:N	2.50	0.42
2:D:5:LEU:HA	2:D:181:SER:O	2.18	0.42
1:E:46:ILE:CG2	2:F:47:TYR:HB3	2.50	0.42
2:F:52:VAL:HG22	2:F:53:ASN:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:176:ASN:O	2:H:177:ASN:CB	2.61	0.42
1:A:120:GLN:OE1	1:A:122:ILE:HD11	2.19	0.42
1:C:163:PHE:C	1:C:165:THR:N	2.72	0.42
1:G:195:ASN:HD21	1:G:197:ILE:HG22	1.85	0.42
3:J:194:LYS:HA	3:J:195:PRO:HD3	1.71	0.42
1:E:122:ILE:CG2	1:E:142:LEU:HB3	2.49	0.42
2:H:50:GLU:CB	2:H:52:VAL:HG12	2.50	0.42
1:A:6:VAL:HG13	1:A:152:LEU:HD21	2.00	0.42
1:A:100:VAL:CG1	2:B:2:VAL:HG23	2.50	0.42
1:A:66:GLY:C	1:A:68:GLN:N	2.70	0.42
1:C:159:GLU:HB2	1:C:166:LYS:NZ	2.34	0.42
1:E:17:LEU:C	1:E:17:LEU:HD23	2.40	0.42
1:E:24:LEU:O	1:E:28:ILE:HG12	2.19	0.42
1:E:47:LYS:HE3	1:E:47:LYS:HB2	1.92	0.42
2:F:163:PRO:HA	2:F:190:ILE:O	2.20	0.42
2:F:166:LEU:C	2:F:166:LEU:HD23	2.40	0.42
2:F:253:LEU:HD23	2:F:288:LEU:HD21	2.02	0.42
1:G:195:ASN:C	1:G:195:ASN:HD22	2.23	0.42
1:A:195:ASN:C	1:A:195:ASN:HD22	2.22	0.42
2:B:89:ILE:C	2:B:90:LEU:HD12	2.40	0.42
2:F:8:PHE:O	2:F:288:LEU:HA	2.20	0.42
2:H:166:LEU:HD23	2:H:166:LEU:C	2.41	0.42
1:C:9:VAL:HG12	1:C:12:ALA:HB2	2.02	0.41
2:H:27:SER:HB3	2:H:224:MET:HG2	2.02	0.41
2:B:291:PRO:HG2	2:B:296:MET:SD	2.60	0.41
1:E:71:LEU:O	1:E:77:ALA:HA	2.20	0.41
1:E:120:GLN:CD	1:E:122:ILE:HD11	2.41	0.41
1:E:167:ILE:HD11	1:E:184:THR:CG2	2.49	0.41
1:G:134:GLY:O	1:G:166:LYS:NZ	2.44	0.41
2:H:264:ASP:OD1	2:H:266:ASP:OD2	2.38	0.41
2:B:82:ASP:O	2:B:83:LYS:O	2.39	0.41
1:E:38:ASP:HB2	1:E:61:THR:HB	2.03	0.41
2:F:11:ILE:HD11	2:F:251:PHE:HB2	2.02	0.41
2:F:49:VAL:HG22	2:F:50:GLU:N	2.36	0.41
1:C:47:LYS:HE3	1:C:47:LYS:HB2	1.87	0.41
1:A:49:LEU:CD2	1:A:55:LYS:HD2	2.43	0.41
1:A:109:SER:O	1:A:113:SER:HB3	2.21	0.41
2:B:232:LEU:HA	2:B:232:LEU:HD12	1.75	0.41
2:B:75:LEU:HA	2:B:75:LEU:HD23	1.86	0.41
2:B:286:ILE:HD12	4:B:332:HOH:O	2.20	0.41
2:F:259:VAL:CG2	2:F:259:VAL:O	2.69	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:74:TYR:CE1	2:B:90:LEU:HD22	2.56	0.41
2:B:226:HIS:CD2	2:B:270:TYR:OH	2.74	0.41
2:B:302:HIS:HB3	2:B:303:GLY:H	1.34	0.41
2:B:305:ILE:HD11	2:F:238:ILE:HG21	2.02	0.41
2:F:53:ASN:OD1	2:F:59:VAL:HG21	2.20	0.41
2:F:234:LYS:HE2	2:F:251:PHE:CZ	2.56	0.41
1:G:130:LEU:HB2	1:G:137:VAL:CG1	2.42	0.41
1:C:167:ILE:HD11	1:C:184:THR:CG2	2.49	0.41
1:E:37:ILE:HD12	1:E:204:TYR:CE1	2.56	0.41
2:F:246:ILE:HG12	3:K:204:PHE:CD2	2.56	0.41
1:G:144:SER:OG	1:G:145:SER:N	2.54	0.41
1:A:91:LEU:HD22	2:B:68:LYS:HA	2.02	0.40
1:C:120:GLN:OE1	1:C:122:ILE:HD11	2.21	0.40
2:F:55:ARG:O	2:F:56:ASN:C	2.60	0.40
1:G:71:LEU:HD11	1:G:104:ILE:CG1	2.40	0.40
2:H:212:GLU:HG2	2:H:213:PHE:HD2	1.87	0.40
1:A:17:LEU:HD23	1:A:17:LEU:C	2.41	0.40
1:A:18:THR:O	1:A:21:LYS:HB3	2.21	0.40
1:E:178:ARG:CA	1:E:180:LYS:HE2	2.43	0.40
2:F:291:PRO:HG2	2:F:296:MET:SD	2.61	0.40
1:G:63:HIS:O	1:G:65:HIS:N	2.54	0.40
2:H:16:TYR:CE1	2:H:20:ILE:HD11	2.57	0.40
2:H:54:SER:OG	2:H:55:ARG:HD2	2.21	0.40
2:B:90:LEU:N	2:B:90:LEU:CD1	2.79	0.40
1:C:46:ILE:HG22	1:C:47:LYS:N	2.36	0.40
2:H:295:SER:HA	3:L:203:LYS:HD3	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:25:THR:OG1	2:F:25:THR:OG1[2_646]	2.06	0.14

