Full wwPDB X-ray Structure Validation Report ⓘ

Apr 29, 2024 – 04:09 PM JST

PDB ID	:	8Z6G
Title	:	the AlgU-MucAcyto complex structure in Pseudomonas aeruginosa
Authors	:	Li, T.; Wang, Y.Z.; Bao, R.
Deposited on	:	2024-04-19
Resolution	:	2.10 Å(reported)

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

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

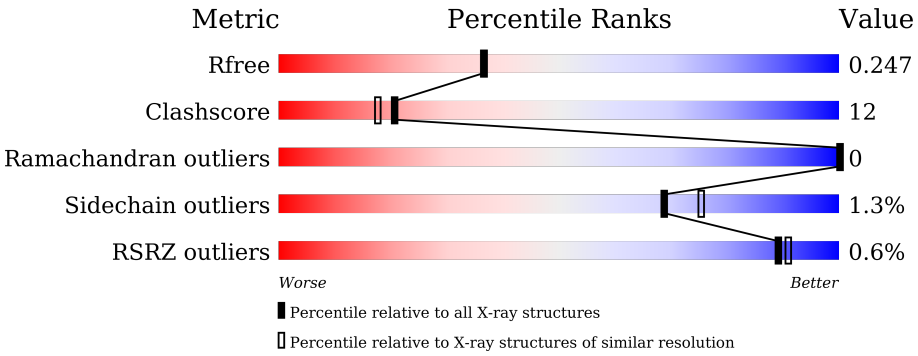
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	89	65% 15% 20%
1	C	89	% 57% 21% • 19%
1	E	89	% 60% 19% • 20%
2	B	201	62% 21% 16%
2	D	201	63% 20% • 16%
2	F	201	62% 20% • 16%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5943 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 Anti sigma-E RseA, N-terminal domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	71	Total	C	N	O	S	0	0	0
			547	333	99	112	3			
1	C	72	Total	C	N	O	S	0	0	0
			555	338	100	113	4			
1	E	71	Total	C	N	O	S	0	0	0
			546	333	99	110	4			

There are 27 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	PRO	-	expression tag	UNP A0A2R3IWP1
A	-7	LEU	-	expression tag	UNP A0A2R3IWP1
A	-6	GLU	-	expression tag	UNP A0A2R3IWP1
A	-5	HIS	-	expression tag	UNP A0A2R3IWP1
A	-4	HIS	-	expression tag	UNP A0A2R3IWP1
A	-3	HIS	-	expression tag	UNP A0A2R3IWP1
A	-2	HIS	-	expression tag	UNP A0A2R3IWP1
A	-1	HIS	-	expression tag	UNP A0A2R3IWP1
A	0	HIS	-	expression tag	UNP A0A2R3IWP1
C	-8	PRO	-	expression tag	UNP A0A2R3IWP1
C	-7	LEU	-	expression tag	UNP A0A2R3IWP1
C	-6	GLU	-	expression tag	UNP A0A2R3IWP1
C	-5	HIS	-	expression tag	UNP A0A2R3IWP1
C	-4	HIS	-	expression tag	UNP A0A2R3IWP1
C	-3	HIS	-	expression tag	UNP A0A2R3IWP1
C	-2	HIS	-	expression tag	UNP A0A2R3IWP1
C	-1	HIS	-	expression tag	UNP A0A2R3IWP1
C	0	HIS	-	expression tag	UNP A0A2R3IWP1
E	-8	PRO	-	expression tag	UNP A0A2R3IWP1
E	-7	LEU	-	expression tag	UNP A0A2R3IWP1
E	-6	GLU	-	expression tag	UNP A0A2R3IWP1
E	-5	HIS	-	expression tag	UNP A0A2R3IWP1
E	-4	HIS	-	expression tag	UNP A0A2R3IWP1

