



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 07:22 PM UTC

PDB ID : 8FFA / pdb_00008ffa
Title : Crystal structure of Apo Dps protein (PA0962) from *Pseudomonas aeruginosa* (cubic form)
Authors : Lovell, S.; Kashipathy, M.M.; Battaile, K.P.; Rivera, M.
Deposited on : 2022-12-08
Resolution : 2.15 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 : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

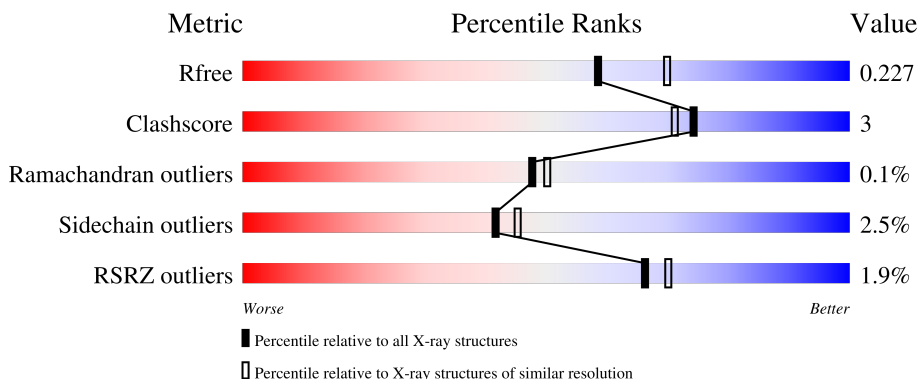
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	156	 92% 6% ..
1	B	156	 92% 6% ..
1	C	156	 91% 8% .
1	D	156	 92% 7% .
1	E	156	 88% 11% .

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Mol	Chain	Length	Quality of chain
1	F	156	<p>4% 90% 9% ..</p>
1	G	156	<p>4% 89% 8% ..</p>
1	H	156	<p>% 94% 5% .</p>
1	I	156	<p>% 88% 10% ..</p>
1	J	156	<p>3% 81% 19% .</p>
1	K	156	<p>% 90% 10% .</p>
1	L	156	<p>5% 90% 10% .</p>
1	M	156	<p>% 91% 7% ..</p>
1	N	156	<p>2% 92% 7% .</p>
1	O	156	<p>2% 92% 6% ..</p>
1	P	156	<p>% 90% 10% .</p>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 20338 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 Probable dna-binding stress protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	155	1195	760	204	225	6	0	0	0
1	B	155	1216	772	210	228	6	0	0	0
1	C	155	1199	763	205	225	6	0	0	0
1	D	155	1197	762	207	222	6	0	0	0
1	E	155	1198	762	208	222	6	0	0	0
1	F	155	1187	757	201	223	6	0	0	0
1	G	155	1195	761	201	227	6	0	0	0
1	H	155	1206	766	206	228	6	0	0	0
1	I	155	1207	765	208	228	6	0	0	0
1	J	155	1182	754	200	222	6	0	0	0
1	K	155	1203	763	207	227	6	0	0	0
1	L	155	1192	759	204	223	6	0	0	0
1	M	155	1207	766	209	226	6	0	0	0
1	N	155	1201	763	205	227	6	0	0	0
1	O	155	1200	762	207	225	6	0	0	0
1	P	155	1190	758	201	225	6	0	0	0

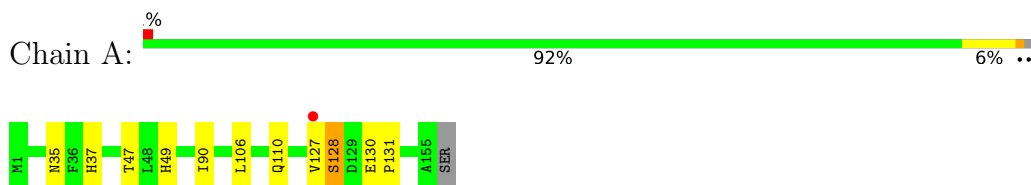
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	72	Total O 72 72	0	0
2	B	99	Total O 99 99	0	0
2	C	61	Total O 61 61	0	0
2	D	55	Total O 55 55	0	0
2	E	79	Total O 79 79	0	0
2	F	43	Total O 43 43	0	0
2	G	51	Total O 51 51	0	0
2	H	108	Total O 108 108	0	0
2	I	101	Total O 101 101	0	0
2	J	63	Total O 63 63	0	0
2	K	72	Total O 72 72	0	0
2	L	60	Total O 60 60	0	0
2	M	98	Total O 98 98	0	0
2	N	59	Total O 59 59	0	0
2	O	74	Total O 74 74	0	0
2	P	68	Total O 68 68	0	0

