Full wwPDB X-ray Structure Validation Report ⓘ

May 26, 2025 – 10:17 AM JST

PDB ID	:	8ZR1 / pdb_00008zr1
Title	:	Cocrystallization of engineered streptavidin with A9 oligo DNA
Authors	:	Minamihata, K.; Adachi, M.
Deposited on	:	2024-06-03
Resolution	:	2.60 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:

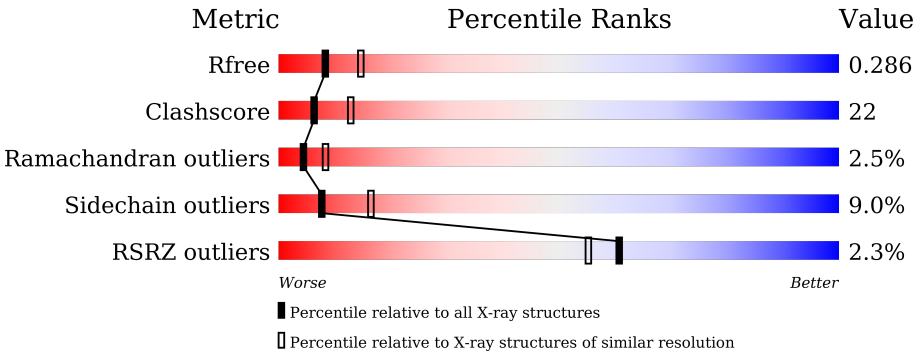
MolProbity	:	4-5-2 with Phenix2.0rc1
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 2.60 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}	164625	3775 (2.60-2.60)
Clashscore	180529	4181 (2.60-2.60)
Ramachandran outliers	177936	4129 (2.60-2.60)
Sidechain outliers	177891	4129 (2.60-2.60)
RSRZ outliers	164620	3775 (2.60-2.60)

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	132	3% 45% 41% 5% • 8%
1	B	132	2% 67% 22% • • 8%
1	C	132	3% 48% 38% 6% 8%
1	D	132	% 53% 36% • 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3784 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 Streptavidin.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	122	Total	C	N	O	0	1	0
			905	566	158	181			
1	B	122	Total	C	N	O	0	1	0
			905	566	158	181			
1	C	122	Total	C	N	O	0	1	0
			905	566	158	181			
1	D	122	Total	C	N	O	0	1	0
			905	566	158	181			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	140	ARG	-	expression tag	UNP P22629
A	141	ARG	-	expression tag	UNP P22629
A	142	ARG	-	expression tag	UNP P22629
A	143	ARG	-	expression tag	UNP P22629
A	144	ARG	-	expression tag	UNP P22629
A	145	ARG	-	expression tag	UNP P22629
A	146	TYR	-	expression tag	UNP P22629
B	140	ARG	-	expression tag	UNP P22629
B	141	ARG	-	expression tag	UNP P22629
B	142	ARG	-	expression tag	UNP P22629
B	143	ARG	-	expression tag	UNP P22629
B	144	ARG	-	expression tag	UNP P22629
B	145	ARG	-	expression tag	UNP P22629
B	146	TYR	-	expression tag	UNP P22629
C	140	ARG	-	expression tag	UNP P22629
C	141	ARG	-	expression tag	UNP P22629
C	142	ARG	-	expression tag	UNP P22629
C	143	ARG	-	expression tag	UNP P22629
C	144	ARG	-	expression tag	UNP P22629
C	145	ARG	-	expression tag	UNP P22629
C	146	TYR	-	expression tag	UNP P22629

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	140	ARG	-	expression tag	UNP P22629
D	141	ARG	-	expression tag	UNP P22629
D	142	ARG	-	expression tag	UNP P22629
D	143	ARG	-	expression tag	UNP P22629
D	144	ARG	-	expression tag	UNP P22629
D	145	ARG	-	expression tag	UNP P22629
D	146	TYR	-	expression tag	UNP P22629

- Molecule 2 is water.