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	-3	HIS	-	expression tag	UNP A0A2R3IWP1
E	-2	HIS	-	expression tag	UNP A0A2R3IWP1
E	-1	HIS	-	expression tag	UNP A0A2R3IWP1
E	0	HIS	-	expression tag	UNP A0A2R3IWP1

- Molecule 2 is a protein called RNA polymerase sigma factor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	168	Total	C	N	O	S	0	0	0
			1369	863	254	249	3			
2	D	169	Total	C	N	O	S	0	0	0
			1377	867	255	252	3			
2	F	169	Total	C	N	O	S	0	0	0
			1377	867	255	252	3			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP A5JL21
B	194	LEU	-	expression tag	UNP A5JL21
B	195	GLU	-	expression tag	UNP A5JL21
B	196	VAL	-	expression tag	UNP A5JL21
B	197	LEU	-	expression tag	UNP A5JL21
B	198	PHE	-	expression tag	UNP A5JL21
B	199	GLN	-	expression tag	UNP A5JL21
B	200	GLY	-	expression tag	UNP A5JL21
D	0	MET	-	initiating methionine	UNP A5JL21
D	194	LEU	-	expression tag	UNP A5JL21
D	195	GLU	-	expression tag	UNP A5JL21
D	196	VAL	-	expression tag	UNP A5JL21
D	197	LEU	-	expression tag	UNP A5JL21
D	198	PHE	-	expression tag	UNP A5JL21
D	199	GLN	-	expression tag	UNP A5JL21
D	200	GLY	-	expression tag	UNP A5JL21
F	0	MET	-	initiating methionine	UNP A5JL21
F	194	LEU	-	expression tag	UNP A5JL21
F	195	GLU	-	expression tag	UNP A5JL21
F	196	VAL	-	expression tag	UNP A5JL21
F	197	LEU	-	expression tag	UNP A5JL21
F	198	PHE	-	expression tag	UNP A5JL21
F	199	GLN	-	expression tag	UNP A5JL21
F	200	GLY	-	expression tag	UNP A5JL21

- Molecule 3 is water.

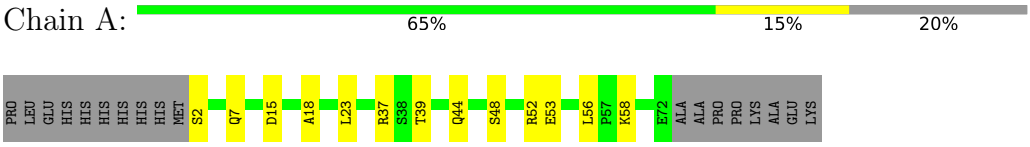
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	24	Total O 24 24	0	0
3	B	27	Total O 27 27	0	0
3	C	24	Total O 24 24	0	0
3	D	35	Total O 35 35	0	0
3	E	26	Total O 26 26	0	0
3	F	36	Total O 36 36	0	0

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.

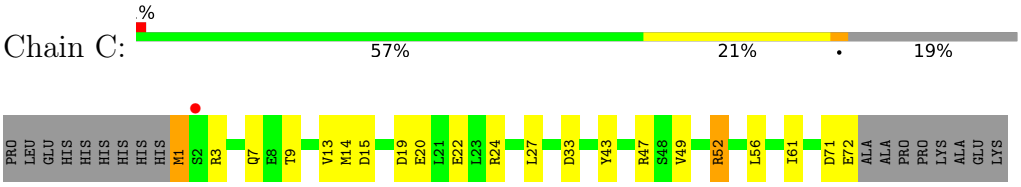
• Molecule 1: Anti sigma-E RseA, N-terminal domain protein

Chain A:



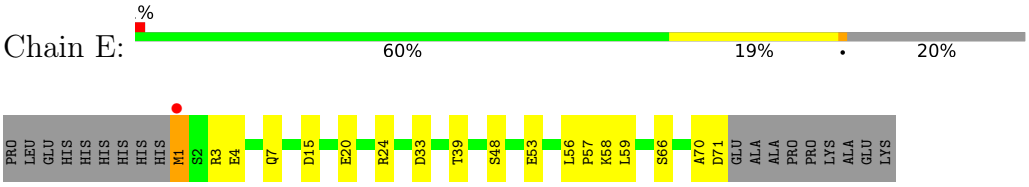
• Molecule 1: Anti sigma-E RseA, N-terminal domain protein

Chain C:



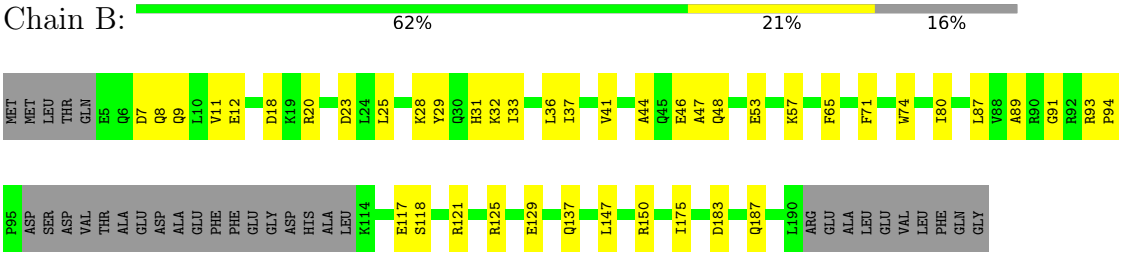
• Molecule 1: Anti sigma-E RseA, N-terminal domain protein

Chain E:



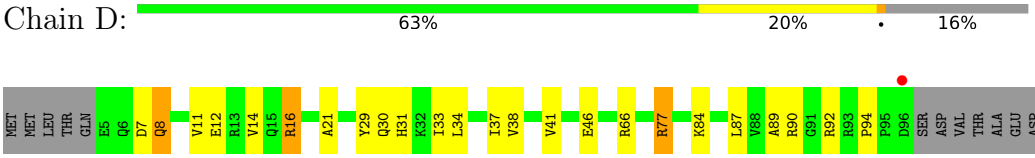
• Molecule 2: RNA polymerase sigma factor

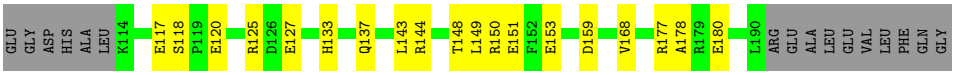
Chain B:



• Molecule 2: RNA polymerase sigma factor

Chain D:





• Molecule 2: RNA polymerase sigma factor

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 32	Depositor
Cell constants a, b, c, α, β, γ	126.53Å 126.53Å 42.84Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	36.52 – 2.10 36.52 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.2 (36.52-2.10) 97.1 (36.52-2.10)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.66 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.11.1_2575, PHENIX 1.11.1_2575	Depositor
R, R_{free}	0.221 , 0.245 0.223 , 0.247	Depositor DCC
R_{free} test set	1972 reflections (4.54%)	wwPDB-VP
Wilson B-factor (Å^2)	25.5	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 28.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.39$, $< L^2 > = 0.22$	Xtriage
Estimated twinning fraction	0.321 for -h,-k,l 0.046 for h,-h-k,-l 0.038 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5943	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 57.94 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1992e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|$ >5	RMSZ	#$\|Z\|$ >5
1	A	0.28	0/552	0.55	0/747
1	C	0.27	0/560	0.51	0/757
1	E	0.36	0/551	0.58	0/745
2	B	0.46	0/1391	0.58	0/1876
2	D	0.38	0/1399	0.60	3/1887 (0.2%)
2	F	0.44	1/1399 (0.1%)	0.59	2/1887 (0.1%)
All	All	0.40	1/5852 (0.0%)	0.58	5/7899 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	117	GLU	CD-OE2	-6.54	1.18	1.25

