Full wwPDB X-ray Structure Validation Report ⓘ

Dec 16, 2023 – 12:05 PM EST

PDB ID	:	4OZD
Title	:	Crystal structure of PdSP15a
Authors	:	Andersen, J.F.; Alvarenga, P.H.
Deposited on	:	2014-02-14
Resolution	:	2.95 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:

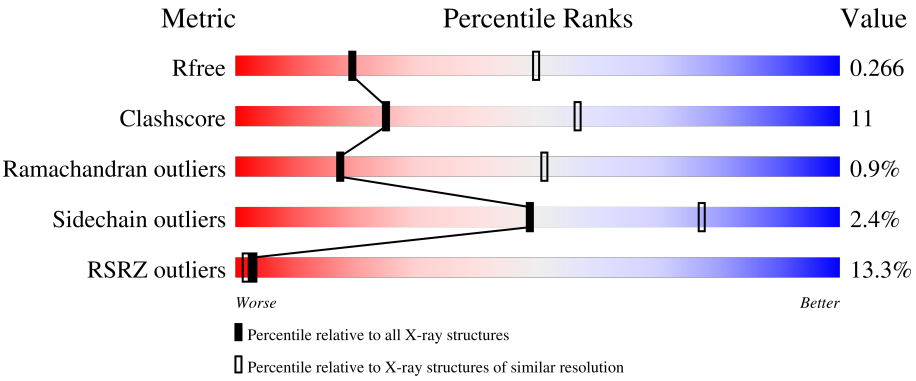
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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	122	8% 80% 17%
1	B	122	8% 80% 18%
1	C	122	16% 77% 20%
1	D	122	12% 80% 19%
1	E	122	11% 64% 27%

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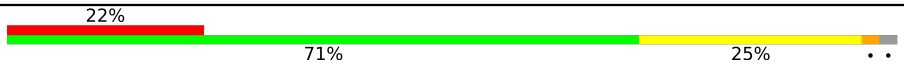
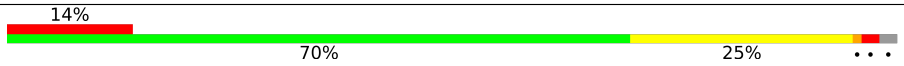
Mol	Chain	Length	Quality of chain
1	F	122	
1	G	122	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7008 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 14.4 kDa salivary protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	120	Total	C	N	O	S	0	0	0
			999	631	176	184	8			
1	B	120	Total	C	N	O	S	0	0	0
			999	631	176	184	8			
1	C	120	Total	C	N	O	S	0	0	0
			999	631	176	184	8			
1	D	120	Total	C	N	O	S	0	0	0
			999	631	176	184	8			
1	E	120	Total	C	N	O	S	0	0	0
			999	631	176	184	8			
1	F	120	Total	C	N	O	S	0	0	0
			999	631	176	184	8			
1	G	120	Total	C	N	O	S	0	0	0
			999	631	176	184	8			

- Molecule 2 is water.

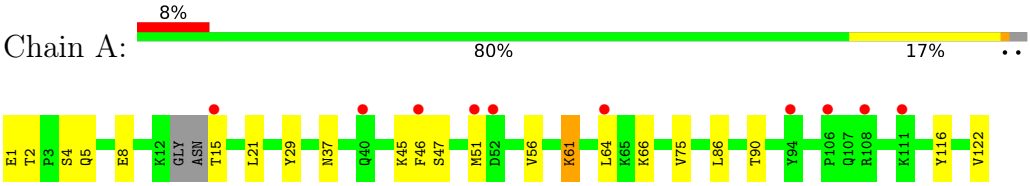
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	O	0	0
			4	4		
2	B	1	Total	O	0	0
			1	1		
2	C	2	Total	O	0	0
			2	2		
2	D	2	Total	O	0	0
			2	2		
2	F	4	Total	O	0	0
			4	4		
2	G	2	Total	O	0	0
			2	2		

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.