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	199/209 (95%)	180 (90%)	17 (8%)	2 (1%)	15	37
1	C	196/209 (94%)	174 (89%)	18 (9%)	4 (2%)	7	19
1	E	199/209 (95%)	180 (90%)	18 (9%)	1 (0%)	29	54
1	G	199/209 (95%)	176 (88%)	21 (11%)	2 (1%)	15	37
2	B	229/306 (75%)	212 (93%)	12 (5%)	5 (2%)	6	17
2	D	208/306 (68%)	196 (94%)	10 (5%)	2 (1%)	15	37
2	F	231/306 (76%)	209 (90%)	19 (8%)	3 (1%)	12	30
2	H	226/306 (74%)	208 (92%)	10 (4%)	8 (4%)	3	8
3	I	20/27 (74%)	20 (100%)	0	0	100	100
3	J	17/27 (63%)	14 (82%)	3 (18%)	0	100	100
3	K	14/27 (52%)	13 (93%)	1 (7%)	0	100	100
3	L	15/27 (56%)	14 (93%)	1 (7%)	0	100	100
All	All	1753/2168 (81%)	1596 (91%)	130 (7%)	27 (2%)	10	26

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	83	LYS
2	B	84	PRO
2	F	56	ASN
2	F	261	ARG
2	H	56	ASN
2	H	261	ARG
1	A	161	GLY
1	C	161	GLY
1	C	195	ASN
1	E	64	HIS
2	H	81	MET
1	A	159	GLU
2	D	196	LYS
1	G	65	HIS
2	H	80	MET
2	H	260	SER
2	B	302	HIS
1	G	161	GLY
1	C	67	ARG

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Mol	Chain	Res	Type
1	C	159	GLU
2	F	196	LYS
2	H	177	ASN
2	H	196	LYS
2	B	196	LYS
2	D	265	ILE
2	H	262	GLY
2	B	303	GLY

