Full wwPDB X-ray Structure Validation Report ⓘ

Dec 9, 2023 – 05:14 pm GMT

PDB ID	:	2BSE
Title	:	Structure of Lactococcal Bacteriophage p2 Receptor Binding Protein in complex with a llama VHH domain
Authors	:	Spinelli, S.; Desmyter, A.; Verrips, C.T.; de Haard, H.J.W.; Moineau, S.; Cambillau, C.
Deposited on	:	2005-05-20
Resolution	:	2.70 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:

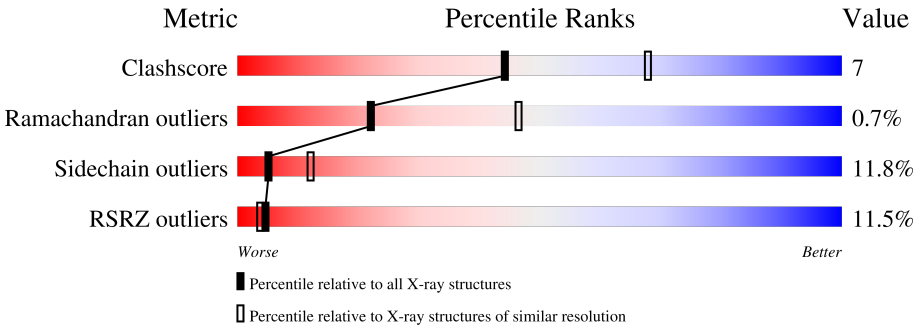
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.70 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))
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	264	34% 6% 59%
1	B	264	34% 6% 59%
1	C	264	34% 6% 59%
2	D	123	11% 65% 28% 6%
2	E	123	24% 74% 21%
2	F	123	20% 64% 32%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 5311 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 RECEPTOR BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			
1	B	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			
1	C	107	Total	C	N	O	S	4	0	0
			832	530	149	152	1			

- Molecule 2 is a protein called LLAMA IMMUNOGLOBULIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			
2	E	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			
2	F	122	Total	C	N	O	S	0	0	0
			938	581	165	186	6			

- Molecule 3 is water.

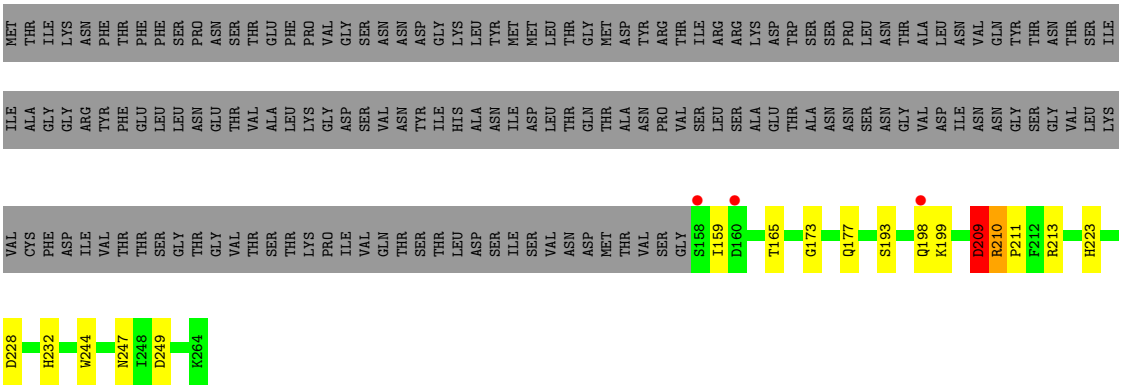
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total	O	0	0
			1	1		

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.