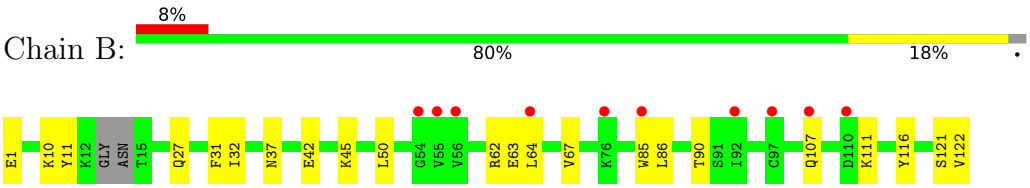
• Molecule 1: 14.4 kDa salivary protein

Chain A:



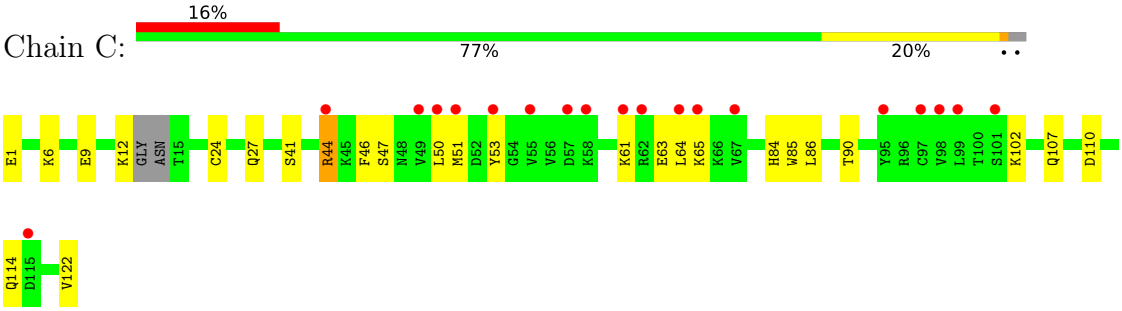
• Molecule 1: 14.4 kDa salivary protein

Chain B:



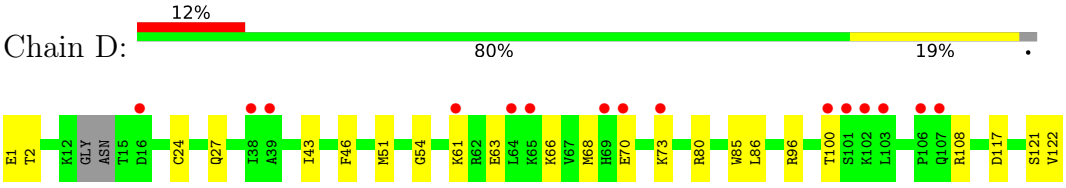
• Molecule 1: 14.4 kDa salivary protein

Chain C:



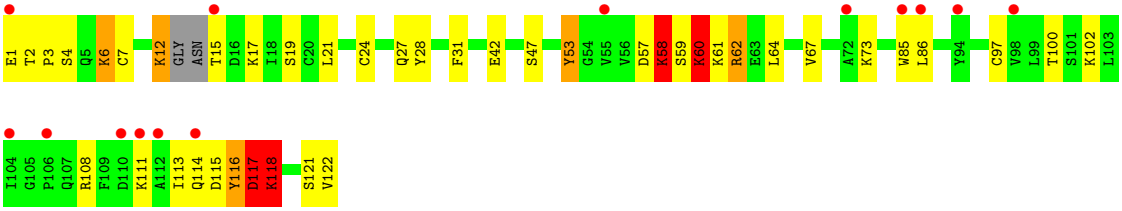
• Molecule 1: 14.4 kDa salivary protein

Chain D:

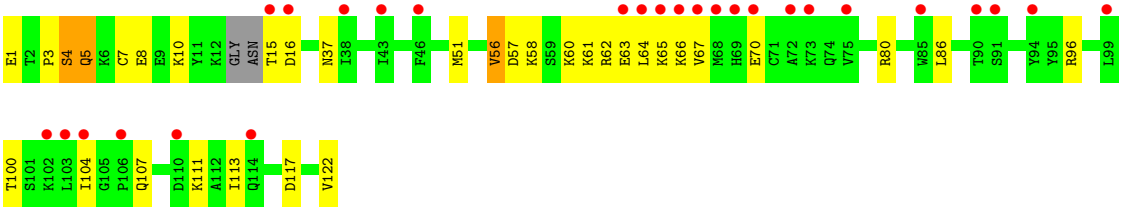


• Molecule 1: 14.4 kDa salivary protein

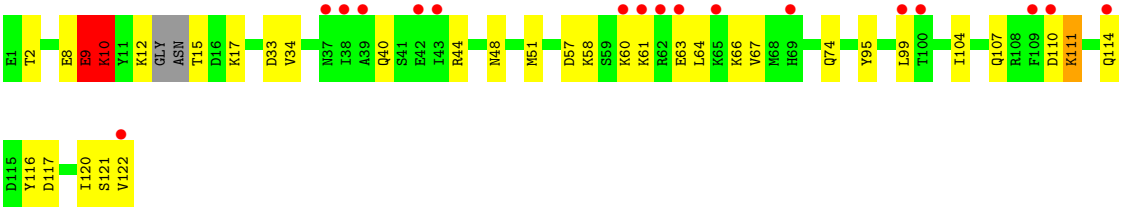
Chain E:



• Molecule 1: 14.4 kDa salivary protein



• Molecule 1: 14.4 kDa salivary protein



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	61.56Å 79.73Å 232.29Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.14 – 2.95 47.69 – 2.95	Depositor EDS
% Data completeness (in resolution range)	97.2 (40.14-2.95) 97.3 (47.69-2.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.42 (at 2.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.200 , 0.263 0.203 , 0.266	Depositor DCC
R_{free} test set	1210 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	77.9	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 72.5	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	7008	wwPDB-VP
Average B, all atoms (Å^2)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.37% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 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	0.22	0/1017	0.44	1/1359 (0.1%)
1	B	0.22	0/1017	0.42	0/1359
1	C	0.29	0/1017	0.49	0/1359
1	D	0.27	0/1017	0.46	0/1359
1	E	0.53	1/1017 (0.1%)	0.80	2/1359 (0.1%)
1	F	0.33	0/1017	0.59	0/1359
1	G	0.31	0/1017	0.66	1/1359 (0.1%)
All	All	0.33	1/7119 (0.0%)	0.57	4/9513 (0.0%)

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	E	0	3
1	F	0	1
1	G	0	1
All	All	0	5

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	6	LYS	CD-CE	-5.15	1.38	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	G	10	LYS	CA-CB-CG	6.93	128.65	113.40
1	E	118	LYS	CG-CD-CE	-5.79	94.53	111.90
1	A	15	THR	N-CA-CB	-5.11	100.59	110.30
1	E	53	TYR	CA-CB-CG	-5.02	103.87	113.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	116	TYR	Peptide
1	E	118	LYS	Peptide
1	E	60	LYS	Peptide
1	F	4	SER	Peptide
1	G	10	LYS	Peptide

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	999	0	1002	14	0
1	B	999	0	1002	13	0
1	C	999	0	1002	28	0
1	D	999	0	1002	16	0
1	E	999	0	1002	36	0
1	F	999	0	1002	29	0
1	G	999	0	1002	21	0
2	A	4	0	0	0	0
2	B	1	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	F	4	0	0	0	0
2	G	2	0	0	0	0
All	All	7008	0	7014	151	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 11.