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	172/177 (97%)	161 (94%)	11 (6%)	17	39
1	C	172/177 (97%)	163 (95%)	9 (5%)	23	49
1	E	172/177 (97%)	162 (94%)	10 (6%)	20	43
1	G	172/177 (97%)	160 (93%)	12 (7%)	15	35
2	B	213/280 (76%)	199 (93%)	14 (7%)	16	38
2	D	193/280 (69%)	179 (93%)	14 (7%)	14	33
2	F	212/280 (76%)	197 (93%)	15 (7%)	14	34
2	H	208/280 (74%)	193 (93%)	15 (7%)	14	34
3	I	21/26 (81%)	21 (100%)	0	100	100
3	J	18/26 (69%)	18 (100%)	0	100	100
3	K	15/26 (58%)	15 (100%)	0	100	100
3	L	16/26 (62%)	16 (100%)	0	100	100
All	All	1584/1932 (82%)	1484 (94%)	100 (6%)	18	40

All (100) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	28	ILE

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Mol	Chain	Res	Type
1	A	37	ILE
1	A	48	ASN
1	A	49	LEU
1	A	64	HIS
1	A	71	LEU
1	A	167	ILE
1	A	181	GLU
1	A	195	ASN
1	A	196	GLU
2	B	52	VAL
2	B	66	LEU
2	B	84	PRO
2	B	85	LEU
2	B	171	ILE
2	B	176	ASN
2	B	178	ARG
2	B	217	THR
2	B	230	LEU
2	B	243	ASN
2	B	260	SER
2	B	275	LEU
2	B	280	LYS
2	B	286	ILE
1	C	3	LYS
1	C	28	ILE
1	C	37	ILE
1	C	71	LEU
1	C	121	LEU
1	C	167	ILE
1	C	181	GLU
1	C	195	ASN
1	C	196	GLU
2	D	11	ILE
2	D	25	THR
2	D	48	ASP
2	D	55	ARG
2	D	60	GLU
2	D	66	LEU
2	D	176	ASN
2	D	217	THR
2	D	232	LEU
2	D	235	ILE

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Mol	Chain	Res	Type
2	D	237	GLN
2	D	246	ILE
2	D	275	LEU
2	D	280	LYS
1	E	26	ASN
1	E	48	ASN
1	E	52	ASP
1	E	64	HIS
1	E	71	LEU
1	E	121	LEU
1	E	167	ILE
1	E	181	GLU
1	E	195	ASN
1	E	196	GLU
2	F	50	GLU
2	F	55	ARG
2	F	66	LEU
2	F	144	ASP
2	F	162	SER
2	F	176	ASN
2	F	189	ILE
2	F	217	THR
2	F	233	GLN
2	F	246	ILE
2	F	260	SER
2	F	268	ILE
2	F	275	LEU
2	F	280	LYS
2	F	287	GLU
1	G	26	ASN
1	G	28	ILE
1	G	37	ILE
1	G	47	LYS
1	G	49	LEU
1	G	52	ASP
1	G	55	LYS
1	G	71	LEU
1	G	167	ILE
1	G	181	GLU
1	G	195	ASN
1	G	196	GLU
2	H	11	ILE

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Mol	Chain	Res	Type
2	H	48	ASP
2	H	55	ARG
2	H	66	LEU
2	H	83	LYS
2	H	176	ASN
2	H	217	THR
2	H	233	GLN
2	H	243	ASN
2	H	263	THR
2	H	264	ASP
2	H	275	LEU
2	H	280	LYS
2	H	285	TYR
2	H	286	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (51) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	48	ASN
1	A	75	ASN
1	A	118	GLN
1	A	195	ASN
2	B	4	GLN
2	B	53	ASN
2	B	57	GLN
2	B	226	HIS
2	B	258	ASN
2	B	269	ASN
2	B	302	HIS
1	C	26	ASN
1	C	63	HIS
1	C	68	GLN
1	C	118	GLN
1	C	195	ASN
2	D	4	GLN
2	D	57	GLN
2	D	167	GLN
2	D	226	HIS
2	D	258	ASN
2	D	269	ASN
2	D	277	ASN