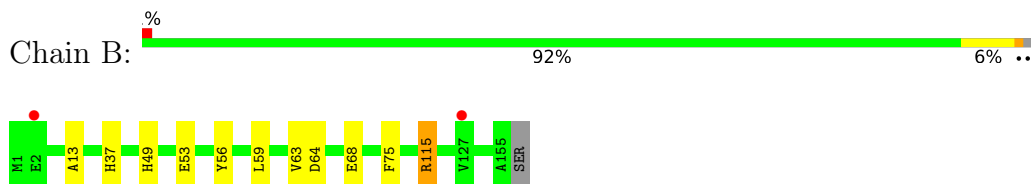
3 Residue-property plots [i](#)

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.

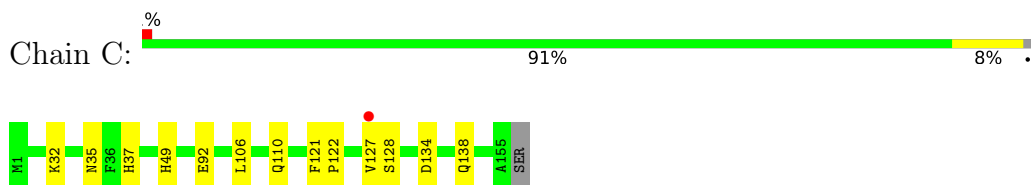
- Molecule 1: Probable dna-binding stress protein



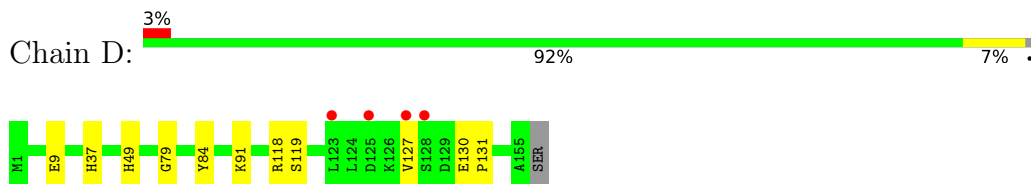
- Molecule 1: Probable dna-binding stress protein



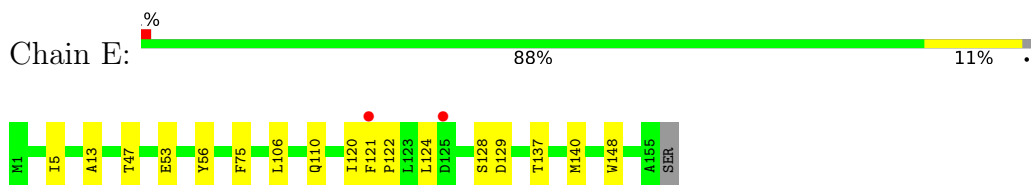
- Molecule 1: Probable dna-binding stress protein



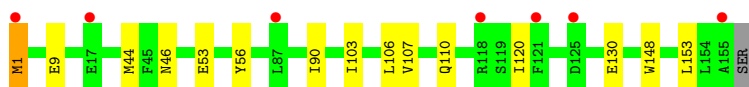
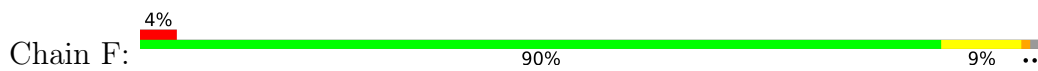
- Molecule 1: Probable dna-binding stress protein



