Full wwPDB X-ray Structure Validation Report ⓘ

Nov 7, 2023 – 12:26 PM EST

PDB ID	:	3BVN
Title	:	High resolution crystal structure of HLA-B*1402 in complex with the latent membrane protein 2 peptide (LMP2) of Epstein-Barr virus
Authors	:	Kumar, P.; Vahedi-Faridi, A.; Saenger, W.; Uchanska-Ziegler, B.; Ziegler, A.
Deposited on	:	2008-01-07
Resolution	:	2.55 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:

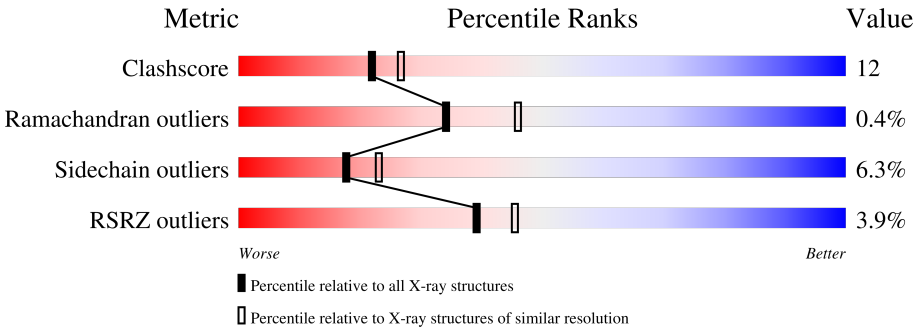
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 2.55 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	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	278	5% 71% 24%
1	D	278	4% 77% 21%
2	B	100	77% 20%
2	E	100	2% 75% 23%
3	C	9	56% 22% 22%
3	F	9	22% 44% 44% 11%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6615 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 HLA class I histocompatibility antigen, B*1402 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	277	Total	C	N	O	S	0	0	0
			2261	1405	411	438	7			
1	D	277	Total	C	N	O	S	0	0	0
			2261	1405	411	438	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP Q56H30
D	0	MET	-	initiating methionine	UNP Q56H30

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			
2	E	99	Total	C	N	O	S	0	0	0
			829	528	140	158	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769
E	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called Latent membrane protein 2 peptide.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			92	56	25	11			
3	F	9	Total	C	N	O	0	0	0
			92	56	25	11			

- Molecule 4 is water.

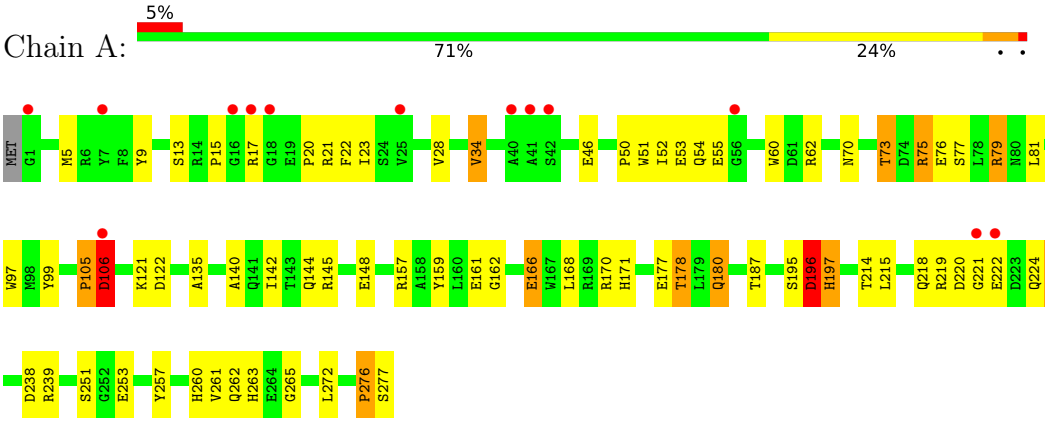
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	85	Total O 85 85	0	0
4	B	27	Total O 27 27	0	0
4	C	5	Total O 5 5	0	0
4	D	94	Total O 94 94	0	0
4	E	33	Total O 33 33	0	0
4	F	7	Total O 7 7	0	0

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.