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Mol	Chain	Res	Type
1	E	26	ASN
1	E	68	GLN
1	E	75	ASN
1	E	118	GLN
1	E	173	HIS
1	E	195	ASN
2	F	4	GLN
2	F	57	GLN
2	F	176	ASN
2	F	205	ASN
2	F	214	GLN
2	F	226	HIS
2	F	258	ASN
2	F	269	ASN
1	G	26	ASN
1	G	68	GLN
1	G	75	ASN
1	G	173	HIS
1	G	195	ASN
2	H	4	GLN
2	H	57	GLN
2	H	214	GLN
2	H	226	HIS
2	H	243	ASN
2	H	258	ASN
2	H	269	ASN
3	I	211	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	203/209 (97%)	0.86	34 (16%) 1 1	35, 77, 120, 127	0
1	C	202/209 (96%)	0.79	28 (13%) 2 2	34, 81, 121, 127	0
1	E	203/209 (97%)	0.60	24 (11%) 4 3	34, 74, 117, 122	0
1	G	203/209 (97%)	0.81	39 (19%) 1 0	34, 79, 118, 122	0
2	B	235/306 (76%)	-0.11	7 (2%) 50 51	28, 45, 72, 111	0
2	D	214/306 (69%)	0.01	15 (7%) 16 14	29, 49, 100, 109	0
2	F	235/306 (76%)	-0.03	13 (5%) 25 24	29, 48, 91, 108	0
2	H	230/306 (75%)	-0.00	11 (4%) 30 28	30, 47, 92, 104	0
3	I	22/27 (81%)	0.10	1 (4%) 33 31	35, 44, 61, 82	0
3	J	19/27 (70%)	0.09	0 100 100	40, 50, 83, 93	0
3	K	16/27 (59%)	-0.30	0 100 100	37, 46, 64, 69	0
3	L	17/27 (62%)	-0.24	0 100 100	36, 46, 70, 85	0
All	All	1799/2168 (82%)	0.33	172 (9%) 8 6	28, 57, 115, 127	0

All (172) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	65	HIS	9.8
1	C	65	HIS	7.9
1	E	65	HIS	7.4
1	A	175	ALA	6.0
2	D	50	GLU	6.0
1	A	181	GLU	5.9
1	A	178	ARG	5.8
1	C	29	LEU	5.6
2	H	261	ARG	5.5
1	C	194	SER	5.4
1	E	29	LEU	5.3

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Mol	Chain	Res	Type	RSRZ
1	A	29	LEU	5.2
1	C	64	HIS	4.9
2	H	54	SER	4.9
1	C	181	GLU	4.9
1	C	30	SER	4.8
1	G	26	ASN	4.7
1	A	11	ARG	4.7
2	B	264	ASP	4.6
1	C	168	ALA	4.5
1	E	181	GLU	4.5
1	A	180	LYS	4.3
1	E	180	LYS	4.3
1	C	26	ASN	4.3
2	D	56	ASN	4.3
1	C	11	ARG	4.2
1	E	2	GLY	4.1
2	D	177	ASN	4.1
2	D	196	LYS	4.1
2	F	176	ASN	4.0
1	A	160	ALA	4.0
1	C	178	ARG	4.0
1	E	153	ILE	3.9
2	F	265	ILE	3.9
1	G	29	LEU	3.9
1	G	153	ILE	3.9
1	G	161	GLY	3.8
1	G	165	THR	3.8
1	G	53	VAL	3.8
2	F	177	ASN	3.8
1	E	152	LEU	3.7
2	D	76	ILE	3.7
1	C	175	ALA	3.6
1	E	137	VAL	3.6
3	I	216	HIS	3.6
1	A	51	ALA	3.6
1	A	162	GLU	3.6
1	E	159	GLU	3.6
1	G	195	ASN	3.6
1	E	30	SER	3.6
1	G	162	GLU	3.6
1	C	119	ARG	3.5
1	C	32	ARG	3.5