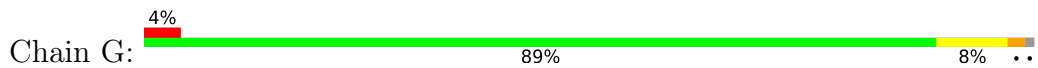
- Molecule 1: Probable dna-binding stress protein



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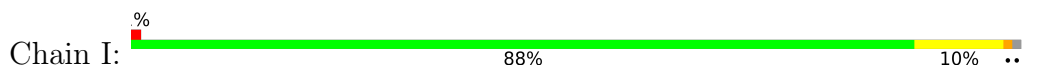
- Molecule 1: Probable dna-binding stress protein



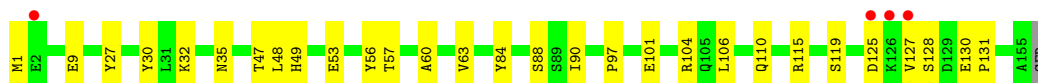
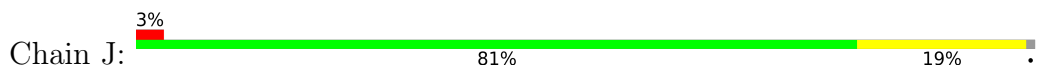
- Molecule 1: Probable dna-binding stress protein



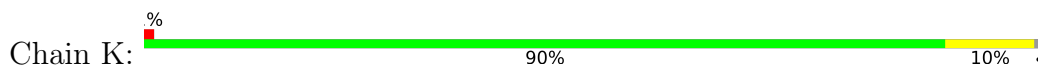
- Molecule 1: Probable dna-binding stress protein



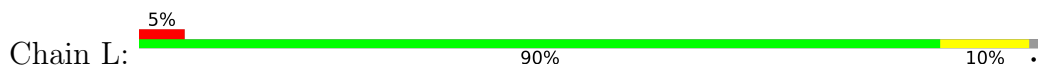
- Molecule 1: Probable dna-binding stress protein




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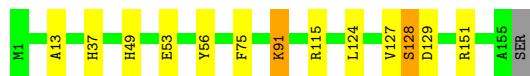


- Molecule 1: Probable dna-binding stress protein

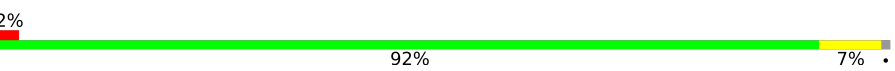


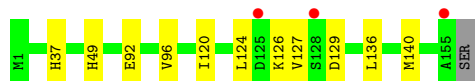
- Molecule 1: Probable dna-binding stress protein

Chain M:  91% 7% ..

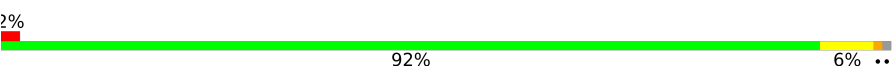


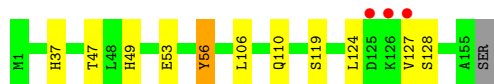
- Molecule 1: Probable dna-binding stress protein

Chain N:  2% 92% 7% .

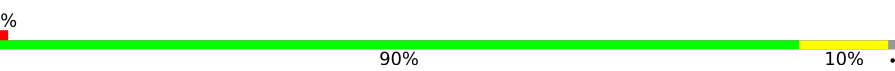


- Molecule 1: Probable dna-binding stress protein

Chain O:  2% 92% 6% ..



- Molecule 1: Probable dna-binding stress protein

Chain P:  1% 90% 10% .



