



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 06:07 am BST

PDB ID : 3Q63
Title : X-ray crystal structure of protein MLL2253 from *Mesorhizobium loti*, Northeast Structural Genomics Consortium Target MIR404.
Authors : Forouhar, F.; Lew, S.; Seetharaman, J.; Wang, D.; Ciccocanti, C.; Sahdev, S.; Nair, R.; Rost, B.; Acton, T.B.; Xiao, R.; Everett, J.K.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on : 2010-12-30
Resolution : 2.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
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) : 2.11

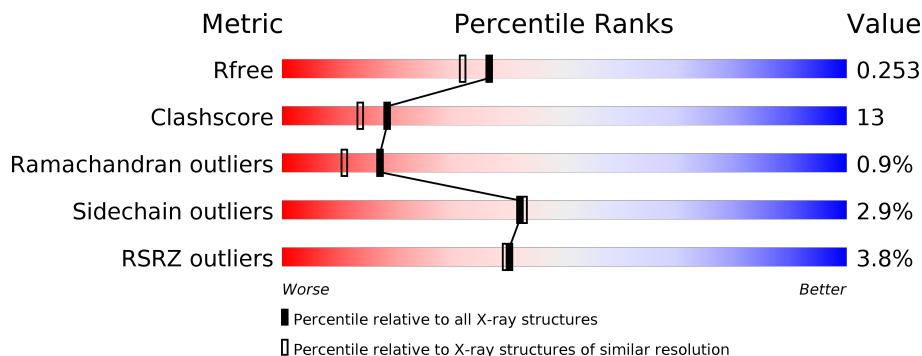
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 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	151	 68% 17% • 13%
1	B	151	 65% 24% • 9%
1	C	151	 62% 28% • 9%
1	D	151	 70% 20% • 10%
1	E	151	 62% 26% • 11%
1	F	151	 63% 27% • 8%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 7357 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 Mll2253 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	132	1077	690	191	192	1	3	0	0	0
1	B	137	1119	714	200	201	1	3	0	0	0
1	C	137	1119	714	200	201	1	3	0	0	0
1	D	136	1111	710	198	199	1	3	0	0	0
1	E	135	1105	705	198	198	1	3	0	0	0
1	F	139	1135	723	202	206	1	3	0	0	0

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	EXPRESSION TAG	UNP Q98IT8
A	144	LEU	-	EXPRESSION TAG	UNP Q98IT8
A	145	GLU	-	EXPRESSION TAG	UNP Q98IT8
A	146	HIS	-	EXPRESSION TAG	UNP Q98IT8
A	147	HIS	-	EXPRESSION TAG	UNP Q98IT8
A	148	HIS	-	EXPRESSION TAG	UNP Q98IT8
A	149	HIS	-	EXPRESSION TAG	UNP Q98IT8
A	150	HIS	-	EXPRESSION TAG	UNP Q98IT8
A	151	HIS	-	EXPRESSION TAG	UNP Q98IT8
B	1	MSE	-	EXPRESSION TAG	UNP Q98IT8
B	144	LEU	-	EXPRESSION TAG	UNP Q98IT8
B	145	GLU	-	EXPRESSION TAG	UNP Q98IT8
B	146	HIS	-	EXPRESSION TAG	UNP Q98IT8
B	147	HIS	-	EXPRESSION TAG	UNP Q98IT8
B	148	HIS	-	EXPRESSION TAG	UNP Q98IT8
B	149	HIS	-	EXPRESSION TAG	UNP Q98IT8
B	150	HIS	-	EXPRESSION TAG	UNP Q98IT8