All (151) 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:C:51:MET:CE	1:C:61:LYS:HD3	1.22	1.58
1:C:51:MET:CE	1:C:61:LYS:CD	2.17	1.22
1:C:51:MET:HE3	1:C:61:LYS:HD3	1.32	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:51:MET:HE1	1:C:61:LYS:HD3	1.13	1.05
1:C:51:MET:HE2	1:C:61:LYS:HD3	1.40	1.00
1:F:63:GLU:HA	1:F:66:LYS:HG2	1.58	0.86
1:F:51:MET:HG2	1:F:61:LYS:HE3	1.59	0.83
1:E:115:ASP:O	1:E:118:LYS:N	2.13	0.79
1:G:111:LYS:HA	1:G:114:GLN:HB3	1.65	0.78
1:G:10:LYS:HA	1:G:12:LYS:HG2	1.66	0.77
1:C:51:MET:HE1	1:C:61:LYS:CD	2.01	0.74
1:B:1:GLU:HA	1:B:122:VAL:HG13	1.70	0.73
1:E:1:GLU:H2	1:E:6:LYS:HE3	1.51	0.73
1:E:58:LYS:HG2	1:E:58:LYS:O	1.86	0.73
1:E:115:ASP:OD1	1:E:116:TYR:N	2.20	0.73
1:E:4:SER:OG	1:E:117:ASP:OD2	2.05	0.71
1:D:54:GLY:O	1:D:108:ARG:NH2	2.24	0.70
1:C:47:SER:OG	1:C:61:LYS:HD2	1.89	0.70
1:E:60:LYS:HA	1:E:62:ARG:HG3	1.74	0.70
1:E:108:ARG:HA	1:E:111:LYS:HE3	1.73	0.69
1:F:1:GLU:HA	1:F:122:VAL:HG23	1.74	0.69
1:D:80:ARG:NH2	1:F:104:ILE:O	2.24	0.69
1:C:41:SER:HA	1:C:44:ARG:HG3	1.72	0.69
1:D:46:PHE:HB3	1:D:68:MET:HE1	1.73	0.69
1:C:41:SER:O	1:C:44:ARG:NH1	2.27	0.68
1:G:40:GLN:O	1:G:44:ARG:HG3	1.94	0.67
1:C:51:MET:HE3	1:C:61:LYS:CD	2.07	0.66
1:E:102:LYS:HD2	1:E:102:LYS:H	1.61	0.65
1:F:51:MET:HG2	1:F:61:LYS:CE	2.26	0.65
1:D:51:MET:SD	1:D:61:LYS:NZ	2.69	0.65
1:C:51:MET:HE2	1:C:61:LYS:CD	2.09	0.64
1:E:1:GLU:O	1:E:121:SER:HA	1.96	0.64
1:E:47:SER:HB3	1:E:61:LYS:HE2	1.78	0.64
1:E:115:ASP:O	1:E:118:LYS:HG2	1.99	0.62
1:C:41:SER:HB2	1:C:44:ARG:HH11	1.63	0.62
1:E:1:GLU:HA	1:E:122:VAL:HA	1.81	0.62
1:D:70:GLU:HA	1:D:73:LYS:HG2	1.83	0.60
1:D:70:GLU:O	1:D:73:LYS:HE2	2.01	0.60
1:G:2:THR:OG1	1:G:117:ASP:O	2.20	0.60
1:C:102:LYS:N	1:C:102:LYS:HD2	2.17	0.59
1:D:122:VAL:HG22	1:F:15:THR:HA	1.84	0.59
1:G:61:LYS:HA	1:G:64:LEU:HB3	1.85	0.59
1:G:63:GLU:O	1:G:67:VAL:HG23	2.03	0.58
1:E:12:LYS:H	1:E:15:THR:HG22	1.68	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:80:ARG:NH2	1:G:104:ILE:O	2.26	0.58
1:F:107:GLN:O	1:F:111:LYS:HG3	2.04	0.57
1:G:48:ASN:HA	1:G:51:MET:HG2	1.87	0.57
1:F:5:GLN:HB3	1:F:8:GLU:H	1.69	0.57
1:E:57:ASP:O	1:E:59:SER:N	2.32	0.57
1:F:57:ASP:OD1	1:F:58:LYS:N	2.37	0.57
1:G:10:LYS:HA	1:G:12:LYS:H	1.70	0.56
1:C:9:GLU:O	1:C:12:LYS:HG2	2.06	0.56