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 3	Depositor
Cell constants a, b, c, α , β , γ	223.47Å 223.47Å 223.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.97 – 2.15 49.97 – 2.15	Depositor EDS
% Data completeness (in resolution range)	100.0 (49.97-2.15) 100.0 (49.97-2.15)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.88 (at 2.16Å)	Xtrriage
Refinement program	PHENIX 1.19rc5_4043	Depositor
R, R_{free}	0.183 , 0.227 0.189 , 0.227	Depositor DCC
R_{free} test set	10047 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	37.7	Xtrriage
Anisotropy	0.000	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.005 for l,-k,h	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	20338	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.82% 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

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	0.51	0/1218	0.62	0/1657
1	B	0.58	0/1239	0.67	0/1681
1	C	0.50	0/1222	0.62	0/1661
1	D	0.49	0/1220	0.60	0/1658
1	E	0.51	0/1221	0.63	0/1660
1	F	0.47	0/1210	0.61	0/1647
1	G	0.50	0/1218	0.64	0/1657
1	H	0.58	0/1229	0.68	0/1670
1	I	0.52	0/1230	0.66	0/1672
1	J	0.51	0/1205	0.61	0/1641
1	K	0.52	0/1226	0.64	0/1667
1	L	0.49	0/1215	0.64	0/1653
1	M	0.52	0/1230	0.65	0/1671
1	N	0.50	0/1224	0.64	0/1664
1	O	0.51	0/1223	0.61	0/1663
1	P	0.49	0/1213	0.58	0/1651
All	All	0.51	0/19543	0.63	0/26573

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	I	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	115	ARG	Sidechain
1	I	115	ARG	Sidechain

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	1195	0	1171	7	0
1	B	1216	0	1212	5	0
1	C	1199	0	1179	7	0
1	D	1197	0	1183	5	0
1	E	1198	0	1182	9	0
1	F	1187	0	1160	10	0
1	G	1195	0	1168	8	0
1	H	1206	0	1190	5	0
1	I	1207	0	1188	10	0
1	J	1182	0	1152	19	0
1	K	1203	0	1182	7	0
1	L	1192	0	1169	8	0
1	M	1207	0	1195	7	0
1	N	1201	0	1179	6	0
1	O	1200	0	1180	4	0
1	P	1190	0	1162	7	0
2	A	72	0	0	0	0
2	B	99	0	0	0	0
2	C	61	0	0	0	0
2	D	55	0	0	0	0
2	E	79	0	0	0	0
2	F	43	0	0	1	0
2	G	51	0	0	0	0
2	H	108	0	0	1	0
2	I	101	0	0	1	0
2	J	63	0	0	2	0
2	K	72	0	0	0	0
2	L	60	0	0	0	0
2	M	98	0	0	1	0
2	N	59	0	0	1	0
2	O	74	0	0	0	0
2	P	68	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	20338	0	18852	118	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 3.