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Chain	Residue	Modelled	Actual	Comment	Reference
B	151	HIS	-	EXPRESSION TAG	UNP Q98IT8
C	1	MSE	-	EXPRESSION TAG	UNP Q98IT8
C	144	LEU	-	EXPRESSION TAG	UNP Q98IT8
C	145	GLU	-	EXPRESSION TAG	UNP Q98IT8
C	146	HIS	-	EXPRESSION TAG	UNP Q98IT8
C	147	HIS	-	EXPRESSION TAG	UNP Q98IT8
C	148	HIS	-	EXPRESSION TAG	UNP Q98IT8
C	149	HIS	-	EXPRESSION TAG	UNP Q98IT8
C	150	HIS	-	EXPRESSION TAG	UNP Q98IT8
C	151	HIS	-	EXPRESSION TAG	UNP Q98IT8
D	1	MSE	-	EXPRESSION TAG	UNP Q98IT8
D	144	LEU	-	EXPRESSION TAG	UNP Q98IT8
D	145	GLU	-	EXPRESSION TAG	UNP Q98IT8
D	146	HIS	-	EXPRESSION TAG	UNP Q98IT8
D	147	HIS	-	EXPRESSION TAG	UNP Q98IT8
D	148	HIS	-	EXPRESSION TAG	UNP Q98IT8
D	149	HIS	-	EXPRESSION TAG	UNP Q98IT8
D	150	HIS	-	EXPRESSION TAG	UNP Q98IT8
D	151	HIS	-	EXPRESSION TAG	UNP Q98IT8
E	1	MSE	-	EXPRESSION TAG	UNP Q98IT8
E	144	LEU	-	EXPRESSION TAG	UNP Q98IT8
E	145	GLU	-	EXPRESSION TAG	UNP Q98IT8
E	146	HIS	-	EXPRESSION TAG	UNP Q98IT8
E	147	HIS	-	EXPRESSION TAG	UNP Q98IT8
E	148	HIS	-	EXPRESSION TAG	UNP Q98IT8
E	149	HIS	-	EXPRESSION TAG	UNP Q98IT8
E	150	HIS	-	EXPRESSION TAG	UNP Q98IT8
E	151	HIS	-	EXPRESSION TAG	UNP Q98IT8
F	1	MSE	-	EXPRESSION TAG	UNP Q98IT8
F	144	LEU	-	EXPRESSION TAG	UNP Q98IT8
F	145	GLU	-	EXPRESSION TAG	UNP Q98IT8
F	146	HIS	-	EXPRESSION TAG	UNP Q98IT8
F	147	HIS	-	EXPRESSION TAG	UNP Q98IT8
F	148	HIS	-	EXPRESSION TAG	UNP Q98IT8
F	149	HIS	-	EXPRESSION TAG	UNP Q98IT8
F	150	HIS	-	EXPRESSION TAG	UNP Q98IT8
F	151	HIS	-	EXPRESSION TAG	UNP Q98IT8

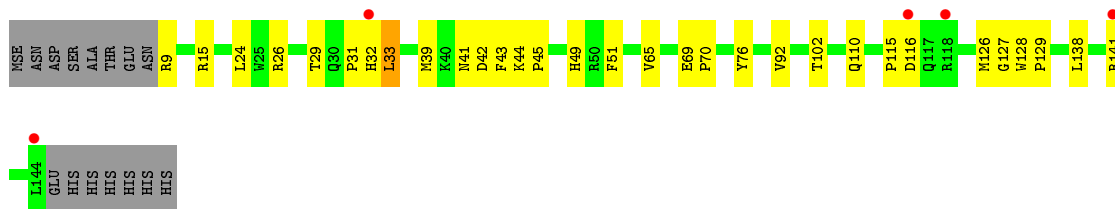
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	118	Total O 118 118	0	0

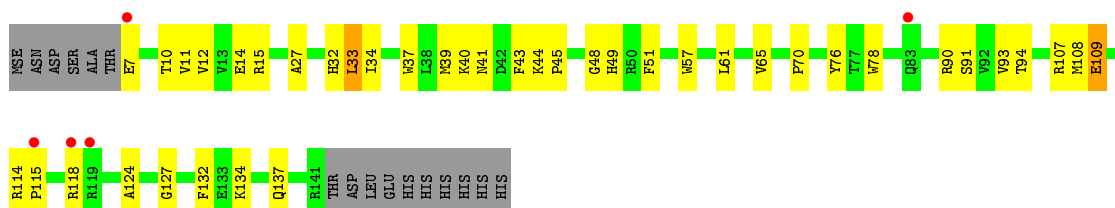
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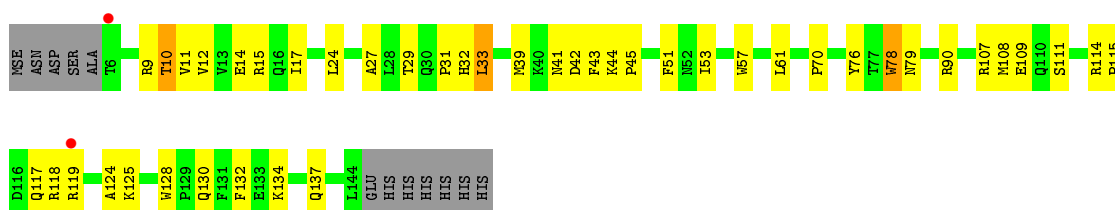
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	110	Total 110	O 110	0	0
2	C	108	Total 108	O 108	0	0
2	D	121	Total 121	O 121	0	0
2	E	103	Total 103	O 103	0	0
2	F	131	Total 131	O 131	0	0