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	16	ARG	CB-CG-CD	-6.38	95.02	111.60
2	F	66	ARG	CB-CA-C	-6.07	98.27	110.40
2	D	77	ARG	CG-CD-NE	5.73	123.83	111.80
2	D	66	ARG	NE-CZ-NH1	-5.71	117.44	120.30
2	F	68	ASP	CB-CG-OD2	-5.23	113.59	118.30

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	547	0	538	15	0
1	C	555	0	550	17	1
1	E	546	0	544	29	0
2	B	1369	0	1383	32	0
2	D	1377	0	1387	31	1
2	F	1377	0	1387	38	0
3	A	24	0	0	7	0
3	B	27	0	0	2	0
3	C	24	0	0	4	0
3	D	35	0	0	3	0
3	E	26	0	0	1	0
3	F	36	0	0	2	0
All	All	5943	0	5789	142	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 12.

All (142) 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:E:1:MET:CE	1:E:3:ARG:HB2	1.43	1.44
1:C:1:MET:HE2	3:C:121:HOH:O	1.04	1.21
2:D:117:GLU:OE2	2:D:125:ARG:NH1	1.73	1.19
1:C:24:ARG:HD3	3:C:109:HOH:O	1.44	1.17
1:E:1:MET:CE	1:E:3:ARG:CB	2.22	1.17
1:E:1:MET:HE2	1:E:3:ARG:H	1.12	1.10
1:A:37:ARG:HD3	3:A:109:HOH:O	1.52	1.09
1:E:1:MET:HE2	1:E:3:ARG:CB	1.88	1.03
1:E:1:MET:CE	1:E:3:ARG:N	2.23	1.01
1:E:1:MET:HE2	1:E:3:ARG:HB2	1.36	0.99
1:E:1:MET:HE2	1:E:3:ARG:N	1.75	0.99
1:E:1:MET:CE	1:E:3:ARG:H	1.75	0.98
1:E:56:LEU:HD23	1:E:59:LEU:HD22	1.46	0.96
1:E:1:MET:HE3	1:E:3:ARG:HB2	1.46	0.95
1:E:1:MET:HE1	1:E:4:GLU:N	1.83	0.93
1:E:1:MET:HE1	1:E:3:ARG:HB2	1.50	0.92
2:D:168:VAL:HG12	3:D:313:HOH:O	1.69	0.91
1:E:7:GLN:HG2	1:E:39:THR:HG21	1.53	0.89
1:A:53:GLU:HB3	3:A:108:HOH:O	1.74	0.86
1:E:1:MET:HE1	1:E:3:ARG:CA	2.06	0.86
1:E:1:MET:CE	1:E:3:ARG:CA	2.53	0.86
1:E:1:MET:HE1	1:E:4:GLU:H	1.41	0.84