1:A:45:LYS:NZ	1:A:116:TYR:OH	2.37	0.55
1:F:4:SER:N	1:F:117:ASP:OD1	2.39	0.55
1:F:122:VAL:HG12	1:G:15:THR:OG1	2.06	0.55
1:C:61:LYS:O	1:C:65:LYS:N	2.32	0.54
1:B:45:LYS:NZ	1:B:116:TYR:OH	2.40	0.54
1:D:1:GLU:HB2	1:D:122:VAL:HG12	1.89	0.54
1:E:53:TYR:CZ	1:E:118:LYS:NZ	2.71	0.53
1:D:63:GLU:OE1	1:D:66:LYS:HE3	2.08	0.53
1:A:51:MET:HE1	1:A:56:VAL:HB	1.90	0.53
1:C:102:LYS:HD2	1:C:102:LYS:H	1.74	0.53
1:F:37:ASN:ND2	1:G:95:TYR:OH	2.43	0.52
1:G:57:ASP:OD1	1:G:58:LYS:N	2.41	0.52
1:D:2:THR:OG1	1:D:117:ASP:O	2.28	0.52
1:A:8:GLU:HG2	1:A:21:LEU:HD11	1.91	0.51
1:E:102:LYS:HD2	1:E:102:LYS:N	2.25	0.51
1:B:50:LEU:HD12	1:B:64:LEU:HD21	1.92	0.51
1:G:60:LYS:HB3	1:G:63:GLU:OE1	2.10	0.51
1:E:1:GLU:N	1:E:6:LYS:HE3	2.23	0.51
1:E:116:TYR:HA	1:E:118:LYS:HG3	1.93	0.50
1:A:56:VAL:HG21	1:A:64:LEU:HD22	1.94	0.50
1:E:64:LEU:O	1:E:67:VAL:HG12	2.12	0.50
1:F:51:MET:SD	1:F:56:VAL:HG13	2.53	0.49
1:B:86:LEU:HA	1:B:90:THR:HG21	1.95	0.49
1:F:7:CYS:HA	1:F:10:LYS:HB3	1.93	0.49
1:F:63:GLU:O	1:F:67:VAL:HG23	2.13	0.48
1:B:27:GLN:HA	1:B:32:ILE:O	2.13	0.48
1:D:121:SER:HA	1:D:122:VAL:HA	1.52	0.48
1:A:29:TYR:O	1:A:45:LYS:NZ	2.44	0.48
1:E:58:LYS:O	1:E:58:LYS:CG	2.60	0.47
1:F:4:SER:O	1:F:5:GLN:HB2	2.12	0.47
1:C:50:LEU:HD12	1:C:64:LEU:HD21	1.95	0.47
1:E:111:LYS:O	1:E:115:ASP:HB3	2.14	0.47
1:C:63:GLU:OE1	1:C:63:GLU:N	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:66:LYS:HB3	1:G:66:LYS:HE2	1.64	0.47
1:C:1:GLU:HA	1:C:122:VAL:HG23	1.97	0.46
1:F:3:PRO:O	1:F:5:GLN:HG2	2.16	0.46
1:A:37:ASN:HA	1:A:86:LEU:HD12	1.98	0.46
1:F:5:GLN:HB3	1:F:7:CYS:N	2.31	0.46
1:F:5:GLN:HG3	1:F:7:CYS:HB2	1.97	0.46
1:G:121:SER:HA	1:G:122:VAL:HA	1.58	0.45
1:B:37:ASN:HA	1:B:86:LEU:HD12	1.97	0.45
1:C:51:MET:HE2	1:C:61:LYS:CG	2.46	0.45
1:A:4:SER:O	1:A:8:GLU:HG3	2.16	0.45
1:E:60:LYS:HE3	1:E:60:LYS:HB3	1.62	0.45
1:F:56:VAL:HG11	1:F:64:LEU:HD22	1.98	0.45
1:E:3:PRO:HG3	1:E:28:TYR:HB3	1.99	0.45
1:E:31:PHE:O	1:E:42:GLU:HB3	2.16	0.45
1:F:60:LYS:HB2	1:F:63:GLU:OE1	2.17	0.45
1:F:107:GLN:H	1:F:107:GLN:CD	2.20	0.45
1:B:31:PHE:O	1:B:42:GLU:HB3	2.17	0.44
1:D:85:TRP:CG	1:D:86:LEU:N	2.85	0.44
1:E:24:CYS:O	1:E:27:GLN:HG2	2.17	0.44
1:A:66:LYS:HE2	1:A:66:LYS:HB2	1.79	0.44
1:A:2:THR:OG1	1:A:5:GLN:HG3	2.17	0.44
1:D:66:LYS:O	1:D:70:GLU:HB2	2.18	0.44