- Molecule 1: Mll2253 protein



- Molecule 1: Mll2253 protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	40.12Å 148.12Å 87.39Å 90.00° 98.33° 90.00°	Depositor
Resolution (Å)	19.99 – 2.00 29.07 – 1.95	Depositor EDS
% Data completeness (in resolution range)	82.1 (19.99-2.00) 93.4 (29.07-1.95)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.58 (at 1.95Å)	Xtrriage
Refinement program	CNS 1.2 & XtalView	Depositor
R, R_{free}	0.202 , 0.244 0.210 , 0.253	Depositor DCC
R_{free} test set	12731 reflections (9.36%)	wwPDB-VP
Wilson B-factor (Å ²)	21.6	Xtrriage
Anisotropy	0.821	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 49.6	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	7357	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.95% 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	0.34	0/1107	0.62	0/1502
1	B	0.34	0/1149	0.58	0/1559
1	C	0.33	0/1149	0.58	0/1559
1	D	0.33	0/1141	0.61	0/1548
1	E	0.33	0/1135	0.57	0/1539
1	F	0.34	0/1165	0.58	0/1581
All	All	0.33	0/6846	0.59	0/9288

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 [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1077	0	1051	29	0
1	B	1119	0	1092	35	0
1	C	1119	0	1092	39	0
1	D	1111	0	1086	19	0
1	E	1105	0	1076	35	0
1	F	1135	0	1105	34	0
2	A	118	0	0	5	0
2	B	110	0	0	2	0
2	C	108	0	0	3	0
2	D	121	0	0	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	E	103	0	0	4	0
2	F	131	0	0	6	0
All	All	7357	0	6502	174	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 (174) 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:80:LEU:HD21	1:B:60:VAL:HG12	1.53	0.91
1:F:11:VAL:HG13	1:F:125:LYS:HD2	1.57	0.87
1:E:10:THR:HG21	2:E:536:HOH:O	1.81	0.81
1:C:41:ASN:HD22	1:C:43:PHE:H	1.28	0.80
1:C:126:MSE:HB2	2:C:527:HOH:O	1.83	0.78
1:C:10:THR:HG22	1:C:111:SER:HB3	1.71	0.73
1:F:130:GLN:O	1:F:134:LYS:HG2	1.90	0.72
1:F:10:THR:HG21	2:F:341:HOH:O	1.90	0.70
1:E:108:MSE:O	1:E:109:GLU:HB2	1.92	0.70
1:B:44:LYS:NZ	1:B:44:LYS:HB3	2.08	0.69
1:E:27:ALA:HA	1:E:33:LEU:HD23	1.76	0.68
1:E:12:VAL:HG22	1:E:109:GLU:HG2	1.75	0.67
1:D:41:ASN:HD22	1:D:43:PHE:H	1.43	0.67
1:F:53:ILE:HD11	1:F:61:LEU:HD12	1.77	0.67
1:E:94:THR:O	1:E:108:MSE:O	2.13	0.66
1:F:32:HIS:HB3	2:F:558:HOH:O	1.96	0.65
1:C:125:LYS:NZ	1:C:126:MSE:HE2	2.13	0.64