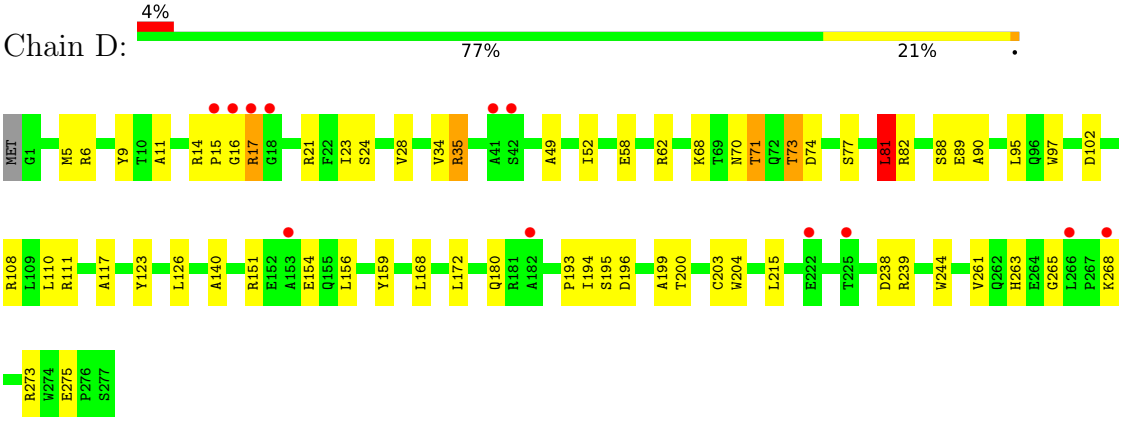
• Molecule 1: HLA class I histocompatibility antigen, B*1402 alpha chain

Chain A:



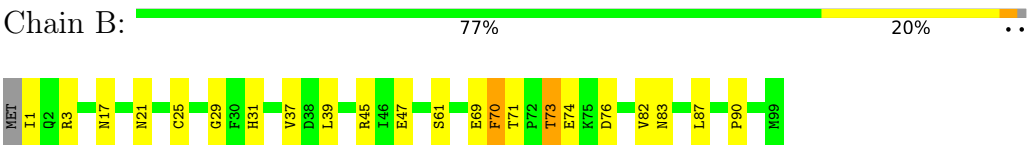
• Molecule 1: HLA class I histocompatibility antigen, B*1402 alpha chain

Chain D:



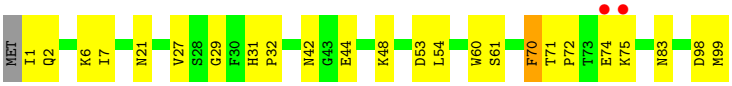
• Molecule 2: Beta-2-microglobulin

Chain B:



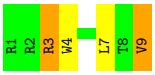
• Molecule 2: Beta-2-microglobulin

Chain E:



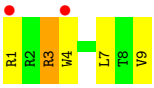
• Molecule 3: Latent membrane protein 2 peptide

Chain C:



• Molecule 3: Latent membrane protein 2 peptide

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	53.38Å 79.95Å 105.44Å 90.00° 99.51° 90.00°	Depositor
Resolution (Å)	50.00 – 2.55 29.63 – 2.55	Depositor EDS
% Data completeness (in resolution range)	80.8 (50.00-2.55) 84.9 (29.63-2.55)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.33 (at 2.54Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.240 , 0.268 0.252 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å^2)	26.9	Xtriage
Anisotropy	0.270	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 43.2	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	0.90	EDS
Total number of atoms	6615	wwPDB-VP
Average B, all atoms (Å^2)	26.0	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 19.84 % 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 9.9120e-03. 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	0.57	1/2325 (0.0%)	0.84	9/3163 (0.3%)
1	D	0.47	0/2325	0.72	3/3163 (0.1%)
2	B	0.44	0/852	0.68	0/1152
2	E	0.53	0/852	0.71	0/1152
3	C	0.46	0/93	0.73	0/121
3	F	0.48	0/93	0.72	0/121
All	All	0.51	1/6540 (0.0%)	0.76	12/8872 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	196	ASP	CB-CG	-5.48	1.40	1.51

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	106	ASP	N-CA-C	-7.43	90.93	111.00
1	A	225	THR	N-CA-C	6.45	128.42	111.00
1	D	81	LEU	CA-CB-CG	6.26	129.69	115.30
1	A	105	PRO	N-CA-C	-6.02	96.44	112.10
1	A	225	THR	N-CA-CB	5.97	121.64	110.30
1	A	28	VAL	N-CA-C	-5.41	96.41	111.00
1	A	230	LEU	CA-CB-CG	5.35	127.61	115.30
1	D	28	VAL	N-CA-C	-5.24	96.85	111.00
1	D	81	LEU	CB-CG-CD2	-5.23	102.11	111.00
1	A	106	ASP	CB-CG-OD1	5.12	122.91	118.30
1	A	106	ASP	CB-CG-OD2	-5.09	113.72	118.30
1	A	225	THR	CB-CA-C	-5.05	97.95	111.60