1:E:6:LYS:N	1:E:6:LYS:HD3	2.31	0.44
1:A:47:SER:O	1:A:51:MET:HG2	2.17	0.44
1:E:6:LYS:HD3	1:E:6:LYS:HA	1.69	0.44
1:B:85:TRP:CG	1:B:86:LEU:N	2.86	0.44
1:E:17:LYS:HE3	1:E:19:SER:HB2	1.98	0.44
1:F:96:ARG:O	1:F:100:THR:HG23	2.17	0.44
1:F:113:ILE:O	1:F:117:ASP:HB2	2.18	0.44
1:E:97:CYS:O	1:E:100:THR:HG22	2.17	0.43
1:C:51:MET:O	1:C:53:TYR:N	2.50	0.43
1:A:1:GLU:HA	1:A:122:VAL:HG23	2.01	0.43
1:E:57:ASP:C	1:E:59:SER:H	2.21	0.43
1:E:85:TRP:CG	1:E:86:LEU:N	2.86	0.43
1:E:116:TYR:HA	1:E:118:LYS:HE3	1.99	0.43
1:B:63:GLU:O	1:B:67:VAL:HG23	2.19	0.43
1:F:62:ARG:HA	1:F:65:LYS:HB2	2.00	0.43
1:G:17:LYS:HA	1:G:17:LYS:HD2	1.87	0.43
1:C:86:LEU:HA	1:C:90:THR:HG21	2.01	0.43
1:F:80:ARG:NE	1:G:99:LEU:O	2.49	0.43
1:C:85:TRP:CG	1:C:86:LEU:N	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:113:ILE:O	1:E:116:TYR:N	2.51	0.43
1:G:8:GLU:O	1:G:9:GLU:O	2.37	0.43
1:E:2:THR:O	1:E:6:LYS:HE2	2.18	0.42
1:B:10:LYS:HE3	1:B:11:TYR:CZ	2.55	0.42
1:E:7:CYS:HB3	1:E:21:LEU:HD12	2.01	0.42
1:F:37:ASN:HA	1:F:86:LEU:HD12	2.01	0.42
1:C:110:ASP:O	1:C:114:GLN:HG2	2.19	0.42
1:B:121:SER:HA	1:B:122:VAL:HA	1.79	0.42
1:E:60:LYS:HA	1:E:62:ARG:CG	2.47	0.42
1:G:10:LYS:CA	1:G:12:LYS:HG2	2.44	0.42
1:A:51:MET:HE2	1:A:61:LYS:HG2	2.02	0.41
1:A:51:MET:CE	1:A:56:VAL:HB	2.50	0.41
1:C:84:HIS:ND1	1:C:85:TRP:O	2.42	0.41
1:D:96:ARG:O	1:D:100:THR:HG23	2.19	0.41
1:B:107:GLN:H	1:B:107:GLN:CD	2.23	0.41
1:C:51:MET:C	1:C:53:TYR:N	2.73	0.41
1:F:107:GLN:OE1	1:F:107:GLN:N	2.42	0.41
1:B:107:GLN:O	1:B:111:LYS:HG3	2.21	0.41
1:D:24:CYS:O	1:D:27:GLN:HG2	2.21	0.41
1:G:116:TYR:CE2	1:G:120:ILE:HD11	2.56	0.41
1:D:43:ILE:HG23	1:D:68:MET:HE2	2.03	0.41
1:A:75:VAL:HG13	1:A:90:THR:HB	2.04	0.41
1:C:6:LYS:HD2	1:C:122:VAL:HG22	2.04	0.40
1:G:33:ASP:OD1	1:G:34:VAL:N	2.51	0.40
1:C:24:CYS:O	1:C:27:GLN:HG2	2.22	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	116/122 (95%)	111 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	116/122 (95%)	111 (96%)	5 (4%)	0	100 100
1	C	116/122 (95%)	108 (93%)	7 (6%)	1 (1%)	17 51
1	D	116/122 (95%)	110 (95%)	6 (5%)	0	100 100
1	E	116/122 (95%)	98 (84%)	15 (13%)	3 (3%)	5 24
1	F	116/122 (95%)	105 (90%)	10 (9%)	1 (1%)	17 51
1	G	116/122 (95%)	111 (96%)	3 (3%)	2 (2%)	9 34
All	All	812/854 (95%)	754 (93%)	51 (6%)	7 (1%)	17 51