1:E:39:MSE:HE1	1:F:57:TRP:CE2	2.33	0.64
1:E:41:ASN:HD22	1:E:43:PHE:H	1.45	0.63
1:F:130:GLN:HB2	2:F:357:HOH:O	1.99	0.62
1:F:14:GLU:HG2	1:F:107:ARG:HG3	1.82	0.62
1:B:137:GLN:HG2	1:B:141:ARG:NH1	2.16	0.61
1:F:10:THR:HG22	2:F:169:HOH:O	2.01	0.60
1:B:137:GLN:HG2	1:B:141:ARG:HH12	1.65	0.60
1:F:41:ASN:HD22	1:F:43:PHE:H	1.48	0.60
1:B:41:ASN:HD22	1:B:43:PHE:H	1.50	0.59
1:E:57:TRP:CD2	1:F:39:MSE:HE1	2.37	0.59
1:A:93:VAL:HB	1:A:108:MSE:HE3	1.85	0.59
1:E:127:GLY:HA3	2:F:300:HOH:O	2.03	0.59
1:B:32:HIS:NE2	1:B:33:LEU:HD13	2.18	0.59
1:B:85:PRO:HB2	1:B:114:ARG:HH22	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:15:ARG:HG3	1:E:132:PHE:HD2	1.67	0.59
1:E:11:VAL:O	1:E:109:GLU:HA	2.04	0.57
1:C:137:GLN:HB2	2:C:530:HOH:O	2.04	0.57
1:D:115:PRO:HG2	2:D:541:HOH:O	2.04	0.57
1:E:134:LYS:HA	1:E:137:GLN:HG2	1.86	0.57
1:A:80:LEU:CD2	1:B:60:VAL:HG12	2.33	0.56
1:E:10:THR:HG22	2:E:169:HOH:O	2.06	0.56
1:F:29:THR:HB	1:F:45:PRO:HG3	1.88	0.56
1:F:15:ARG:HG3	1:F:132:PHE:HD2	1.70	0.56
1:F:15:ARG:HG3	1:F:132:PHE:CD2	2.41	0.56
1:C:10:THR:CG2	1:C:111:SER:HB3	2.36	0.56
1:D:138:LEU:HA	1:D:141:ARG:NH2	2.21	0.56
1:E:78:TRP:HB3	1:E:91:SER:OG	2.06	0.55
1:E:11:VAL:HG21	1:E:124:ALA:HB3	1.88	0.55
1:C:65:VAL:HA	1:C:76:TYR:HB3	1.90	0.54
1:A:22:GLU:O	1:A:26:ARG:HG3	2.08	0.54
1:A:93:VAL:HA	1:A:108:MSE:HE1	1.90	0.53
1:D:29:THR:HB	1:D:45:PRO:HG3	1.90	0.53
1:C:10:THR:HG22	1:C:111:SER:CB	2.39	0.53
1:D:127:GLY:HA3	2:D:205:HOH:O	2.08	0.53
1:C:69:GLU:HG2	1:C:72:LYS:HB2	1.91	0.53
1:F:27:ALA:HA	1:F:33:LEU:HD23	1.90	0.52
1:F:76:TYR:HE2	1:F:78:TRP:HE1	1.57	0.52
1:C:78:TRP:CE3	1:C:93:VAL:HG21	2.45	0.52
1:C:15:ARG:HH12	1:C:129:PRO:HA	1.75	0.51
1:A:39:MSE:HE1	1:B:57:TRP:CD2	2.46	0.51
1:C:57:TRP:CE2	1:D:39:MSE:HE1	2.46	0.50
1:F:42:ASP:OD1	1:F:51:PHE:HB2	2.11	0.50
1:B:108:MSE:HB2	1:B:132:PHE:HZ	1.76	0.50
1:C:138:LEU:O	1:C:141:ARG:HG2	2.12	0.50
1:F:17:ILE:HD12	1:F:24:LEU:HD22	1.93	0.50
1:C:122:GLY:HA2	1:C:125:LYS:HE3	1.92	0.50
1:C:144:LEU:H	1:C:144:LEU:HD22	1.75	0.50
1:B:44:LYS:HB3	1:B:44:LYS:HZ3	1.76	0.50
1:A:92:VAL:O	1:A:110:GLN:HA	2.11	0.50
1:A:127:GLY:HA3	2:A:154:HOH:O	2.10	0.50
1:F:10:THR:HB	1:F:111:SER:HA	1.94	0.49
1:E:48:GLY:HA2	2:E:350:HOH:O	2.12	0.49
1:B:30:GLN:HB2	1:B:33:LEU:HB2	1.95	0.49
1:C:79:ASN:OD1	1:C:90:ARG:HA	2.12	0.49