All (118) 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:J:127:VAL:HG12	1:J:128:SER:H	1.61	0.66
1:G:147:ALA:O	1:G:151:ARG:HG2	1.97	0.65
1:J:127:VAL:HG12	1:J:128:SER:N	2.11	0.65
1:L:124:LEU:HD22	1:L:129:ASP:HB3	1.79	0.64
1:A:127:VAL:HG12	1:A:128:SER:H	1.62	0.63
1:J:130:GLU:OE1	1:J:130:GLU:N	2.33	0.61
1:J:32:LYS:NZ	2:J:203:HOH:O	2.34	0.59
1:C:127:VAL:HG12	1:C:128:SER:N	2.18	0.59
1:H:106:LEU:O	1:H:110:GLN:HG2	2.04	0.58
1:K:13:ALA:HB2	1:K:75:PHE:CZ	2.39	0.57
1:C:127:VAL:HG12	1:C:128:SER:H	1.69	0.56
1:P:106:LEU:O	1:P:110:GLN:HG2	2.06	0.55
1:J:106:LEU:O	1:J:110:GLN:HG2	2.06	0.55
1:A:127:VAL:HG12	1:A:128:SER:N	2.23	0.53
1:D:118:ARG:NH1	1:E:5:ILE:O	2.41	0.53
1:L:121:PHE:O	1:L:124:LEU:N	2.35	0.53
1:G:121:PHE:O	1:G:123:LEU:O	2.26	0.52
1:J:97:PRO:HB3	1:J:101:GLU:HG2	1.91	0.52
1:P:124:LEU:HD22	1:P:129:ASP:HB3	1.93	0.51
1:H:115:ARG:NH2	2:H:203:HOH:O	2.43	0.51
1:B:13:ALA:HB2	1:B:75:PHE:CZ	2.46	0.51
1:D:37:HIS:HE1	2:F:227:HOH:O	1.94	0.51
1:G:37:HIS:CE1	1:G:49:HIS:CE1	3.00	0.50
1:L:123:LEU:O	1:L:127:VAL:HG23	2.11	0.50
1:O:106:LEU:O	1:O:110:GLN:HG2	2.12	0.50
1:J:84:TYR:O	1:J:88:SER:HB2	2.12	0.50
1:F:46:ASN:ND2	1:L:51:MET:SD	2.80	0.49
1:G:127:VAL:HG12	1:G:128:SER:H	1.77	0.49
1:I:51:MET:SD	1:L:46:ASN:ND2	2.77	0.49
1:M:151:ARG:HD3	2:M:224:HOH:O	2.13	0.49
1:F:1:MET:HE3	1:J:104:ARG:HG2	1.93	0.49
1:P:121:PHE:N	1:P:122:PRO:CD	2.76	0.49
1:L:37:HIS:CE1	1:L:49:HIS:CE1	3.01	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:13:ALA:HB2	1:E:75:PHE:CZ	2.49	0.48
1:F:130:GLU:OE1	1:F:130:GLU:N	2.38	0.48
1:J:125:ASP:O	1:J:127:VAL:O	2.31	0.48
1:B:64:ASP:O	1:B:68:GLU:HG3	2.14	0.48
1:N:96:VAL:HG22	2:N:214:HOH:O	2.13	0.48
1:D:37:HIS:HD2	1:D:49:HIS:O	1.98	0.47
1:B:37:HIS:CE1	1:B:49:HIS:CE1	3.03	0.47
1:A:106:LEU:O	1:A:110:GLN:HG2	2.15	0.47
1:F:44:MET:HE1	1:F:153:LEU:HD22	1.96	0.47
1:I:35:ASN:OD1	1:I:35:ASN:C	2.58	0.47
1:J:53:GLU:HA	1:J:56:TYR:CE2	2.51	0.46
1:I:59:LEU:O	1:I:63:VAL:HG13	2.15	0.46
1:C:106:LEU:O	1:C:110:GLN:HG2	2.15	0.46
1:M:37:HIS:CE1	1:M:49:HIS:CE1	3.03	0.46
1:J:35:ASN:C	1:J:35:ASN:OD1	2.59	0.46
1:K:106:LEU:O	1:K:110:GLN:HG2	2.16	0.46
1:M:127:VAL:O	1:M:128:SER:CB	2.63	0.46
1:J:60:ALA:O	1:J:63:VAL:HG22	2.16	0.46
1:J:130:GLU:N	1:J:131:PRO:CD	2.79	0.46
1:L:123:LEU:O	1:L:123:LEU:HD12	2.16	0.46
1:I:124:LEU:O	1:I:127:VAL:O	2.34	0.46
1:H:124:LEU:O	1:H:127:VAL:O	2.34	0.45
1:O:124:LEU:O	1:O:127:VAL:O	2.34	0.45
1:E:124:LEU:HD22	1:E:129:ASP:HB3	1.99	0.45
1:I:85:ALA:O	1:M:91:LYS:HE3	2.16	0.45
1:M:124:LEU:HD22	1:M:129:ASP:HB3	1.98	0.45
1:C:121:PHE:N	1:C:122:PRO:CD	2.78	0.45
1:E:53:GLU:HA	1:E:56:TYR:CE2	2.52	0.45
1:I:120:ILE:HG22	1:I:120:ILE:O	2.17	0.45
1:H:13:ALA:HB2	1:H:75:PHE:CZ	2.52	0.45
1:E:106:LEU:O	1:E:110:GLN:HG2	2.18	0.44
1:L:121:PHE:O	1:L:122:PRO:C	2.60	0.44
1:B:59:LEU:O	1:B:63:VAL:HG13	2.17	0.44
1:K:53:GLU:HA	1:K:56:TYR:CE2	2.53	0.44
1:F:106:LEU:O	1:F:110:GLN:HG2	2.18	0.44
1:P:53:GLU:HA	1:P:56:TYR:CE2	2.52	0.44
1:K:121:PHE:N	1:K:122:PRO:CD	2.81	0.44