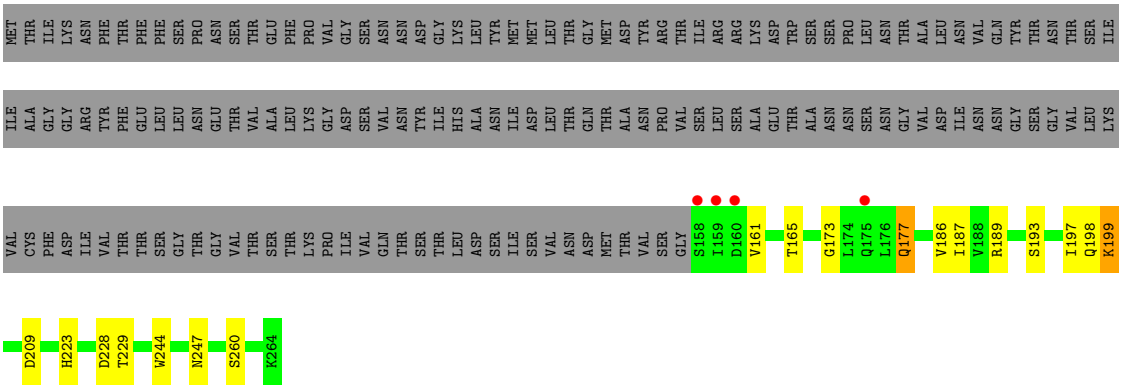
• Molecule 1: RECEPTOR BINDING PROTEIN

Chain A:



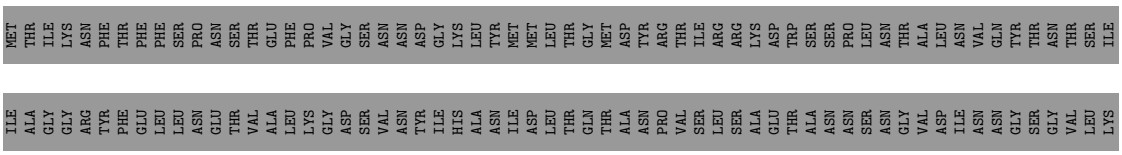
• Molecule 1: RECEPTOR BINDING PROTEIN

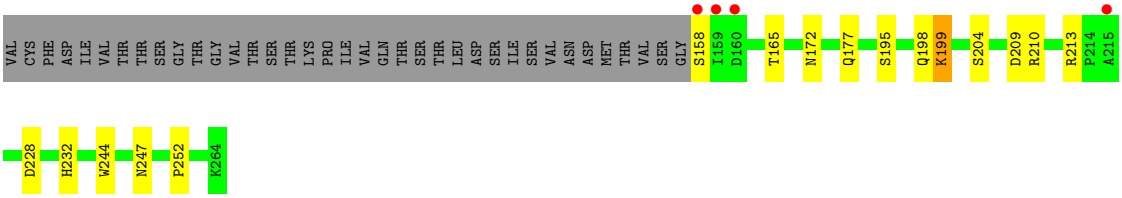
Chain B:



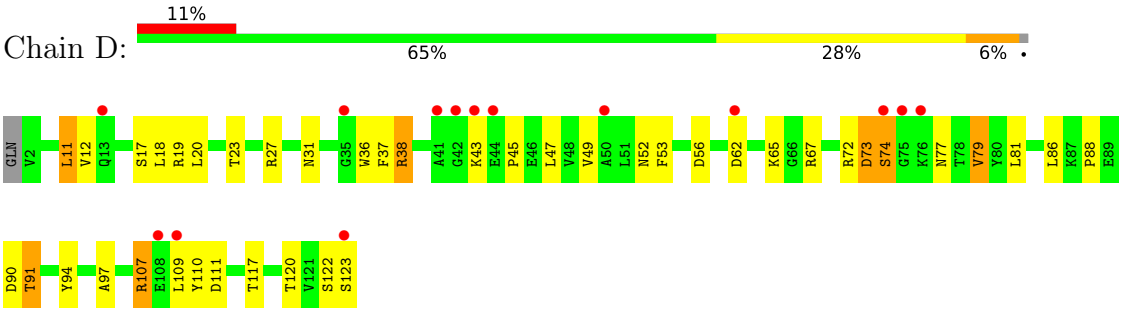
• Molecule 1: RECEPTOR BINDING PROTEIN

Chain C:

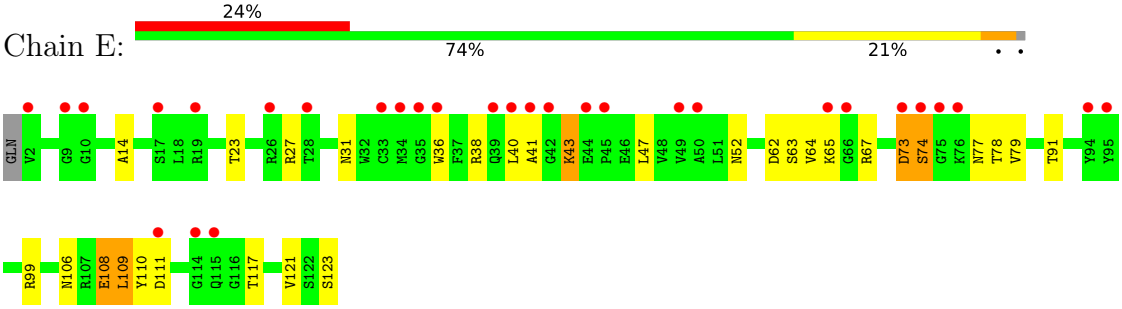




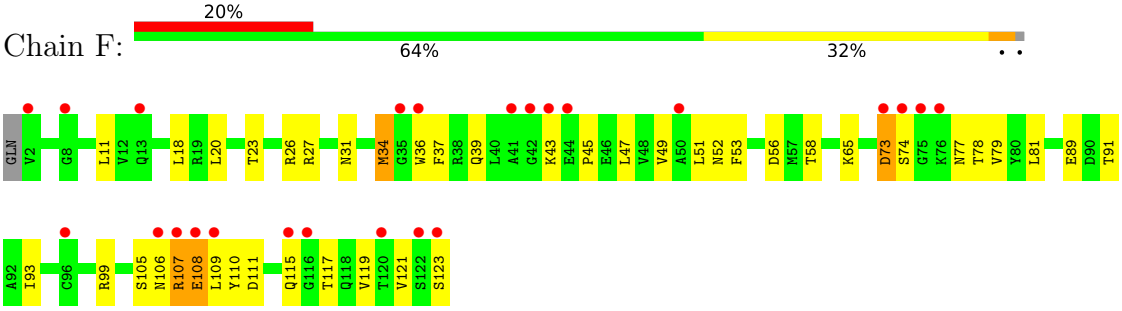
• Molecule 2: LLAMA IMMUNOGLOBULIN



• Molecule 2: LLAMA IMMUNOGLOBULIN



• Molecule 2: LLAMA IMMUNOGLOBULIN



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	74.76Å 83.94Å 137.79Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 2.70 19.99 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (15.00-2.70) 99.0 (19.99-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.31 (at 2.71Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.251 , 0.294 0.243 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	52.5	Xtriage
Anisotropy	0.491	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 28.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	5311	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.50% 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	0.34	0/853	0.66	2/1161 (0.2%)
1	B	0.33	0/853	0.66	1/1161 (0.1%)
1	C	0.35	0/853	0.66	1/1161 (0.1%)
2	D	0.36	0/956	0.70	4/1289 (0.3%)
2	E	0.33	0/956	0.65	3/1289 (0.2%)
2	F	0.32	0/956	0.66	3/1289 (0.2%)
All	All	0.34	0/5427	0.67	14/7350 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	73	ASP	CB-CG-OD2	5.89	123.60	118.30
2	D	56	ASP	CB-CG-OD2	5.78	123.50	118.30
1	B	209	ASP	CB-CG-OD2	5.76	123.49	118.30
2	F	111	ASP	CB-CG-OD2	5.74	123.47	118.30
1	C	209	ASP	CB-CG-OD2	5.54	123.29	118.30
2	E	111	ASP	CB-CG-OD2	5.42	123.18	118.30
2	E	73	ASP	CB-CG-OD2	5.37	123.13	118.30
2	F	56	ASP	CB-CG-OD2	5.32	123.09	118.30
2	E	62	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	209	ASP	CB-CG-OD2	5.15	122.94	118.30
2	F	73	ASP	CB-CG-OD2	5.15	122.93	118.30
2	D	62	ASP	CB-CG-OD2	5.13	122.92	118.30
1	A	249	ASP	CB-CG-OD2	5.08	122.87	118.30
2	D	111	ASP	CB-CG-OD2	5.00	122.80	118.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	832	0	819	9	0
1	B	832	0	819	11	0
1	C	832	0	819	14	0
2	D	938	0	891	13	0
2	E	938	0	891	11	0
2	F	938	0	891	19	0
3	D	1	0	0	0	0
All	All	5311	0	5130	69	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 7.