1:C:92:VAL:O	1:C:110:GLN:HA	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:42:ASP:O	1:D:49:HIS:HE1	1.95	0.49
1:C:144:LEU:N	1:C:144:LEU:HD22	2.27	0.48
1:E:40:LYS:HG2	1:F:119:ARG:NH2	2.28	0.48
1:C:125:LYS:HZ2	1:C:126:MSE:HE2	1.77	0.48
1:C:22:GLU:H	1:C:22:GLU:CD	2.17	0.48
1:E:43:PHE:HE2	1:E:45:PRO:HG3	1.78	0.48
1:B:126:MSE:C	1:B:129:PRO:HD2	2.34	0.48
1:B:26:ARG:HD2	2:B:401:HOH:O	2.13	0.48
1:A:80:LEU:HD21	1:B:60:VAL:CG1	2.37	0.47
1:F:108:MSE:HE2	1:F:128:TRP:CG	2.49	0.47
1:E:32:HIS:NE2	1:E:33:LEU:HD13	2.29	0.47
1:E:78:TRP:CE3	1:E:93:VAL:HG21	2.49	0.47
1:B:90:ARG:NH2	1:C:50:ARG:HD2	2.29	0.47
1:B:97:LEU:N	1:B:97:LEU:HD12	2.30	0.47
1:E:34:ILE:HA	1:E:37:TRP:NE1	2.30	0.47
1:C:137:GLN:HE21	1:C:141:ARG:NH2	2.13	0.47
1:F:9:ARG:HH22	1:F:118:ARG:HG2	1.80	0.47
1:C:21:PRO:HG2	1:C:22:GLU:OE2	2.14	0.46
1:B:22:GLU:HB3	1:B:26:ARG:HH22	1.79	0.46
1:E:15:ARG:HG3	1:E:132:PHE:CD2	2.50	0.46
1:F:134:LYS:O	1:F:137:GLN:HG2	2.16	0.46
1:F:53:ILE:CG1	1:F:61:LEU:HB2	2.46	0.46
1:A:14:GLU:HG2	1:A:107:ARG:HG3	1.97	0.45
1:B:36:GLU:HG2	1:B:138:LEU:HD13	1.97	0.45
1:B:43:PHE:HE2	1:B:45:PRO:HG3	1.80	0.45
1:C:41:ASN:ND2	1:C:43:PHE:H	2.02	0.45
2:A:189:HOH:O	1:B:80:LEU:HD11	2.17	0.45
1:D:44:LYS:HD3	1:D:49:HIS:NE2	2.32	0.45
1:C:107:ARG:HD3	2:C:165:HOH:O	2.16	0.45
1:B:121:TYR:CE2	1:B:125:LYS:HD2	2.51	0.45
1:F:114:ARG:NH1	1:F:117:GLN:NE2	2.65	0.45
1:C:126:MSE:C	1:C:129:PRO:HD2	2.37	0.45
1:D:15:ARG:NH2	1:D:129:PRO:HB3	2.32	0.45
1:A:56:ASP:HB3	1:B:123:GLY:O	2.16	0.45
1:D:102:THR:HG23	2:D:531:HOH:O	2.16	0.45
1:D:32:HIS:CD2	1:D:33:LEU:HD13	2.52	0.45
1:E:108:MSE:O	1:E:109:GLU:CB	2.62	0.45
1:A:108:MSE:HE1	1:A:109:GLU:O	2.17	0.44
1:F:31:PRO:HA	1:F:41:ASN:HD21	1.82	0.44
1:C:29:THR:HB	1:C:45:PRO:HG3	1.98	0.44
1:A:32:HIS:O	1:A:36:GLU:HG2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:85:PRO:CB	1:B:114:ARG:HH22	2.30	0.44
1:A:93:VAL:HA	1:A:108:MSE:CE	2.48	0.44
1:A:54:SER:HB2	2:A:625:HOH:O	2.17	0.44
1:F:11:VAL:HG21	1:F:124:ALA:HB3	1.99	0.44
1:B:92:VAL:O	1:B:110:GLN:HA	2.17	0.44
1:C:36:GLU:OE2	1:C:138:LEU:HD13	2.18	0.43
1:A:76:TYR:O	1:A:93:VAL:HG22	2.18	0.43
1:B:42:ASP:OD2	1:B:51:PHE:HB2	2.19	0.43
1:A:29:THR:HB	1:A:45:PRO:HG3	2.01	0.43
1:C:15:ARG:HH22	1:C:129:PRO:HB3	1.84	0.43
1:D:116:ASP:HB3	2:D:657:HOH:O	2.19	0.43
1:A:119:ARG:HB3	2:A:595:HOH:O	2.19	0.43