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:159:ASP:OD2	3:D:302:HOH:O	1.96	0.83
2:D:118:SER:OG	2:D:120:GLU:OE2	1.95	0.83
2:F:8:GLN:NE2	2:F:12:GLU:OE2	2.14	0.81
1:E:1:MET:HE1	1:E:3:ARG:CB	2.05	0.80
2:D:7:ASP:OD2	2:D:29:TYR:OH	2.00	0.80
2:F:117:GLU:OE1	2:F:125:ARG:NH1	2.14	0.80
2:D:117:GLU:CD	2:D:125:ARG:HH11	1.86	0.79
2:D:11:VAL:HA	2:D:14:VAL:HG22	1.66	0.76
2:F:129:GLU:O	2:F:133:HIS:ND1	2.20	0.75
2:F:156:SER:OG	2:F:159:ASP:OD1	2.06	0.74
1:E:15:ASP:OD2	2:F:157:TYR:OH	2.04	0.72
2:F:117:GLU:HG3	2:F:121:ARG:HB2	1.71	0.71
1:C:3:ARG:NH1	1:C:33:ASP:OD2	2.26	0.69
1:A:52:ARG:HD3	2:F:94:PRO:HG3	1.73	0.69
1:E:1:MET:HE2	1:E:3:ARG:CA	2.18	0.68
2:F:87:LEU:HD22	2:F:92:ARG:NH1	2.09	0.67
1:A:53:GLU:CB	3:A:108:HOH:O	2.38	0.66
2:F:87:LEU:HD22	2:F:92:ARG:HH12	1.60	0.65
1:A:58:LYS:HB2	2:B:121:ARG:HH12	1.61	0.64
2:F:90:ARG:HB3	3:F:304:HOH:O	1.97	0.63
1:A:23:LEU:HD22	2:B:9:GLN:HE21	1.64	0.63
2:B:8:GLN:HE21	2:B:12:GLU:CD	2.01	0.63
2:D:144:ARG:O	2:D:148:THR:OG1	2.12	0.62
2:F:117:GLU:CG	2:F:121:ARG:HB2	2.28	0.62
1:A:52:ARG:NH2	2:F:85:ASN:OD1	2.33	0.61
1:E:1:MET:HE1	1:E:3:ARG:C	2.21	0.61
3:A:108:HOH:O	2:B:32:LYS:CE	2.49	0.60
2:F:38:VAL:HA	2:F:41:VAL:HG12	1.84	0.60
2:D:84:LYS:HD3	2:D:94:PRO:HB2	1.84	0.60
2:F:41:VAL:HG11	2:F:47:ALA:HB2	1.84	0.60
3:A:108:HOH:O	2:B:32:LYS:HE2	2.00	0.59
2:D:143:LEU:HB3	2:D:178:ALA:HB2	1.85	0.58
1:E:71:ASP:O	3:E:101:HOH:O	2.17	0.58
2:D:168:VAL:CG1	3:D:313:HOH:O	2.36	0.58
1:A:15:ASP:HB3	2:B:150:ARG:HD3	1.86	0.58
2:F:120:GLU:OE2	2:F:120:GLU:N	2.30	0.57
2:D:149:LEU:O	2:D:153:GLU:HB2	2.03	0.57
1:A:7:GLN:HG2	1:A:39:THR:HG21	1.85	0.56
1:C:49:VAL:O	3:C:101:HOH:O	2.18	0.56
2:F:135:THR:HG21	2:F:182:ILE:HA	1.87	0.55
2:B:33:ILE:O	2:B:37:ILE:HG12	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:36:LEU:HD21	2:B:80:ILE:HG12	1.88	0.55
2:B:87:LEU:HD23	2:B:94:PRO:HA	1.89	0.54
1:E:56:LEU:H	2:F:31:HIS:CD2	2.26	0.54
1:C:14:MET:SD	1:C:43:TYR:HB3	2.49	0.53
1:C:1:MET:HB3	3:C:121:HOH:O	2.09	0.52
2:F:35:GLY:O	2:F:38:VAL:HG12	2.10	0.52
1:A:48:SER:HB3	1:A:53:GLU:HB2	1.92	0.52
2:B:117:GLU:OE2	2:B:125:ARG:NH1	2.43	0.52
2:F:116:ILE:HG13	2:F:116:ILE:O	2.08	0.52
2:B:7:ASP:OD1	2:B:28:LYS:NZ	2.37	0.52
2:F:53:GLU:HA	2:F:56:ILE:HD12	1.92	0.51
2:B:28:LYS:HE2	2:B:29:TYR:CZ	2.46	0.51
1:C:47:ARG:HE	2:D:151:GLU:CD	2.14	0.51
1:C:27:LEU:HD11	2:D:21:ALA:HB2	1.92	0.51
2:F:86:HIS:O	2:F:90:ARG:NH2	2.44	0.50
1:C:3:ARG:O	1:C:7:GLN:N	2.34	0.49
2:D:177:ARG:NH1	2:D:180:GLU:OE1	2.46	0.49
2:F:92:ARG:NE	3:F:304:HOH:O	2.45	0.49
1:C:15:ASP:CG	2:D:150:ARG:HE	2.16	0.48