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	2261	0	2104	61	0
1	D	2261	0	2104	54	0
2	B	829	0	794	14	0
2	E	829	0	794	22	0
3	C	92	0	104	4	0
3	F	92	0	104	4	0
4	A	85	0	0	9	0
4	B	27	0	0	3	0
4	C	5	0	0	0	0
4	D	94	0	0	5	0
4	E	33	0	0	3	0
4	F	7	0	0	1	0
All	All	6615	0	6004	146	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 12.

All (146) 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:D:82:ARG:HD2	1:D:89:GLU:OE1	1.39	1.22
1:A:196:ASP:HB3	1:A:197:HIS:ND1	1.63	1.11
1:D:17:ARG:CB	1:D:17:ARG:HH11	1.64	1.09
1:A:105:PRO:O	1:A:106:ASP:HB3	1.51	1.07
1:D:17:ARG:HH11	1:D:17:ARG:HB2	1.22	1.01
1:A:196:ASP:HB3	1:A:197:HIS:CE1	1.99	0.97
1:D:21:ARG:HE	1:D:23:ILE:HD11	1.32	0.89
1:A:162:GLY:O	1:A:166:GLU:HG3	1.73	0.89
1:D:82:ARG:CD	1:D:89:GLU:OE1	2.24	0.84
1:A:79:ARG:HH11	1:A:79:ARG:HG2	1.45	0.81
1:A:214:THR:HB	1:A:262:GLN:HG3	1.62	0.80
2:E:1:ILE:HG23	2:E:2:GLN:H	1.46	0.80
2:E:7:ILE:HD12	2:E:27:VAL:HG12	1.65	0.79
2:E:74:GLU:HG2	4:E:120:HOH:O	1.82	0.78
2:E:1:ILE:HG23	2:E:2:GLN:N	2.00	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:ASP:CB	1:A:197:HIS:CE1	2.69	0.74
1:A:79:ARG:HG2	1:A:79:ARG:NH1	2.03	0.73
1:A:77:SER:HB3	3:C:9:VAL:HG13	1.72	0.71
1:D:151:ARG:HH11	1:D:151:ARG:HG3	1.56	0.71
1:A:70:ASN:HA	1:A:73:THR:HG23	1.74	0.69
1:D:17:ARG:HB2	1:D:17:ARG:NH1	2.03	0.69
1:D:17:ARG:HH11	1:D:17:ARG:CG	2.05	0.69
1:A:276:PRO:O	1:A:277:SER:HB2	1.93	0.68
1:A:263:HIS:CD2	1:A:265:GLY:H	2.14	0.66
1:D:17:ARG:CB	1:D:17:ARG:NH1	2.49	0.65
1:A:20:PRO:HD3	1:A:75:ARG:HH21	1.61	0.65
1:A:162:GLY:O	1:A:166:GLU:CG	2.45	0.64
1:A:105:PRO:O	1:A:106:ASP:CB	2.34	0.62
1:D:263:HIS:CD2	1:D:265:GLY:H	2.17	0.62
1:D:70:ASN:HA	1:D:73:THR:HG23	1.83	0.61
1:D:151:ARG:HD2	1:D:154:GLU:OE2	2.01	0.60
1:A:238:ASP:O	1:A:239:ARG:HB2	2.02	0.60
1:A:178:THR:HB	4:A:343:HOH:O	2.01	0.59
1:D:126:LEU:HD22	1:D:156:LEU:HD13	1.84	0.59
2:E:1:ILE:CG2	2:E:2:GLN:H	2.15	0.59
1:A:220:ASP:O	1:A:222:GLU:N	2.36	0.58
1:A:121:LYS:HG3	2:B:1:ILE:HG13	1.85	0.58
1:D:151:ARG:HG3	1:D:151:ARG:NH1	2.18	0.58
1:A:79:ARG:HH11	1:A:79:ARG:CG	2.17	0.57
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.84	0.57
1:D:17:ARG:NH1	1:D:17:ARG:CG	2.63	0.57
1:D:24:SER:HB2	4:D:341:HOH:O	2.05	0.57
1:A:224:GLN:NE2	4:A:290:HOH:O	2.38	0.56
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.41	0.56