1:C:9:ARG:HG3	1:C:9:ARG:HH11	1.84	0.43
1:A:22:GLU:H	1:A:22:GLU:CD	2.22	0.43
1:A:83:GLN:HG2	2:A:164:HOH:O	2.18	0.43
1:D:92:VAL:O	1:D:110:GLN:HA	2.18	0.43
1:F:79:ASN:OD1	1:F:90:ARG:HA	2.19	0.43
1:A:76:TYR:CE2	1:A:93:VAL:HG21	2.54	0.42
1:C:8:ASN:N	1:C:121:TYR:HH	2.18	0.42
1:A:108:MSE:CE	1:A:109:GLU:O	2.66	0.42
1:A:32:HIS:NE2	1:A:33:LEU:HD13	2.34	0.42
1:B:128:TRP:N	1:B:129:PRO:CD	2.83	0.42
1:B:50:ARG:HG2	1:B:50:ARG:H	1.56	0.42
1:B:50:ARG:NH2	1:C:90:ARG:HD2	2.34	0.42
1:E:14:GLU:HG2	1:E:107:ARG:HG3	2.02	0.42
1:F:44:LYS:HE2	1:F:44:LYS:HB3	1.82	0.42
1:A:108:MSE:CE	1:A:109:GLU:C	2.88	0.42
1:D:42:ASP:OD1	1:D:51:PHE:HB2	2.19	0.42
1:E:40:LYS:HG2	1:F:119:ARG:HH22	1.84	0.42
1:A:38:LEU:HB3	1:A:39:MSE:H	1.58	0.42
1:F:53:ILE:O	1:F:53:ILE:HG13	2.20	0.42
1:D:26:ARG:HG3	2:D:163:HOH:O	2.19	0.42
1:C:108:MSE:HB2	1:C:132:PHE:HZ	1.85	0.42
1:A:57:TRP:CD2	1:B:39:MSE:HE1	2.55	0.42
1:D:65:VAL:HA	1:D:76:TYR:HB3	2.02	0.42
1:E:7:GLU:N	1:E:7:GLU:OE2	2.53	0.41
1:D:128:TRP:N	1:D:129:PRO:CD	2.83	0.41
1:A:27:ALA:HA	1:A:33:LEU:HD23	2.01	0.41
1:B:108:MSE:HE2	1:B:128:TRP:CG	2.54	0.41
1:E:65:VAL:HA	1:E:76:TYR:HB3	2.01	0.41
1:A:43:PHE:HE1	1:A:45:PRO:HG3	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:49:HIS:CE1	1:E:51:PHE:HB3	2.55	0.41
1:A:57:TRP:CE2	1:B:39:MSE:HE1	2.56	0.41
1:C:31:PRO:HG3	1:C:43:PHE:O	2.20	0.41
1:C:60:VAL:O	1:C:80:LEU:HD23	2.21	0.41
1:B:50:ARG:CZ	1:C:90:ARG:HD2	2.51	0.41
1:D:31:PRO:HA	1:D:41:ASN:HD21	1.85	0.41
1:E:90:ARG:HG2	1:E:90:ARG:HH11	1.86	0.41
1:F:12:VAL:HG13	1:F:109:GLU:HG2	2.03	0.41
1:B:91:SER:HB2	1:B:111:SER:O	2.21	0.41
1:E:44:LYS:HA	1:E:45:PRO:HD3	1.88	0.41
1:E:114:ARG:HB3	1:E:115:PRO:HD2	2.03	0.41
1:F:115:PRO:HG2	2:F:686:HOH:O	2.20	0.40
1:C:19:HIS:CD2	1:C:139:LEU:HB3	2.56	0.40
1:C:144:LEU:H	1:C:144:LEU:CD2	2.34	0.40
1:E:118:ARG:HD3	1:E:118:ARG:HA	1.97	0.40
1:B:119:ARG:HD2	2:B:320:HOH:O	2.21	0.40
1:C:57:TRP:CD2	1:D:39:MSE:HE1	2.57	0.40
1:E:108:MSE:SE	1:E:109:GLU:N	3.04	0.40
1:E:137:GLN:HG3	2:E:445:HOH:O	2.21	0.40
1:E:61:LEU:HD11	1:F:57:TRP:HE3	1.87	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	130/151 (86%)	122 (94%)	7 (5%)	1 (1%)	19 13
1	B	135/151 (89%)	124 (92%)	10 (7%)	1 (1%)	22 16
1	C	135/151 (89%)	124 (92%)	10 (7%)	1 (1%)	22 16
1	D	134/151 (89%)	125 (93%)	8 (6%)	1 (1%)	22 16