2:B:18:ASP:OD2	2:B:20:ARG:NH2	2.34	0.48
1:E:20:GLU:O	1:E:24:ARG:HG3	2.12	0.48
2:B:46:GLU:OE2	3:B:301:HOH:O	2.20	0.48
1:C:20:GLU:O	1:C:24:ARG:HG3	2.12	0.48
1:C:56:LEU:H	2:D:31:HIS:CD2	2.32	0.47
2:F:161:ALA:HB1	2:F:166:CYS:O	2.15	0.47
2:B:129:GLU:OE1	2:F:93:ARG:NH2	2.48	0.47
2:B:137:GLN:HB2	2:F:91:GLY:HA3	1.97	0.47
1:E:1:MET:CE	1:E:4:GLU:H	2.22	0.46
1:E:57:PRO:O	1:E:58:LYS:HB2	2.15	0.46
2:B:89:ALA:O	2:D:144:ARG:HD2	2.14	0.46
2:D:89:ALA:HB3	2:D:90:ARG:HH22	1.81	0.46
3:A:108:HOH:O	2:B:32:LYS:HE3	2.13	0.46
2:B:44:ALA:O	2:B:48:GLN:HG3	2.16	0.45
2:F:22:PHE:O	2:F:26:VAL:HG23	2.17	0.45
2:F:114:LYS:O	2:F:116:ILE:HG23	2.17	0.45
1:C:52:ARG:HH21	1:C:52:ARG:HG2	1.80	0.45
2:B:183:ASP:O	2:B:187:GLN:HG3	2.16	0.45
2:F:28:LYS:HE2	2:F:29:TYR:CZ	2.52	0.45
2:F:66:ARG:HB2	2:F:68:ASP:OD2	2.17	0.45
2:D:89:ALA:HB3	2:D:90:ARG:NH2	2.32	0.44
1:E:56:LEU:HD23	1:E:59:LEU:CD2	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:93:ARG:HG2	2:D:133:HIS:CG	2.51	0.44
1:C:19:ASP:OD1	1:C:22:GLU:HG2	2.17	0.44
2:D:87:LEU:CD2	2:D:92:ARG:HH21	2.30	0.44
1:E:3:ARG:NH1	1:E:33:ASP:OD2	2.51	0.44
1:A:48:SER:O	1:A:52:ARG:N	2.50	0.44
2:F:161:ALA:HA	2:F:166:CYS:SG	2.58	0.44
2:D:33:ILE:O	2:D:37:ILE:HG12	2.19	0.43
2:F:41:VAL:CG1	2:F:47:ALA:HB2	2.47	0.43
2:D:16:ARG:CG	2:D:16:ARG:HH11	2.31	0.43
2:D:34:LEU:O	2:D:38:VAL:HG23	2.18	0.43
2:B:23:ASP:OD1	3:B:302:HOH:O	2.21	0.43
2:D:8:GLN:NE2	2:D:12:GLU:OE2	2.52	0.43
1:C:9:THR:O	1:C:13:VAL:HG23	2.19	0.43
2:B:41:VAL:CG2	2:B:47:ALA:HB2	2.49	0.43
2:B:91:GLY:HA3	2:D:137:GLN:HB2	2.00	0.43
1:A:23:LEU:HD22	2:B:9:GLN:NE2	2.33	0.42
2:F:41:VAL:HG11	2:F:47:ALA:CB	2.48	0.42
1:A:56:LEU:H	2:B:31:HIS:CD2	2.38	0.42
1:A:18:ALA:HB3	2:B:9:GLN:HE22	1.85	0.42
2:D:41:VAL:CG1	2:D:46:GLU:HB3	2.50	0.42
2:B:25:LEU:HD13	2:B:71:PHE:CE2	2.55	0.41
1:C:61:ILE:H	2:D:30:GLN:NE2	2.17	0.41
1:C:71:ASP:O	1:C:72:GLU:HB2	2.20	0.41
2:D:87:LEU:HD23	2:D:92:ARG:HH21	1.85	0.41
2:F:35:GLY:HA2	2:F:38:VAL:HG12	2.02	0.41
2:F:66:ARG:HG3	2:F:68:ASP:OD2	2.20	0.41
2:B:147:LEU:HA	2:B:175:ILE:HG12	2.03	0.41
2:B:53:GLU:O	2:B:57:LYS:HB2	2.20	0.41
1:E:48:SER:HB3	1:E:53:GLU:HB2	2.01	0.41
1:E:66:SER:O	1:E:70:ALA:N	2.54	0.41
2:F:139:LEU:O	2:F:144:ARG:NH2	2.53	0.41
2:F:149:LEU:O	2:F:153:GLU:HB2	2.21	0.41
2:F:177:ARG:HD3	2:F:177:ARG:HA	1.85	0.41
2:D:177:ARG:HA	2:D:177:ARG:HD3	1.80	0.41
1:A:44:GLN:NE2	3:A:102:HOH:O	2.35	0.40
2:B:65:PHE:HB2	2:B:74:TRP:CZ2	2.56	0.40
2:B:7:ASP:O	2:B:11:VAL:HG23	2.21	0.40
2:F:117:GLU:HG3	2:F:121:ARG:CB	2.47	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)
1:C:24:ARG:NH2	2:D:127:GLU:OE2[1_556]	2.16	0.04