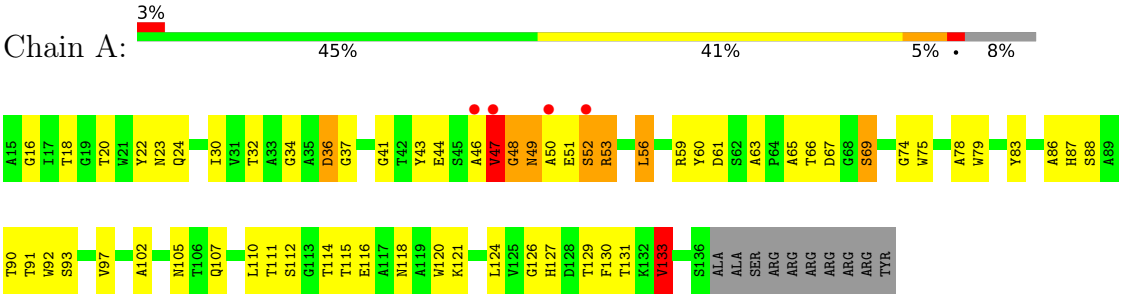
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	37	Total O 37 37	0	0
2	B	38	Total O 38 38	0	0
2	C	39	Total O 39 39	0	0
2	D	50	Total O 50 50	0	0

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.

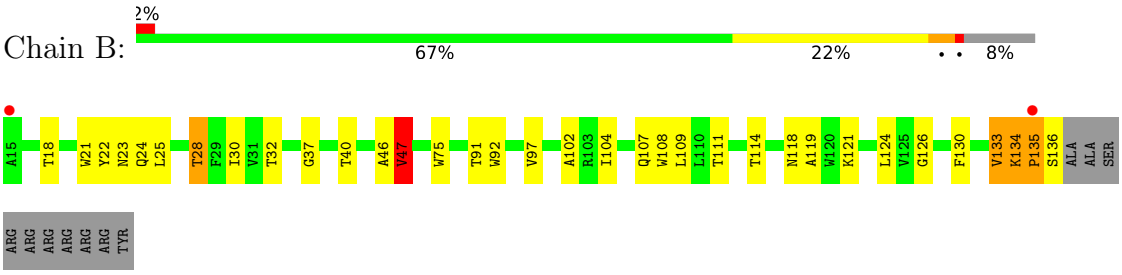
• Molecule 1: Streptavidin

Chain A:



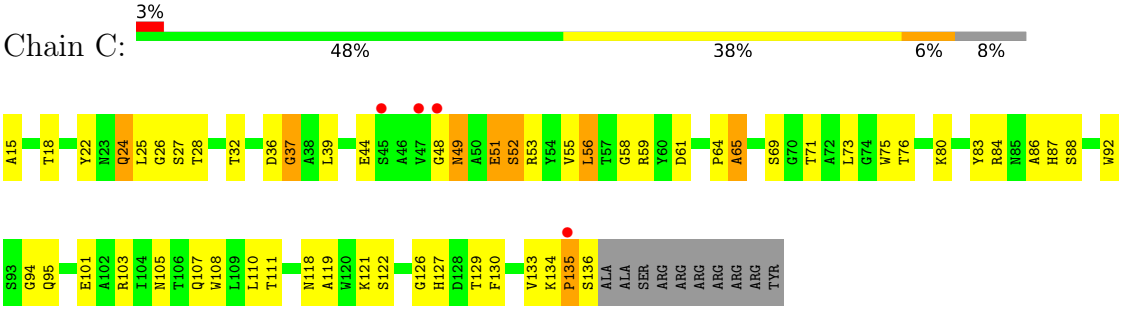
• Molecule 1: Streptavidin

Chain B:



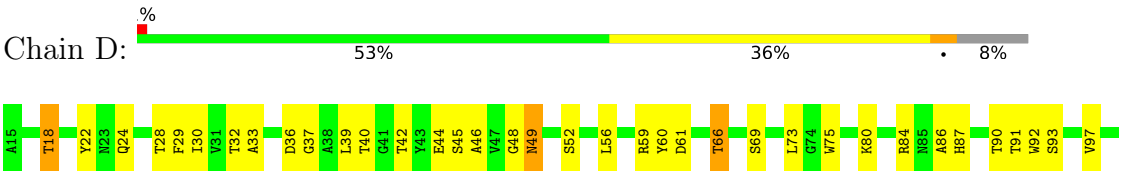
• Molecule 1: Streptavidin

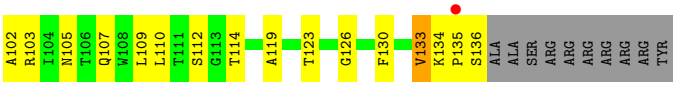
Chain C:



• Molecule 1: Streptavidin

Chain D:




A102
R103
I104
N105
T106
Q107
W108
L109
L110
T111
S112
G113
T114
A119
T123
G126
F130
V133
K134
P135
S136
ALA
ALA
SER
ARG
ARG
ARG
ARG
ARG
ARG
TYR

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	46.08Å 58.01Å 57.79Å 90.65° 107.54° 98.84°	Depositor
Resolution (Å)	37.66 – 2.60 37.66 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.6 (37.66-2.60) 88.4 (37.66-2.60)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.88 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.198 , 0.281 0.201 , 0.286	Depositor DCC
R_{free} test set	15873 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	24.0	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.40 , 73.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	3784	wwPDB-VP
Average B, all atoms (Å^2)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.46% 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	0.56	0/928	0.83	3/1271 (0.2%)
1	B	0.58	0/928	0.90	1/1271 (0.1%)
1	C	0.55	0/928	0.82	1/1271 (0.1%)
1	D	0.54	0/928	0.83	0/1271
All	All	0.56	0/3712	0.85	5/5084 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	133	VAL	N-CA-C	6.51	118.19	106.61
1	C	52	SER	N-CA-C	-5.68	106.01	113.17
1	A	133	VAL	N-CA-C	5.20	115.34	107.80
1	A	63	ALA	CA-C-N	-5.08	115.55	120.98
1	A	63	ALA	C-N-CA	-5.08	115.55	120.98

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	905	0	848	51	0
1	B	905	0	848	27	0
1	C	905	0	848	54	0
1	D	905	0	848	38	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	37	0	0	6	0
2	B	38	0	0	2	0
2	C	39	0	0	13	0
2	D	50	0	0	6	0
All	All	3784	0	3392	153	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 22.