1:C:37:HIS:CE1	1:C:49:HIS:CE1	3.06	0.43
1:I:46:ASN:HB2	2:I:246:HOH:O	2.18	0.43
1:A:130:GLU:N	1:A:131:PRO:CD	2.81	0.43
1:H:35:ASN:OD1	1:H:35:ASN:C	2.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:GLY:HA2	1:D:84:TYR:CZ	2.54	0.43
1:F:1:MET:HE3	1:J:104:ARG:CG	2.48	0.43
1:J:127:VAL:CG1	1:J:128:SER:N	2.81	0.43
1:N:37:HIS:CE1	1:N:49:HIS:CE1	3.07	0.43
1:A:37:HIS:CE1	1:A:49:HIS:CE1	3.07	0.43
1:E:121:PHE:N	1:E:122:PRO:CD	2.81	0.43
1:C:32:LYS:O	1:C:35:ASN:HB3	2.19	0.42
1:D:130:GLU:N	1:D:131:PRO:CD	2.82	0.42
1:G:121:PHE:HA	1:G:124:LEU:HD22	2.01	0.42
1:O:37:HIS:CE1	1:O:49:HIS:CE1	3.07	0.42
1:I:37:HIS:CE1	1:I:49:HIS:CE1	3.07	0.42
1:E:137:THR:HA	1:E:140:MET:HE3	2.02	0.42
1:J:88:SER:HB3	2:J:201:HOH:O	2.20	0.42
1:N:120:ILE:HG22	1:N:120:ILE:O	2.19	0.42
1:P:35:ASN:OD1	1:P:35:ASN:C	2.62	0.42
1:I:130:GLU:OE1	1:I:130:GLU:N	2.45	0.42
1:P:53:GLU:HA	1:P:56:TYR:CD2	2.54	0.42
1:G:125:ASP:OD1	1:G:125:ASP:C	2.63	0.42
1:M:13:ALA:HB2	1:M:75:PHE:CZ	2.55	0.42
1:A:35:ASN:OD1	1:A:35:ASN:C	2.63	0.42
1:C:134:ASP:O	1:C:138:GLN:HG2	2.20	0.42
1:M:53:GLU:HA	1:M:56:TYR:CE2	2.55	0.42
1:F:53:GLU:HA	1:F:56:TYR:CD2	2.55	0.42
1:B:53:GLU:HA	1:B:56:TYR:CE2	2.55	0.41
1:I:53:GLU:HA	1:I:56:TYR:CE2	2.55	0.41
1:O:53:GLU:HA	1:O:56:TYR:CD2	2.55	0.41
1:F:103:ILE:O	1:F:107:VAL:HG23	2.21	0.41
1:N:136:LEU:O	1:N:140:MET:HG3	2.20	0.41
1:E:120:ILE:C	1:E:122:PRO:HD2	2.45	0.41
1:F:53:GLU:HA	1:F:56:TYR:CE2	2.56	0.41
1:G:130:GLU:N	1:G:131:PRO:CD	2.83	0.41
1:K:37:HIS:CE1	1:K:49:HIS:CE1	3.09	0.41
1:N:124:LEU:O	1:N:127:VAL:O	2.39	0.41
1:P:147:ALA:O	1:P:151:ARG:HG2	2.21	0.41
1:F:120:ILE:O	1:F:120:ILE:HG22	2.21	0.41
1:J:9:GLU:C	1:J:9:GLU:OE1	2.63	0.41
1:N:124:LEU:HD22	1:N:129:ASP:HB3	2.03	0.40
1:E:56:TYR:C	1:E:56:TYR:CD1	2.99	0.40
1:K:130:GLU:N	1:K:131:PRO:CD	2.84	0.40
1:A:130:GLU:N	1:A:130:GLU:OE1	2.54	0.40
1:G:13:ALA:HB2	1:G:75:PHE:CZ	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:35:ASN:OD1	1:K:35:ASN:C	2.65	0.40
1:J:27:TYR:O	1:J:30:TYR:HB3	2.22	0.40
1:J:48:LEU:O	1:J:49:HIS:C	2.65	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	153/156 (98%)	148 (97%)	5 (3%)	0	100	100
1	B	153/156 (98%)	150 (98%)	3 (2%)	0	100	100
1	C	153/156 (98%)	148 (97%)	5 (3%)	0	100	100
1	D	153/156 (98%)	147 (96%)	6 (4%)	0	100	100
1	E	153/156 (98%)	148 (97%)	5 (3%)	0	100	100
1	F	153/156 (98%)	147 (96%)	6 (4%)	0	100	100
1	G	153/156 (98%)	146 (95%)	7 (5%)	0	100	100
1	H	153/156 (98%)	150 (98%)	3 (2%)	0	100	100
1	I	153/156 (98%)	150 (98%)	3 (2%)	0	100	100
1	J	153/156 (98%)	145 (95%)	8 (5%)	0	100	100
1	K	153/156 (98%)	152 (99%)	1 (1%)	0	100	100
1	L	153/156 (98%)	146 (95%)	7 (5%)	0	100	100
1	M	153/156 (98%)	148 (97%)	4 (3%)	1 (1%)	18	13
1	N	153/156 (98%)	150 (98%)	2 (1%)	1 (1%)	18	13
1	O	153/156 (98%)	150 (98%)	3 (2%)	0	100	100
1	P	153/156 (98%)	150 (98%)	3 (2%)	0	100	100
All	All	2448/2496 (98%)	2375 (97%)	71 (3%)	2 (0%)	48	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	N	126	LYS
1	M	128	SER