All (69) 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)
2:F:108:GLU:HG3	2:F:109:LEU:N	1.54	1.18
2:F:108:GLU:CG	2:F:109:LEU:H	1.64	1.08
1:C:199:LYS:H	1:C:247:ASN:ND2	1.64	0.94
2:F:108:GLU:HG3	2:F:109:LEU:H	0.76	0.91
1:C:198:GLN:HA	1:C:247:ASN:HD22	1.42	0.83
2:F:91:THR:HG22	2:F:121:VAL:H	1.45	0.82
2:E:91:THR:HG22	2:E:121:VAL:H	1.47	0.80
1:B:198:GLN:HA	1:B:247:ASN:OD1	1.83	0.78
1:A:244:TRP:HE1	2:E:31:ASN:HD21	1.39	0.69
1:A:223:HIS:ND1	1:C:232:HIS:HD2	1.91	0.69
2:D:88:PRO:O	2:D:91:THR:HG22	1.95	0.66
1:C:198:GLN:CA	1:C:247:ASN:HD22	2.12	0.63
1:C:199:LYS:N	1:C:247:ASN:ND2	2.44	0.61
2:D:37:PHE:CE1	2:D:47:LEU:HD23	2.38	0.59
2:F:20:LEU:HD12	2:F:81:LEU:HD23	1.85	0.59
1:A:232:HIS:HD2	1:B:223:HIS:ND1	2.02	0.58
1:B:198:GLN:CA	1:B:247:ASN:OD1	2.51	0.56
1:C:199:LYS:H	1:C:247:ASN:HD21	1.52	0.56
2:E:36:TRP:HZ3	2:E:79:VAL:HG12	1.71	0.55
1:B:199:LYS:N	1:B:247:ASN:OD1	2.40	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:72:ARG:HH21	2:D:74:SER:HA	1.72	0.54
2:F:108:GLU:CG	2:F:109:LEU:N	2.38	0.54
2:D:20:LEU:HD12	2:D:81:LEU:HD23	1.90	0.53
1:B:244:TRP:HE1	2:D:31:ASN:HD21	1.58	0.52
2:E:99:ARG:HB3	2:E:110:TYR:CD2	2.45	0.52
1:C:199:LYS:H	1:C:247:ASN:HD22	1.53	0.51
2:F:99:ARG:HB3	2:F:110:TYR:HA	1.92	0.50
2:F:51:LEU:HD12	2:F:58:THR:HG22	1.93	0.50
1:A:223:HIS:ND1	1:C:232:HIS:CD2	2.76	0.50
2:F:49:VAL:HG11	2:F:81:LEU:HD13	1.94	0.50
1:C:244:TRP:HE1	2:F:31:ASN:HD21	1.58	0.50
1:C:172:ASN:HD21	1:C:204:SER:H	1.60	0.49
1:C:210:ARG:HA	1:C:213:ARG:HD2	1.95	0.49
2:F:107:ARG:N	2:F:107:ARG:HD3	2.29	0.48
2:E:23:THR:HG22	2:E:78:THR:HG23	1.95	0.47
2:F:34:MET:HG3	2:F:53:PHE:CE1	2.49	0.47
1:B:177:GLN:OE1	1:B:189:ARG:NH1	2.48	0.47
2:E:64:VAL:HA	2:E:67:ARG:HH11	1.79	0.46
2:E:91:THR:HG22	2:E:121:VAL:N	2.25	0.46
1:B:229:THR:HB	1:C:228:ASP:HB2	1.98	0.46
2:F:23:THR:HG22	2:F:78:THR:HG23	1.97	0.46
2:D:11:LEU:HG	2:D:120:THR:HB	1.97	0.45
1:A:173:GLY:HA3	1:A:193:SER:O	2.16	0.45
2:D:67:ARG:NH2	2:D:90:ASP:OD2	2.50	0.45
2:D:36:TRP:CZ3	2:D:79:VAL:HG12	2.52	0.44
1:A:198:GLN:HA	1:A:247:ASN:OD1	2.17	0.44
2:F:18:LEU:HD23	2:F:119:VAL:HG13	2.00	0.44
2:E:14:ALA:HB2	2:E:123:SER:HA	2.00	0.44
2:E:40:LEU:HB2	2:E:43:LYS:HB2	1.99	0.44
2:F:37:PHE:CE1	2:F:47:LEU:HD23	2.52	0.44
2:F:20:LEU:HB2	2:F:81:LEU:HB3	2.00	0.43
2:D:12:VAL:HB	2:D:18:LEU:HD13	2.00	0.43
1:B:186:VAL:O	1:B:260:SER:HA	2.19	0.42
1:C:199:LYS:N	1:C:247:ASN:HD22	2.13	0.42
1:A:232:HIS:CD2	1:B:223:HIS:ND1	2.85	0.42
2:E:36:TRP:CZ3	2:E:79:VAL:HG12	2.53	0.42
1:B:187:ILE:HG12	1:B:260:SER:HB3	2.00	0.42
1:C:195:SER:HB3	1:C:252:PRO:HA	2.01	0.41
1:A:209:ASP:HB3	1:A:211:PRO:HD2	2.03	0.41
2:D:45:PRO:HG2	2:D:107:ARG:HH22	1.85	0.41
2:F:39:GLN:HG3	2:F:45:PRO:HG3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:53:PHE:CE2	2:D:72:ARG:HD2	2.56	0.41
2:F:106:ASN:HA	2:F:107:ARG:HH11	1.86	0.41
1:A:210:ARG:HA	1:A:213:ARG:HD2	2.02	0.41
2:D:38:ARG:HD2	2:D:94:TYR:OH	2.21	0.41
2:E:108:GLU:CG	2:E:109:LEU:N	2.83	0.41
2:D:97:ALA:HB1	2:D:110:TYR:CD2	2.57	0.40
2:F:36:TRP:CZ3	2:F:79:VAL:HG12	2.55	0.40
1:B:173:GLY:HA3	1:B:193:SER:O	2.21	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	105/264 (40%)	102 (97%)	3 (3%)	0	100 100
1	B	105/264 (40%)	102 (97%)	3 (3%)	0	100 100
1	C	105/264 (40%)	102 (97%)	3 (3%)	0	100 100
2	D	120/123 (98%)	114 (95%)	5 (4%)	1 (1%)	19 43
2	E	120/123 (98%)	114 (95%)	3 (2%)	3 (2%)	5 14
2	F	120/123 (98%)	113 (94%)	6 (5%)	1 (1%)	19 43
All	All	675/1161 (58%)	647 (96%)	23 (3%)	5 (1%)	22 46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	74	SER
2	E	108	GLU
2	F	74	SER
2	E	41	ALA
2	E	74	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	90/228 (40%)	83 (92%)	7 (8%)	12 29
1	B	90/228 (40%)	84 (93%)	6 (7%)	16 37
1	C	90/228 (40%)	86 (96%)	4 (4%)	28 56
2	D	99/100 (99%)	79 (80%)	20 (20%)	1 3
2	E	99/100 (99%)	86 (87%)	13 (13%)	4 10
2	F	99/100 (99%)	82 (83%)	17 (17%)	2 5
All	All	567/984 (58%)	500 (88%)	67 (12%)	5 12