All (153) 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:27:SER:N	2:C:203:HOH:O	1.89	1.05
1:A:44:GLU:OE2	1:A:49:ASN:O	1.73	1.05
1:D:48:GLY:O	1:D:49:ASN:HB2	1.53	1.04
1:C:15:ALA:O	2:C:201:HOH:O	1.77	1.02
1:B:136:SER:HA	2:B:221:HOH:O	1.62	0.98
1:C:36:ASP:OD2	2:C:202:HOH:O	1.87	0.90
1:C:26:GLY:C	2:C:203:HOH:O	2.11	0.90
1:B:121:LYS:HG3	1:B:121:LYS:O	1.73	0.86
1:C:44:GLU:OE2	1:C:53:ARG:HD3	1.74	0.86
1:A:24:GLN:HG2	2:A:208:HOH:O	1.79	0.82
1:C:24:GLN:OE1	1:C:135:PRO:HG3	1.80	0.82
1:C:121:LYS:O	1:C:121:LYS:HG3	1.80	0.78
1:A:44:GLU:OE2	1:A:50:ALA:HA	1.83	0.78
1:D:48:GLY:O	1:D:49:ASN:CB	2.28	0.77
1:A:44:GLU:HA	1:A:52:SER:O	1.85	0.76
1:C:52:SER:OG	2:C:204:HOH:O	2.05	0.75
1:B:121:LYS:O	1:B:121:LYS:CG	2.36	0.73
1:D:90:THR:OG1	1:D:110:LEU:HD13	1.89	0.73
1:D:66:THR:O	1:D:66:THR:HG23	1.88	0.73
1:C:121:LYS:O	1:C:121:LYS:CG	2.36	0.73
1:D:30:ILE:HD13	2:D:223:HOH:O	1.89	0.71
1:C:24:GLN:OE1	1:C:135:PRO:CG	2.39	0.70
1:D:135:PRO:O	1:D:136:SER:C	2.36	0.68
1:D:61:ASP:OD1	1:D:61:ASP:C	2.38	0.66
1:A:131:THR:HB	2:A:207:HOH:O	1.96	0.66
1:A:87:HIS:HA	1:C:61:ASP:OD2	1.95	0.65
1:C:118:ASN:O	1:C:119:ALA:C	2.39	0.65
1:D:59:ARG:NH2	2:D:202:HOH:O	2.20	0.64
1:D:103:ARG:HE	1:D:105:ASN:HD21	1.44	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:GLU:O	1:A:51:GLU:HG3	1.99	0.63
1:C:15:ALA:N	2:C:201:HOH:O	2.32	0.63
1:C:103:ARG:NH1	2:C:207:HOH:O	2.31	0.63
1:B:133:VAL:HG12	1:B:133:VAL:O	1.98	0.62
1:C:119:ALA:O	1:C:122:SER:HB3	2.00	0.62
1:A:65:ALA:HB2	1:C:87:HIS:CD2	2.36	0.60
1:D:22:TYR:O	1:D:130:PHE:HA	2.01	0.60
1:B:18:THR:HG23	1:B:32:THR:HA	1.83	0.60
1:C:88:SER:HB2	1:C:111:THR:O	2.02	0.59
1:A:110:LEU:HD23	1:A:124:LEU:HD12	1.83	0.59
1:A:51:GLU:HA	1:A:83:TYR:CD2	2.38	0.58
1:C:48:GLY:O	1:C:49:ASN:HB2	2.03	0.58
1:A:51:GLU:HA	1:A:83:TYR:HD2	1.67	0.58
1:C:39:LEU:O	1:C:58:GLY:N	2.34	0.58
1:C:88:SER:N	2:C:208:HOH:O	2.32	0.58
1:C:48:GLY:O	1:C:49:ASN:CB	2.52	0.57
1:D:44:GLU:HG2	1:D:46:ALA:O	2.04	0.57
1:A:105:ASN:OD1	1:A:129:THR:HG23	2.03	0.57
1:A:91:THR:HG21	1:C:92:TRP:O	2.05	0.57
1:D:29:PHE:HB2	1:D:42:THR:O	2.04	0.57
1:A:115:THR:O	1:A:116:GLU:C	2.49	0.56
1:B:22:TYR:O	1:B:130:PHE:HA	2.06	0.56
1:D:24:GLN:NE2	2:D:205:HOH:O	2.39	0.56
1:A:36:ASP:N	1:A:36:ASP:OD1	2.39	0.56
1:A:53:ARG:NH1	2:A:204:HOH:O	2.39	0.55
1:A:97[A]:VAL:O	1:A:102:ALA:HA	2.07	0.55
1:B:97[A]:VAL:O	1:B:102:ALA:HA	2.07	0.55
1:C:101:GLU:CB	2:C:223:HOH:O	2.54	0.55
1:B:133:VAL:O	1:B:134:LYS:O	2.25	0.55
1:B:46:ALA:O	1:B:47:VAL:C	2.49	0.55
1:B:91:THR:HG21	1:D:92:TRP:O	2.08	0.54
1:C:18:THR:HG23	1:C:32:THR:HA	1.88	0.54
1:B:114:THR:O	1:D:69:SER:HA	2.07	0.54
1:C:51:GLU:HB3	1:C:83:TYR:CD2	2.44	0.53
1:B:107:GLN:HE22	1:C:126:GLY:HA2	1.74	0.53
1:C:135:PRO:O	1:C:136:SER:C	2.51	0.53
1:D:37:GLY:O	1:D:59:ARG:HA	2.09	0.53
1:B:114:THR:OG1	1:B:119:ALA:HA	2.09	0.52
1:A:46:ALA:O	1:A:47:VAL:O	2.27	0.52
1:C:101:GLU:CB	2:C:207:HOH:O	2.57	0.52
1:C:24:GLN:HA	1:C:135:PRO:HG2	1.92	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:18:THR:HG23	1:A:32:THR:HA	1.92	0.51
1:B:23:ASN:HB3	1:B:130:PHE:CD2	2.45	0.51
1:C:108:TRP:CE2	1:C:126:GLY:HA3	2.45	0.51
1:A:107:GLN:HE22	1:D:126:GLY:HA2	1.76	0.51
1:B:24:GLN:HG2	1:B:25:LEU:HG	1.92	0.51
1:B:91:THR:HB	1:D:91:THR:HB	1.93	0.51
1:A:133:VAL:O	1:A:133:VAL:HG12	2.11	0.51
1:A:37:GLY:O	1:A:59:ARG:HA	2.12	0.49
1:C:103:ARG:HD3	2:C:207:HOH:O	2.13	0.49
1:C:94:GLY:HA3	1:C:105:ASN:O	2.13	0.49