1:D:5:MET:HB2	1:D:168:LEU:HD13	1.88	0.56
1:A:20:PRO:HD3	1:A:75:ARG:NH2	2.22	0.55
1:D:16:GLY:C	1:D:17:ARG:HG2	2.27	0.55
2:E:6:LYS:O	2:E:7:ILE:HD13	2.07	0.55
2:E:1:ILE:CG2	2:E:2:GLN:N	2.70	0.54
1:A:180:GLN:HA	4:A:319:HOH:O	2.06	0.54
1:A:219:ARG:C	1:A:220:ASP:O	2.44	0.53
1:A:77:SER:CB	3:C:9:VAL:HG13	2.38	0.53
1:D:16:GLY:O	1:D:17:ARG:HG2	2.10	0.52
1:D:215:LEU:HD23	1:D:261:VAL:HG22	1.90	0.52
1:A:50:PRO:O	1:A:53:GLU:HG2	2.10	0.52
2:B:90:PRO:HA	4:B:112:HOH:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:55:GLU:CD	1:A:170:ARG:HH21	2.13	0.52
2:B:73:THR:OG1	2:B:76:ASP:HB2	2.10	0.52
1:D:273:ARG:HB3	4:D:315:HOH:O	2.11	0.51
1:A:218:GLN:OE1	1:A:260:HIS:NE2	2.44	0.51
1:D:62:ARG:NH1	4:D:311:HOH:O	2.40	0.51
1:A:159:TYR:CD1	3:C:3:ARG:HG2	2.45	0.50
2:B:37:VAL:HG22	2:B:82:VAL:HG22	1.94	0.50
2:E:7:ILE:CD1	2:E:27:VAL:HG12	2.39	0.50
2:B:71:THR:HG21	1:D:108:ARG:NH2	2.27	0.50
1:D:21:ARG:NE	1:D:23:ILE:HD11	2.14	0.49
1:D:49:ALA:O	1:D:52:ILE:HG22	2.12	0.49
1:A:15:PRO:HG3	1:A:90:ALA:O	2.12	0.49
2:E:42:ASN:HB2	4:E:108:HOH:O	2.12	0.48
1:D:81:LEU:HD22	3:F:9:VAL:HG21	1.95	0.48
1:D:77:SER:HB3	3:F:9:VAL:HG22	1.95	0.48
1:A:20:PRO:HG2	1:A:22:PHE:CE1	2.48	0.48
1:A:218:GLN:O	1:A:257:TYR:HA	2.13	0.48
1:D:82:ARG:HH11	1:D:89:GLU:CD	2.14	0.48
1:D:11:ALA:HB3	1:D:95:LEU:HB3	1.96	0.47
2:B:17:ASN:ND2	2:B:74:GLU:HG3	2.29	0.47
1:D:6:ARG:NH1	1:D:102:ASP:OD1	2.44	0.47
1:A:224:GLN:HE21	1:A:224:GLN:HA	1.80	0.47
2:B:29:GLY:HA2	2:B:61:SER:HB2	1.96	0.47
2:B:3:ARG:NH1	2:B:61:SER:HB3	2.30	0.47
1:A:62:ARG:HD2	4:A:348:HOH:O	2.15	0.47
1:A:187:THR:OG1	1:A:272:LEU:HD21	2.15	0.47
1:A:263:HIS:HD2	1:A:265:GLY:H	1.60	0.47
1:A:76:GLU:OE2	1:A:79:ARG:NH1	2.48	0.47
1:D:172:LEU:O	1:D:180:GLN:NE2	2.45	0.47
1:A:159:TYR:CG	3:C:3:ARG:HG2	2.49	0.46
2:E:21:ASN:HB3	2:E:70:PHE:CE1	2.51	0.46
1:A:21:ARG:NH2	1:A:23:ILE:HD11	2.30	0.46
1:D:21:ARG:HE	1:D:23:ILE:CD1	2.15	0.46
1:D:14:ARG:HA	1:D:15:PRO:HD2	1.75	0.46
2:E:27:VAL:HG23	2:E:27:VAL:O	2.16	0.46
1:D:196:ASP:OD2	1:D:196:ASP:N	2.42	0.46
1:D:35:ARG:HD3	2:E:53:ASP:OD1	2.15	0.46
1:A:157:ARG:O	1:A:161:GLU:HB2	2.15	0.46
1:A:171:HIS:HE1	4:A:279:HOH:O	1.98	0.45
1:D:159:TYR:CD1	3:F:3:ARG:HG2	2.51	0.45
2:E:29:GLY:HA2	2:E:61:SER:OG	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:70:ASN:HA	1:D:73:THR:CG2	2.46	0.45
2:B:25:CYS:HB2	2:B:39:LEU:HD21	1.99	0.45