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	121/129 (94%)	118 (98%)	3 (2%)	42	45
1	B	126/129 (98%)	125 (99%)	1 (1%)	73	79
1	C	121/129 (94%)	120 (99%)	1 (1%)	73	79
1	D	121/129 (94%)	117 (97%)	4 (3%)	33	34
1	E	121/129 (94%)	118 (98%)	3 (2%)	42	45
1	F	119/129 (92%)	115 (97%)	4 (3%)	32	33
1	G	121/129 (94%)	116 (96%)	5 (4%)	27	26
1	H	124/129 (96%)	124 (100%)	0	100	100
1	I	124/129 (96%)	120 (97%)	4 (3%)	34	36
1	J	118/129 (92%)	112 (95%)	6 (5%)	21	18
1	K	123/129 (95%)	121 (98%)	2 (2%)	55	61
1	L	120/129 (93%)	115 (96%)	5 (4%)	26	25
1	M	124/129 (96%)	122 (98%)	2 (2%)	55	61
1	N	122/129 (95%)	121 (99%)	1 (1%)	73	79
1	O	122/129 (95%)	118 (97%)	4 (3%)	33	34
1	P	120/129 (93%)	116 (97%)	4 (3%)	33	34
All	All	1947/2064 (94%)	1898 (98%)	49 (2%)	42	45