1:D:97[A]:VAL:O	1:D:102:ALA:HA	2.13	0.49
1:B:135:PRO:O	1:B:136:SER:OG	2.28	0.49
1:A:47:VAL:O	1:A:48:GLY:C	2.55	0.49
1:B:107:GLN:NE2	1:C:126:GLY:HA2	2.28	0.49
1:C:80:LYS:HA	1:C:84:ARG:O	2.13	0.49
1:A:61:ASP:OD2	1:C:87:HIS:HA	2.14	0.48
1:D:33:ALA:HB1	1:D:60:TYR:CE1	2.48	0.48
1:A:110:LEU:HB3	1:A:124:LEU:HB2	1.96	0.48
1:B:92:TRP:O	1:D:91:THR:HG21	2.13	0.47
1:D:30:ILE:CD1	2:D:223:HOH:O	2.55	0.47
1:A:22:TYR:O	1:A:130:PHE:HA	2.14	0.47
1:A:20:THR:HG23	1:A:30:ILE:HG13	1.96	0.47
1:A:67:ASP:OD1	1:A:69:SER:OG	2.33	0.47
1:A:114:THR:O	1:C:69:SER:HA	2.14	0.47
1:A:112:SER:O	1:A:114:THR:HG23	2.14	0.47
1:A:107:GLN:HA	1:A:127:HIS:HA	1.97	0.46
1:A:23:ASN:HB3	1:A:130:PHE:CE2	2.51	0.46
1:A:44:GLU:CD	1:A:49:ASN:O	2.52	0.46
1:A:43:TYR:O	1:A:53:ARG:HA	2.15	0.46
1:C:64:PRO:HD2	2:C:217:HOH:O	2.15	0.46
1:C:86:ALA:O	1:C:87:HIS:C	2.60	0.45
1:C:134:LYS:HA	1:C:135:PRO:HD3	1.78	0.45
1:B:111:THR:OG1	2:B:201:HOH:O	2.16	0.45
1:C:133:VAL:HG12	1:C:134:LYS:O	2.17	0.45
1:D:39:LEU:HD11	1:D:60:TYR:HB3	1.99	0.45
1:D:18:THR:HB	1:D:32:THR:HA	1.97	0.45
1:A:90:THR:OG1	1:A:110:LEU:HD13	2.17	0.45
1:A:120:TRP:CE2	1:A:121:LYS:HG3	2.52	0.45
1:D:102:ALA:O	1:D:103:ARG:HB3	2.17	0.45
1:C:108:TRP:CZ2	1:C:126:GLY:HA3	2.52	0.44
1:A:65:ALA:HB2	1:C:87:HIS:NE2	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:22:TYR:CD2	1:D:134:LYS:HG2	2.53	0.44
1:A:56:LEU:C	1:A:56:LEU:HD23	2.43	0.44
1:C:56:LEU:C	1:C:56:LEU:HD23	2.43	0.44
1:C:71:THR:O	1:C:95:GLN:HA	2.18	0.43
1:B:109:LEU:HD11	1:D:109:LEU:HG	1.99	0.43
1:A:126:GLY:HA2	1:D:107:GLN:HE22	1.82	0.43
1:D:36:ASP:OD1	1:D:36:ASP:N	2.51	0.43
1:A:74:GLY:O	1:C:76:THR:HG21	2.19	0.43
1:C:36:ASP:OD1	1:C:36:ASP:N	2.39	0.43
1:A:75:TRP:NE1	1:A:92:TRP:CE3	2.86	0.43
1:C:24:GLN:O	1:C:25:LEU:HG	2.18	0.43
1:B:124:LEU:HA	1:B:124:LEU:HD23	1.81	0.43
1:C:73:LEU:HD13	1:C:75:TRP:HZ3	1.83	0.43
1:A:111:THR:HG21	1:C:94:GLY:HA2	2.01	0.43
1:C:64:PRO:C	1:C:65:ALA:O	2.61	0.43
1:D:133:VAL:O	1:D:133:VAL:HG12	2.18	0.43
1:A:23:ASN:OD1	1:A:23:ASN:C	2.61	0.42
1:A:79:TRP:HB2	1:A:86:ALA:HB3	2.01	0.42
1:D:134:LYS:NZ	2:D:201:HOH:O	2.14	0.42
1:D:75:TRP:NE1	1:D:92:TRP:CE3	2.87	0.42
1:A:88:SER:HA	1:A:111:THR:O	2.19	0.42
1:D:110:LEU:O	1:D:123:THR:HA	2.20	0.42
1:A:78:ALA:N	2:A:205:HOH:O	2.41	0.42
1:B:75:TRP:NE1	1:B:92:TRP:CE3	2.88	0.41
1:A:127:HIS:ND1	2:A:203:HOH:O	2.33	0.41
1:B:21:TRP:CZ3	1:B:104:ILE:HG13	2.54	0.41
1:C:22:TYR:O	1:C:130:PHE:HA	2.21	0.41
1:A:86:ALA:O	1:A:87:HIS:HB2	2.19	0.41
1:C:37:GLY:O	1:C:59:ARG:HA	2.20	0.41
1:D:86:ALA:O	1:D:87:HIS:C	2.64	0.41
1:D:114:THR:OG1	1:D:119:ALA:HA	2.21	0.41
1:A:30:ILE:O	1:A:41:GLY:HA3	2.21	0.41
1:A:34:GLY:O	1:A:60:TYR:OH	2.27	0.41
1:D:46:ALA:HB3	1:D:52:SER:OG	2.21	0.41
1:D:80:LYS:HA	1:D:84:ARG:O	2.20	0.41
1:C:55:VAL:HG23	2:C:218:HOH:O	2.20	0.41
1:A:87:HIS:N	2:A:206:HOH:O	2.46	0.41
1:B:108:TRP:CZ2	1:B:126:GLY:HA3	2.56	0.41
1:B:21:TRP:O	1:B:28:THR:HG23	2.21	0.40
1:B:23:ASN:HB3	1:B:130:PHE:CE2	2.56	0.40
1:D:92:TRP:NE1	2:D:204:HOH:O	2.39	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:107:GLN:HA	1:C:127:HIS:HA	2.04	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	120/132 (91%)	109 (91%)	8 (7%)	3 (2%)	4 8
1	B	120/132 (91%)	107 (89%)	9 (8%)	4 (3%)	3 5
1	C	120/132 (91%)	100 (83%)	16 (13%)	4 (3%)	3 5
1	D	120/132 (91%)	110 (92%)	9 (8%)	1 (1%)	16 34
All	All	480/528 (91%)	426 (89%)	42 (9%)	12 (2%)	4 8