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	159	ILE
1	A	165	THR
1	A	177	GLN
1	A	199	LYS
1	A	209	ASP
1	A	210	ARG
1	A	228	ASP
1	B	161	VAL
1	B	165	THR
1	B	177	GLN
1	B	197	ILE
1	B	199	LYS
1	B	228	ASP
1	C	158	SER
1	C	165	THR
1	C	177	GLN
1	C	199	LYS
2	D	11	LEU
2	D	17	SER
2	D	19	ARG
2	D	23	THR
2	D	27	ARG

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Mol	Chain	Res	Type
2	D	38	ARG
2	D	43	LYS
2	D	49	VAL
2	D	52	ASN
2	D	65	LYS
2	D	73	ASP
2	D	77	ASN
2	D	79	VAL
2	D	86	LEU
2	D	91	THR
2	D	107	ARG
2	D	109	LEU
2	D	117	THR
2	D	122	SER
2	D	123	SER
2	E	27	ARG
2	E	38	ARG
2	E	43	LYS
2	E	47	LEU
2	E	52	ASN
2	E	63	SER
2	E	65	LYS
2	E	73	ASP
2	E	74	SER
2	E	77	ASN
2	E	106	ASN
2	E	109	LEU
2	E	117	THR
2	F	11	LEU
2	F	26	ARG
2	F	27	ARG
2	F	34	MET
2	F	43	LYS
2	F	52	ASN
2	F	65	LYS
2	F	73	ASP
2	F	77	ASN
2	F	89	GLU
2	F	93	ILE
2	F	105	SER
2	F	107	ARG
2	F	108	GLU