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	58	LYS
1	E	62	ARG
1	E	117	ASP
1	F	5	GLN
1	G	9	GLU
1	G	107	GLN
1	C	44	ARG

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	113/114 (99%)	111 (98%)	2 (2%)	59 82
1	B	113/114 (99%)	112 (99%)	1 (1%)	78 91
1	C	113/114 (99%)	111 (98%)	2 (2%)	59 82
1	D	113/114 (99%)	113 (100%)	0	100 100
1	E	113/114 (99%)	106 (94%)	7 (6%)	18 48
1	F	113/114 (99%)	110 (97%)	3 (3%)	44 74
1	G	113/114 (99%)	109 (96%)	4 (4%)	36 68
All	All	791/798 (99%)	772 (98%)	19 (2%)	49 77

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	PHE
1	A	61	LYS
1	B	62	ARG
1	C	46	PHE
1	C	107	GLN
1	E	12	LYS
1	E	58	LYS
1	E	60	LYS
1	E	73	LYS
1	E	114	GLN
1	E	117	ASP
1	E	118	LYS
1	F	16	ASP
1	F	56	VAL
1	F	70	GLU
1	G	9	GLU
1	G	74	GLN
1	G	110	ASP
1	G	111	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	107	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 monosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	120/122 (98%)	0.63	10 (8%)	11	6	48, 71, 110, 138	0
1	B	120/122 (98%)	0.62	10 (8%)	11	6	49, 74, 118, 157	0
1	C	120/122 (98%)	1.02	19 (15%)	2	1	46, 77, 124, 153	0
1	D	120/122 (98%)	0.92	15 (12%)	3	2	55, 80, 115, 153	0
1	E	120/122 (98%)	0.90	14 (11%)	4	2	55, 96, 156, 177	0
1	F	120/122 (98%)	1.02	27 (22%)	0	0	56, 97, 152, 166	0
1	G	120/122 (98%)	1.02	17 (14%)	2	1	61, 94, 143, 179	0
All	All	840/854 (98%)	0.88	112 (13%)	3	2	46, 82, 139, 179	0