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	47	THR
1	A	90	ILE

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Mol	Chain	Res	Type
1	A	128	SER
1	B	115	ARG
1	C	92	GLU
1	D	9	GLU
1	D	91	LYS
1	D	119	SER
1	D	127	VAL
1	E	47	THR
1	E	128	SER
1	E	148	TRP
1	F	1	MET
1	F	9	GLU
1	F	90	ILE
1	F	148	TRP
1	G	1	MET
1	G	92	GLU
1	G	124	LEU
1	G	125	ASP
1	G	127	VAL
1	I	2	GLU
1	I	115	ARG
1	I	127	VAL
1	I	128	SER
1	J	1	MET
1	J	47	THR
1	J	57	THR
1	J	90	ILE
1	J	115	ARG
1	J	119	SER
1	K	92	GLU
1	K	127	VAL
1	L	90	ILE
1	L	92	GLU
1	L	119	SER
1	L	128	SER
1	L	148	TRP
1	M	91	LYS
1	M	115	ARG
1	N	92	GLU
1	O	47	THR
1	O	56	TYR
1	O	119	SER

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Mol	Chain	Res	Type
1	O	128	SER
1	P	47	THR
1	P	90	ILE
1	P	92	GLU
1	P	148	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	4	ASN
1	D	49	HIS
1	E	49	HIS
1	G	55	GLN
1	I	37	HIS
1	I	49	HIS
1	M	37	HIS
1	M	49	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 oligosaccharides 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

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	155/156 (99%)	0.01	1 (0%) 85 87	33, 40, 56, 74	0
1	B	155/156 (99%)	-0.26	2 (1%) 75 78	28, 34, 46, 65	0
1	C	155/156 (99%)	0.23	1 (0%) 85 87	34, 42, 57, 74	0
1	D	155/156 (99%)	0.30	4 (2%) 57 61	34, 43, 64, 84	0
1	E	155/156 (99%)	0.04	2 (1%) 75 78	32, 40, 56, 64	0
1	F	155/156 (99%)	0.52	7 (4%) 38 43	37, 45, 62, 69	0
1	G	155/156 (99%)	0.24	6 (3%) 43 48	32, 43, 65, 90	0
1	H	155/156 (99%)	-0.28	2 (1%) 75 78	27, 33, 45, 62	0
1	I	155/156 (99%)	-0.16	1 (0%) 85 87	29, 38, 51, 65	0
1	J	155/156 (99%)	0.52	4 (2%) 57 61	38, 44, 60, 78	0
1	K	155/156 (99%)	-0.15	1 (0%) 85 87	29, 36, 57, 74	0
1	L	155/156 (99%)	0.31	8 (5%) 33 36	30, 43, 67, 85	0
1	M	155/156 (99%)	-0.27	0 100 100	30, 37, 46, 58	0
1	N	155/156 (99%)	-0.03	3 (1%) 66 70	32, 40, 57, 80	0
1	O	155/156 (99%)	0.01	3 (1%) 66 70	33, 40, 57, 79	0
1	P	155/156 (99%)	-0.05	1 (0%) 85 87	34, 40, 54, 65	0
All	All	2480/2496 (99%)	0.06	46 (1%) 66 70	27, 40, 57, 90	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	127	VAL	4.6
1	O	127	VAL	4.2
1	G	127	VAL	3.8
1	D	127	VAL	3.2
1	C	127	VAL	3.0

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Mol	Chain	Res	Type	RSRZ
1	L	127	VAL	3.0
1	F	121	PHE	2.8
1	F	125	ASP	2.8
1	L	8	GLY	2.8
1	L	124	LEU	2.7
1	G	124	LEU	2.7
1	J	125	ASP	2.7
1	N	125	ASP	2.6
1	N	128	SER	2.6
1	L	155	ALA	2.6
1	O	125	ASP	2.6
1	J	126	LYS	2.5
1	F	155	ALA	2.4
1	L	125	ASP	2.4
1	D	128	SER	2.4
1	A	127	VAL	2.4
1	O	126	LYS	2.4
1	L	2	GLU	2.3
1	N	155	ALA	2.3
1	E	125	ASP	2.3
1	H	1	MET	2.3
1	B	127	VAL	2.3
1	D	125	ASP	2.3
1	K	123	LEU	2.3
1	J	2	GLU	2.2
1	F	118	ARG	2.2
1	E	121	PHE	2.2
1	G	70	ILE	2.2
1	L	7	ILE	2.2
1	H	127	VAL	2.2
1	D	123	LEU	2.2
1	F	1	MET	2.2
1	P	155	ALA	2.1
1	G	128	SER	2.1
1	G	126	LYS	2.1
1	L	1	MET	2.1
1	F	17	GLU	2.0
1	I	1	MET	2.0
1	F	87	LEU	2.0
1	G	123	LEU	2.0
1	B	2	GLU	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 oligosaccharides 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.