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	69/89 (78%)	68 (99%)	1 (1%)	0	100	100
1	C	70/89 (79%)	69 (99%)	1 (1%)	0	100	100
1	E	69/89 (78%)	67 (97%)	2 (3%)	0	100	100
2	B	164/201 (82%)	163 (99%)	1 (1%)	0	100	100
2	D	165/201 (82%)	165 (100%)	0	0	100	100
2	F	165/201 (82%)	164 (99%)	1 (1%)	0	100	100
All	All	702/870 (81%)	696 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	57/72 (79%)	56 (98%)	1 (2%)	59	65
1	C	58/72 (81%)	56 (97%)	2 (3%)	37	39
1	E	57/72 (79%)	56 (98%)	1 (2%)	59	65
2	B	143/170 (84%)	142 (99%)	1 (1%)	84	88

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	D	144/170 (85%)	142 (99%)	2 (1%)	67 73
2	F	144/170 (85%)	143 (99%)	1 (1%)	84 88
All	All	603/726 (83%)	595 (99%)	8 (1%)	69 75

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	SER
2	B	118	SER
1	C	1	MET
1	C	52	ARG
2	D	8	GLN
2	D	77	ARG
1	E	1	MET
2	F	118	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	8	GLN
2	B	31	HIS
2	B	48	GLN
2	B	64	ASN
2	B	134	GLN
1	C	16	ASN
2	D	8	GLN
2	D	30	GLN
2	D	31	HIS
2	D	86	HIS
2	F	31	HIS
2	F	81	ASN
2	F	86	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	71/89 (79%)	-0.37	0 100 100	14, 23, 41, 59	0
1	C	72/89 (80%)	-0.11	1 (1%) 75 78	18, 29, 43, 63	0
1	E	71/89 (79%)	-0.24	1 (1%) 75 78	14, 28, 41, 56	0
2	B	168/201 (83%)	-0.37	0 100 100	17, 31, 48, 54	0
2	D	169/201 (84%)	-0.23	1 (0%) 89 91	20, 33, 51, 59	0
2	F	169/201 (84%)	-0.26	1 (0%) 89 91	15, 31, 49, 59	0
All	All	720/870 (82%)	-0.27	4 (0%) 89 91	14, 31, 49, 63	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1	MET	2.6
2	D	96	ASP	2.2
1	C	2	SER	2.1
2	F	66	ARG	2.0

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.