1:A:60:TRP:HB3	4:A:301:HOH:O	2.16	0.45
1:A:135:ALA:HB1	1:A:140:ALA:HB3	1.99	0.44
2:B:87:LEU:HB2	4:B:112:HOH:O	2.16	0.44
1:A:52:ILE:O	1:A:52:ILE:HG13	2.18	0.44
1:A:75:ARG:HG3	4:A:332:HOH:O	2.17	0.44
1:D:74:ASP:HA	1:D:77:SER:HB2	1.99	0.44
1:A:15:PRO:O	1:A:17:ARG:HG3	2.18	0.44
1:A:9:TYR:HB2	1:A:97:TRP:HB3	2.00	0.44
1:D:238:ASP:O	1:D:239:ARG:CB	2.65	0.44
1:D:123:TYR:CZ	1:D:140:ALA:HA	2.53	0.44
1:A:144:GLN:O	1:A:148:GLU:HG3	2.17	0.43
1:D:110:LEU:O	1:D:111:ARG:HB3	2.19	0.43
1:A:215:LEU:HD23	1:A:261:VAL:HG22	2.00	0.43
1:D:15:PRO:HG3	1:D:90:ALA:O	2.19	0.43
1:A:238:ASP:O	1:A:239:ARG:CB	2.67	0.43
1:D:9:TYR:HB2	1:D:97:TRP:HB3	2.00	0.43
1:A:20:PRO:CD	1:A:75:ARG:HH21	2.29	0.42
1:D:273:ARG:HD2	4:D:315:HOH:O	2.19	0.42
1:D:275:GLU:HB2	4:D:369:HOH:O	2.18	0.42
2:E:29:GLY:HA2	2:E:61:SER:CB	2.49	0.42
1:A:177:GLU:HB2	4:A:333:HOH:O	2.19	0.42
1:D:193:PRO:HA	1:D:199:ALA:HA	2.02	0.42
1:D:194:ILE:HD11	1:D:200:THR:OG1	2.20	0.42
2:E:31:HIS:CD2	2:E:32:PRO:HA	2.54	0.42
1:A:142:ILE:HA	1:A:145:ARG:NH1	2.35	0.41
1:A:9:TYR:CE1	1:A:99:TYR:HE1	2.37	0.41
1:D:23:ILE:HG21	2:E:54:LEU:HB3	2.02	0.41
1:D:68:LYS:O	1:D:71:THR:HB	2.20	0.41
2:E:71:THR:HA	2:E:72:PRO:HD2	1.90	0.41
2:B:17:ASN:HD21	2:B:74:GLU:HG3	1.84	0.41
3:F:1:ARG:NH2	4:F:11:HOH:O	2.52	0.41
1:D:215:LEU:CD2	1:D:261:VAL:HG22	2.50	0.41
2:B:45:ARG:NH2	4:B:116:HOH:O	2.54	0.41
1:A:51:TRP:HZ3	1:A:171:HIS:CD2	2.39	0.41
1:A:195:SER:HB2	1:A:196:ASP:H	1.66	0.41
4:A:362:HOH:O	2:B:31:HIS:HD2	2.03	0.41
2:B:21:ASN:HB3	2:B:70:PHE:CE1	2.56	0.41
1:A:9:TYR:O	1:A:96:GLN:HA	2.21	0.41
1:A:13:SER:HA	1:A:20:PRO:HB3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:34:VAL:HA	1:A:46:GLU:O	2.21	0.41
1:A:121:LYS:O	1:A:122:ASP:C	2.60	0.41
2:E:29:GLY:HA2	2:E:61:SER:HB2	2.02	0.41
2:E:48:LYS:O	2:E:48:LYS:HG3	2.20	0.41
2:E:99:MET:HE3	4:E:126:HOH:O	2.20	0.40
1:D:17:ARG:NH1	1:D:17:ARG:HG3	2.36	0.40
1:D:203:CYS:O	1:D:244:TRP:HA	2.21	0.40
1:D:204:TRP:HZ2	2:E:98:ASP:O	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	275/278 (99%)	256 (93%)	16 (6%)	3 (1%)	14	19
1	D	275/278 (99%)	259 (94%)	16 (6%)	0	100	100
2	B	97/100 (97%)	96 (99%)	1 (1%)	0	100	100
2	E	97/100 (97%)	96 (99%)	1 (1%)	0	100	100
3	C	7/9 (78%)	7 (100%)	0	0	100	100
3	F	7/9 (78%)	7 (100%)	0	0	100	100
All	All	758/774 (98%)	721 (95%)	34 (4%)	3 (0%)	34	46