All (112) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	103	LEU	6.1
1	F	94	TYR	5.4
1	G	43	ILE	5.3
1	E	112	ALA	5.2
1	F	67	VAL	5.2
1	C	64	LEU	4.9
1	G	69	HIS	4.8
1	C	50	LEU	4.5
1	G	38	ILE	4.5
1	F	106	PRO	4.3
1	F	15	THR	4.1
1	F	70	GLU	4.0
1	C	115	ASP	4.0
1	E	55	VAL	3.9
1	E	1	GLU	3.6
1	F	102	LYS	3.6
1	G	62	ARG	3.6

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Mol	Chain	Res	Type	RSRZ
1	G	110	ASP	3.6
1	E	106	PRO	3.5
1	E	15	THR	3.5
1	C	58	LYS	3.5
1	D	107	GLN	3.4
1	F	72	ALA	3.3
1	D	61	LYS	3.3
1	C	98	VAL	3.3
1	F	46	PHE	3.2
1	G	61	LYS	3.2
1	F	66	LYS	3.2
1	A	108	ARG	3.2
1	C	99	LEU	3.2
1	D	38	ILE	3.1
1	D	64	LEU	3.1
1	A	64	LEU	3.0
1	C	95	TYR	3.0
1	E	98	VAL	3.0
1	C	62	ARG	3.0
1	G	122	VAL	3.0
1	E	114	GLN	2.9
1	A	15	THR	2.9
1	D	103	LEU	2.9
1	C	44	ARG	2.9
1	C	51	MET	2.8
1	C	49	VAL	2.8
1	E	86	LEU	2.8
1	G	39	ALA	2.8
1	E	110	ASP	2.8
1	D	69	HIS	2.7
1	F	99	LEU	2.7
1	C	61	LYS	2.7
1	F	104	ILE	2.7
1	D	100	THR	2.6
1	G	99	LEU	2.6
1	C	65	LYS	2.6
1	G	60	LYS	2.6
1	E	104	ILE	2.6
1	F	75	VAL	2.6
1	A	111	LYS	2.6
1	G	109	PHE	2.6
1	B	64	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	94	TYR	2.5
1	D	102	LYS	2.5
1	G	42	GLU	2.5
1	B	85	TRP	2.4
1	C	57	ASP	2.4
1	B	55	VAL	2.4
1	F	64	LEU	2.4
1	G	63	GLU	2.4
1	F	69	HIS	2.4
1	G	114	GLN	2.4
1	E	72	ALA	2.4
1	F	91	SER	2.4
1	G	37	ASN	2.3
1	F	90	THR	2.3
1	F	114	GLN	2.3
1	A	40	GLN	2.3
1	D	39	ALA	2.3
1	E	94	TYR	2.3
1	B	56	VAL	2.3
1	D	70	GLU	2.3
1	D	16	ASP	2.3
1	F	65	LYS	2.3
1	F	73	LYS	2.3
1	C	97	CYS	2.2
1	G	100	THR	2.2
1	E	85	TRP	2.2
1	F	63	GLU	2.2
1	E	111	LYS	2.2
1	A	52	ASP	2.2
1	B	54	GLY	2.2
1	D	101	SER	2.2
1	C	55	VAL	2.2
1	B	76	LYS	2.2
1	C	67	VAL	2.2
1	F	85	TRP	2.2
1	F	16	ASP	2.2
1	F	110	ASP	2.2
1	C	101	SER	2.2
1	F	38	ILE	2.1
1	B	92	ILE	2.1
1	D	65	LYS	2.1
1	F	68	MET	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	107	GLN	2.1
1	B	110	ASP	2.1
1	C	53	TYR	2.1
1	B	97	CYS	2.1
1	A	46	PHE	2.1
1	G	65	LYS	2.1
1	F	43	ILE	2.0
1	A	106	PRO	2.0
1	D	106	PRO	2.0
1	D	73	LYS	2.0
1	A	51	MET	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 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.