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	133/151 (88%)	122 (92%)	9 (7%)	2 (2%)	10	4
1	F	137/151 (91%)	130 (95%)	6 (4%)	1 (1%)	22	16
All	All	804/906 (89%)	747 (93%)	50 (6%)	7 (1%)	17	11

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	70	PRO
1	E	70	PRO
1	E	109	GLU
1	A	70	PRO
1	F	70	PRO
1	B	70	PRO
1	D	70	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	116/130 (89%)	111 (96%)	5 (4%)	29	26
1	B	121/130 (93%)	117 (97%)	4 (3%)	38	37
1	C	121/130 (93%)	118 (98%)	3 (2%)	47	49
1	D	120/130 (92%)	115 (96%)	5 (4%)	30	27
1	E	119/130 (92%)	118 (99%)	1 (1%)	81	86
1	F	123/130 (95%)	120 (98%)	3 (2%)	49	51
All	All	720/780 (92%)	699 (97%)	21 (3%)	42	43

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	24	LEU
1	A	33	LEU
1	A	38	LEU

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Mol	Chain	Res	Type
1	A	40	LYS
1	A	108	MSE
1	B	24	LEU
1	B	33	LEU
1	B	44	LYS
1	B	50	ARG
1	C	8	ASN
1	C	16	GLN
1	C	119	ARG
1	D	9	ARG
1	D	24	LEU
1	D	33	LEU
1	D	69	GLU
1	D	126	MSE
1	E	33	LEU
1	F	10	THR
1	F	33	LEU
1	F	78	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	16	GLN
1	A	30	GLN
1	A	49	HIS
1	A	137	GLN
1	B	41	ASN
1	B	49	HIS
1	C	8	ASN
1	C	16	GLN
1	C	30	GLN
1	C	41	ASN
1	C	49	HIS
1	C	71	ASN
1	C	83	GLN
1	C	137	GLN
1	D	41	ASN
1	D	49	HIS
1	D	71	ASN
1	E	8	ASN
1	E	16	GLN
1	E	30	GLN

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Mol	Chain	Res	Type
1	E	41	ASN
1	E	49	HIS
1	E	130	GLN
1	E	137	GLN
1	F	8	ASN
1	F	30	GLN
1	F	41	ASN
1	F	49	HIS
1	F	83	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	129/151 (85%)	0.02	2 (1%) 72 70	13, 21, 31, 40	0
1	B	134/151 (88%)	0.21	9 (6%) 17 17	14, 22, 43, 58	0
1	C	134/151 (88%)	0.25	7 (5%) 27 26	14, 23, 37, 44	0
1	D	133/151 (88%)	0.10	5 (3%) 40 39	14, 21, 34, 41	0
1	E	132/151 (87%)	0.15	5 (3%) 40 39	15, 24, 36, 47	0
1	F	136/151 (90%)	0.07	2 (1%) 73 72	13, 21, 35, 45	0
All	All	798/906 (88%)	0.13	30 (3%) 40 39	13, 22, 36, 58	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	6	THR	5.2
1	B	118	ARG	4.8
1	E	119	ARG	4.5
1	C	141	ARG	4.0
1	B	115	PRO	3.4
1	F	119	ARG	3.1
1	D	144	LEU	3.0
1	E	118	ARG	2.9
1	C	8	ASN	2.9
1	E	83	GLN	2.8
1	C	118	ARG	2.8
1	E	7	GLU	2.7
1	D	116	ASP	2.7
1	A	116	ASP	2.7
1	B	119	ARG	2.7
1	A	9	ARG	2.6
1	B	116	ASP	2.6
1	B	85	PRO	2.5
1	C	144	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	D	118	ARG	2.4
1	C	115	PRO	2.4
1	B	9	ARG	2.2
1	B	8	ASN	2.1
1	C	83	GLN	2.1
1	C	143	ASP	2.1
1	D	141	ARG	2.0
1	B	83	GLN	2.0
1	D	32	HIS	2.0
1	B	141	ARG	2.0
1	E	115	PRO	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.