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	106	ASP
1	A	221	GLY
1	A	276	PRO

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	236/237 (100%)	219 (93%)	17 (7%)	14	18
1	D	236/237 (100%)	226 (96%)	10 (4%)	30	40
2	B	94/95 (99%)	89 (95%)	5 (5%)	22	30
2	E	94/95 (99%)	90 (96%)	4 (4%)	29	39
3	C	9/9 (100%)	5 (56%)	4 (44%)	0	0
3	F	9/9 (100%)	6 (67%)	3 (33%)	0	0
All	All	678/682 (99%)	635 (94%)	43 (6%)	18	23

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	VAL
1	A	54	GLN
1	A	73	THR
1	A	75	ARG
1	A	79	ARG
1	A	81	LEU
1	A	106	ASP
1	A	166	GLU
1	A	178	THR
1	A	180	GLN
1	A	196	ASP
1	A	197	HIS
1	A	225	THR
1	A	230	LEU
1	A	231	VAL
1	A	251	SER
1	A	253	GLU
2	B	47	GLU
2	B	69	GLU
2	B	70	PHE
2	B	73	THR
2	B	83	ASN

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Mol	Chain	Res	Type
3	C	3	ARG
3	C	4	TRP
3	C	7	LEU
3	C	9	VAL
1	D	17	ARG
1	D	34	VAL
1	D	35	ARG
1	D	58	GLU
1	D	71	THR
1	D	73	THR
1	D	81	LEU
1	D	88	SER
1	D	195	SER
1	D	268	LYS
2	E	44	GLU
2	E	70	PHE
2	E	75	LYS
2	E	83	ASN
3	F	3	ARG
3	F	4	TRP
3	F	7	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	72	GLN
1	A	141	GLN
1	A	171	HIS
1	A	224	GLN
1	A	263	HIS
2	B	31	HIS
2	B	83	ASN
1	D	115	GLN
1	D	141	GLN
1	D	171	HIS
1	D	192	HIS
1	D	263	HIS
2	E	31	HIS
2	E	83	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

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	277/278 (99%)	0.40	14 (5%) 28 33	15, 26, 34, 41	0
1	D	277/278 (99%)	0.33	12 (4%) 35 42	16, 26, 34, 39	0
2	B	99/100 (99%)	0.36	0 100 100	19, 27, 35, 37	0
2	E	99/100 (99%)	0.41	2 (2%) 65 72	17, 27, 36, 39	0
3	C	9/9 (100%)	0.59	0 100 100	20, 23, 29, 32	0
3	F	9/9 (100%)	0.71	2 (22%) 0 0	18, 21, 26, 29	1 (11%)
All	All	770/774 (99%)	0.37	30 (3%) 39 45	15, 26, 35, 41	1 (0%)

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	18	GLY	4.1
1	A	16	GLY	4.0
1	A	17	ARG	3.6
2	E	75	LYS	3.2
1	A	1	GLY	3.2
1	D	41	ALA	3.1
1	D	18	GLY	3.0
1	A	90	ALA	2.9
1	D	42	SER	2.7
1	D	182	ALA	2.7
1	A	221	GLY	2.7
1	D	16	GLY	2.6
1	A	42	SER	2.5
1	A	106	ASP	2.5
2	E	74	GLU	2.5
1	D	268	LYS	2.5
1	D	15	PRO	2.4
1	D	225	THR	2.4
1	D	17	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
3	F	1	ARG	2.3
1	A	25	VAL	2.2
1	A	56	GLY	2.2
1	D	222	GLU	2.2
1	A	222	GLU	2.2
1	A	40	ALA	2.2
1	D	266	LEU	2.1
1	A	41	ALA	2.1
1	D	153	ALA	2.1
1	A	7	TYR	2.0
3	F	4	TRP	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.