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Mol	Chain	Res	Type
2	F	115	GLN
2	F	117	THR
2	F	123	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	172	ASN
1	A	175	GLN
1	A	177	GLN
1	A	232	HIS
1	A	236	ASN
1	B	164	GLN
1	B	172	ASN
1	B	175	GLN
1	B	183	ASN
1	B	232	HIS
1	B	236	ASN
1	C	172	ASN
1	C	177	GLN
1	C	183	ASN
1	C	232	HIS
1	C	236	ASN
1	C	247	ASN
2	D	31	ASN
2	D	52	ASN
2	D	106	ASN
2	E	31	ASN
2	E	52	ASN
2	E	106	ASN
2	F	31	ASN
2	F	52	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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	107/264 (40%)	-0.04	3 (2%)	53	54	13, 20, 31, 41	1 (0%)
1	B	107/264 (40%)	-0.14	4 (3%)	41	41	14, 20, 31, 41	1 (0%)
1	C	107/264 (40%)	-0.18	4 (3%)	41	41	14, 20, 31, 41	1 (0%)
2	D	122/123 (99%)	0.75	14 (11%)	4	4	19, 26, 34, 38	0
2	E	122/123 (99%)	1.40	30 (24%)	0	0	20, 26, 33, 37	0
2	F	122/123 (99%)	1.06	24 (19%)	1	0	20, 26, 34, 37	0
All	All	687/1161 (59%)	0.51	79 (11%)	4	4	13, 23, 34, 41	3 (0%)

All (79) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	2	VAL	10.2
2	E	41	ALA	8.8
2	D	42	GLY	8.7
2	D	75	GLY	7.8
2	D	123	SER	7.7
2	E	42	GLY	7.3
2	E	39	GLN	7.2
2	F	123	SER	6.9
2	E	76	LYS	6.5
2	D	74	SER	5.6
2	F	75	GLY	5.6
2	F	109	LEU	5.1
2	E	75	GLY	5.0
2	F	2	VAL	5.0
2	F	76	LYS	4.9
2	D	109	LEU	4.8
2	E	114	GLY	4.7
1	C	160	ASP	4.6
2	F	74	SER	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	160	ASP	4.2
2	E	45	PRO	4.2
2	F	42	GLY	4.2
2	F	41	ALA	4.1
2	F	44	GLU	4.0
2	F	108	GLU	3.8
2	E	9	GLY	3.8
2	E	35	GLY	3.7
2	E	73	ASP	3.7
2	E	74	SER	3.5
2	D	44	GLU	3.4
2	E	66	GLY	3.4
2	E	26	ARG	3.4
2	F	73	ASP	3.4
2	E	28	THR	3.3
2	E	36	TRP	3.3
1	B	158	SER	3.3
2	F	13	GLN	3.3
2	D	41	ALA	3.2
2	F	35	GLY	3.1
1	C	158	SER	3.1
2	E	49	VAL	3.1
2	E	17	SER	3.0
2	F	107	ARG	3.0
2	F	106	ASN	2.9
2	E	44	GLU	2.9
2	D	76	LYS	2.8
2	D	35	GLY	2.8
1	A	160	ASP	2.8
2	E	10	GLY	2.8
2	F	36	TRP	2.7
2	E	115	GLN	2.7
2	E	40	LEU	2.7
2	F	43	LYS	2.6
1	C	159	ILE	2.6
1	A	158	SER	2.6
2	D	108	GLU	2.5
2	D	43	LYS	2.5
2	E	33	CYS	2.5
2	E	65	LYS	2.4
2	D	13	GLN	2.4
1	B	175	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
2	E	50	ALA	2.3
2	F	8	GLY	2.3
2	F	115	GLN	2.3
2	F	116	GLY	2.3
1	B	159	ILE	2.3
2	F	122	SER	2.2
2	F	96	CYS	2.2
2	E	94	TYR	2.2
1	A	198	GLN	2.2
2	D	62	ASP	2.2
2	F	120	THR	2.2
2	E	111	ASP	2.1
2	E	95	TYR	2.1
1	C	215	ALA	2.1
2	D	50	ALA	2.1
2	E	19	ARG	2.1
2	E	34	MET	2.0
2	F	50	ALA	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.