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Mol	Chain	Res	Type	RSRZ
1	G	178	ARG	3.5
1	C	33	ASP	3.5
1	A	174	LEU	3.5
2	B	176	ASN	3.4
1	C	176	GLU	3.4
1	E	64	HIS	3.4
1	G	30	SER	3.3
2	H	176	ASN	3.3
1	G	66	GLY	3.3
1	C	177	ILE	3.3
1	C	165	THR	3.3
1	G	32	ARG	3.3
1	G	152	LEU	3.2
1	A	64	HIS	3.2
1	C	180	LYS	3.2
1	C	25	SER	3.1
1	G	134	GLY	3.1
1	G	52	ASP	3.1
2	F	48	ASP	3.1
1	G	64	HIS	3.1
1	A	155	LEU	3.1
1	G	11	ARG	3.1
1	C	162	GLU	3.1
1	C	153	ILE	3.1
2	D	265	ILE	3.1
1	E	67	ARG	3.1
1	G	148	PHE	3.0
1	C	158	ASP	3.0
2	B	265	ILE	3.0
1	E	32	ARG	3.0
2	F	54	SER	3.0
1	G	160	ALA	3.0
2	H	50	GLU	3.0
1	G	133	ASP	3.0
1	G	180	LYS	3.0
2	F	262	GLY	2.9
1	C	67	ARG	2.9
2	D	55	ARG	2.9
1	A	2	GLY	2.9
2	F	55	ARG	2.9
2	F	57	GLN	2.9
1	A	153	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
2	H	56	ASN	2.8
1	G	176	GLU	2.8
1	C	133	ASP	2.8
1	G	159	GLU	2.7
1	C	50	PRO	2.7
1	G	31	VAL	2.7
1	G	154	GLU	2.7
1	G	163	PHE	2.7
2	H	55	ARG	2.7
1	A	131	ILE	2.7
1	A	159	GLU	2.6
2	B	301	ALA	2.6
2	H	48	ASP	2.6
1	A	66	GLY	2.6
2	H	196	LYS	2.6
2	D	58	LEU	2.6
2	D	301	ALA	2.5
1	A	32	ARG	2.5
1	G	189	LEU	2.5
1	A	3	LYS	2.5
1	A	26	ASN	2.5
1	A	12	ALA	2.5
1	A	161	GLY	2.5
1	C	152	LEU	2.4
2	B	177	ASN	2.4
1	G	183	LYS	2.4
1	E	155	LEU	2.4
2	D	54	SER	2.4
1	C	71	LEU	2.4
1	G	50	PRO	2.4
1	A	52	ASP	2.4
1	A	154	GLU	2.4
1	G	51	ALA	2.3
2	B	88	ARG	2.3
1	A	151	LEU	2.3
2	H	82	ASP	2.3
2	B	196	LYS	2.3
2	D	240	GLU	2.3
1	E	139	LEU	2.3
1	A	25	SER	2.3
1	A	139	LEU	2.3
1	A	152	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	154	GLU	2.2
1	G	117	MET	2.2
1	E	141	ASN	2.2
1	G	139	LEU	2.2
2	F	158	ASN	2.2
1	E	160	ALA	2.2
1	A	183	LYS	2.2
1	G	168	ALA	2.2
1	A	164	GLU	2.2
1	E	178	ARG	2.2
1	G	143	PHE	2.2
2	D	47	TYR	2.2
2	F	144	ASP	2.2
1	A	143	PHE	2.2
1	G	67	ARG	2.1
1	A	179	ALA	2.1
1	E	133	ASP	2.1
1	G	70	VAL	2.1
1	G	119	ARG	2.1
1	A	188	SER	2.1
2	H	52	VAL	2.1
1	A	119	ARG	2.1
1	E	138	ARG	2.1
2	F	261	ARG	2.1
2	D	51	ASN	2.1
2	F	58	LEU	2.0
2	D	74	TYR	2.0
1	C	19	GLU	2.0
1	E	117	MET	2.0
1	E	136	THR	2.0
2	F	46	SER	2.0
2	H	160	SER	2.0
1	E	140	VAL	2.0
1	G	167	ILE	2.0
2	D	270	TYR	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 [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.