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	VAL
1	B	47	VAL
1	B	134	LYS
1	C	49	ASN
1	D	49	ASN
1	A	48	GLY
1	B	135	PRO
1	A	16	GLY
1	C	65	ALA
1	C	135	PRO
1	B	37	GLY
1	C	37	GLY

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	89/98 (91%)	78 (88%)	11 (12%)	4 7
1	B	89/98 (91%)	84 (94%)	5 (6%)	17 38
1	C	89/98 (91%)	83 (93%)	6 (7%)	13 29
1	D	89/98 (91%)	79 (89%)	10 (11%)	5 9
All	All	356/392 (91%)	324 (91%)	32 (9%)	8 16

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	ASP
1	A	47	VAL
1	A	49	ASN
1	A	52	SER
1	A	53	ARG
1	A	56	LEU
1	A	66	THR
1	A	69	SER
1	A	93	SER
1	A	118	ASN
1	A	133	VAL
1	B	28	THR
1	B	30	ILE
1	B	40	THR
1	B	47	VAL
1	B	118	ASN
1	C	24	GLN
1	C	28	THR
1	C	51	GLU
1	C	56	LEU
1	C	110	LEU
1	C	129	THR
1	D	18	THR
1	D	28	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	40	THR
1	D	45	SER
1	D	56	LEU
1	D	66	THR
1	D	73	LEU
1	D	93	SER
1	D	112	SER
1	D	133	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	107	GLN
1	B	105	ASN
1	B	107	GLN
1	C	105	ASN
1	C	118	ASN
1	D	105	ASN

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 (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	122/132 (92%)	-0.19	4 (3%)	49	43	12, 26, 52, 76	0
1	B	122/132 (92%)	-0.21	2 (1%)	70	65	14, 25, 50, 78	0
1	C	122/132 (92%)	-0.11	4 (3%)	49	43	14, 27, 49, 74	0
1	D	122/132 (92%)	-0.26	1 (0%)	82	79	13, 24, 47, 80	0
All	All	488/528 (92%)	-0.20	11 (2%)	61	55	12, 26, 52, 80	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	45	SER	5.7
1	A	46	ALA	4.5
1	A	50	ALA	3.4
1	C	47	VAL	3.1
1	C	135	PRO	2.9
1	A	47	VAL	2.8
1	C	48	GLY	2.7
1	B	135	PRO	2.5
1	A	52	SER	2.4
1	D	135	PRO	2.2
1	B	15	ALA	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

There are no such residues in this entry.