Full wwPDB X-ray Structure Validation Report ⓘ

Jun 25, 2024 – 12:58 PM EDT

PDB ID	:	6G9R
Title	:	Murine class I major histocompatibility complex H-2 Db in complex with self-antigen derived from dopamine monooxygenase.
Authors	:	Achour, A.; Sandalova, T.; Allerbring, E.
Deposited on	:	2018-04-11
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:

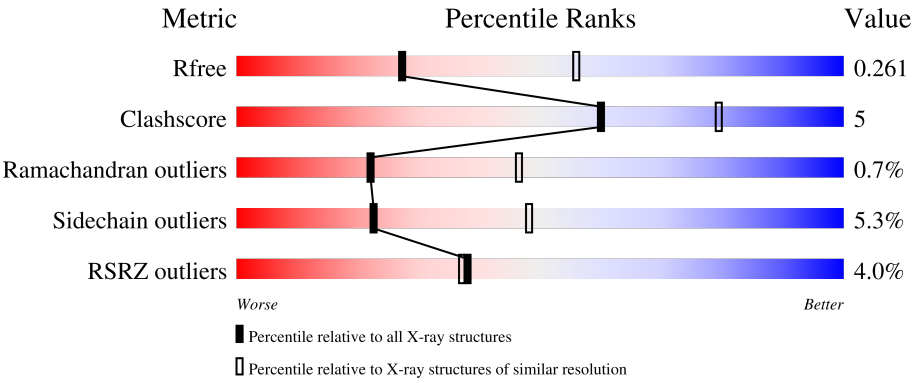
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.70 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))
R_{free}	130704	2808 (2.70-2.70)
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	276	4% 88% 10% ·
1	C	276	5% 87% 12% ·
1	E	276	6% 88% 11% ·
1	G	276	6% 83% 16% ·
2	B	99	92% 7% ·

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Mol	Chain	Length	Quality of chain
2	D	99	2% 93% 6%
2	F	99	91% 8%
2	H	99	87% 12%
3	I	9	100%
3	J	9	78% 11% 11%
3	K	9	56% 44%
3	P	9	78% 22%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 12665 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 H-2 class I histocompatibility antigen, D-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2265	1430	400	426	9			
1	C	276	Total	C	N	O	S	0	1	0
			2275	1436	403	427	9			
1	E	276	Total	C	N	O	S	0	1	0
			2272	1435	402	426	9			
1	G	276	Total	C	N	O	S	0	1	0
			2272	1435	402	426	9			

- 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
			819	523	138	152	6			
2	D	99	Total	C	N	O	S	0	0	0
			819	523	138	152	6			
2	F	99	Total	C	N	O	S	0	0	0
			819	523	138	152	6			
2	H	99	Total	C	N	O	S	0	0	0
			819	523	138	152	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	85	ASP	ALA	variant	UNP P01887
D	85	ASP	ALA	variant	UNP P01887
F	85	ASP	ALA	variant	UNP P01887
H	85	ASP	ALA	variant	UNP P01887

- Molecule 3 is a protein called Dopamine beta-hydroxylase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	P	9	Total	C	N	O	0	0	0
			74	50	10	14			
3	I	9	Total	C	N	O	0	0	0
			74	50	10	14			
3	J	9	Total	C	N	O	0	0	0
			74	50	10	14			
3	K	9	Total	C	N	O	0	0	0
			74	50	10	14			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	3	PRO	LEU	engineered mutation	UNP Q64237
I	3	PRO	LEU	engineered mutation	UNP Q64237
J	3	PRO	LEU	engineered mutation	UNP Q64237
K	3	PRO	LEU	engineered mutation	UNP Q64237

- Molecule 4 is water.

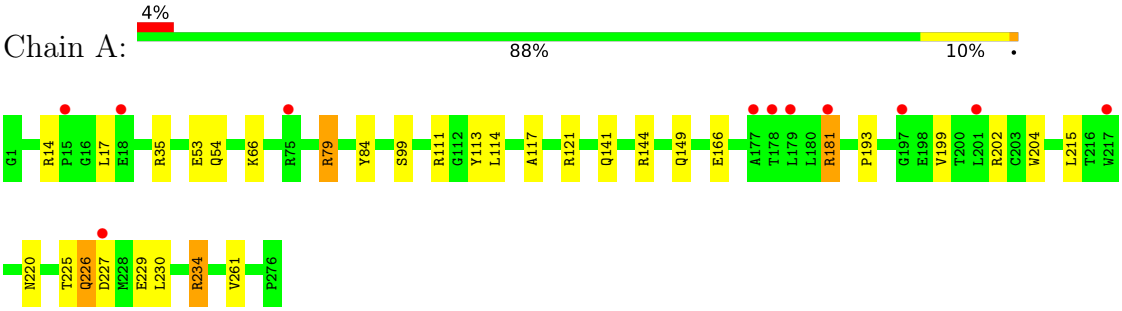
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	3	Total	O	0	0
			3	3		
4	B	1	Total	O	0	0
			1	1		
4	C	1	Total	O	0	0
			1	1		
4	E	1	Total	O	0	0
			1	1		
4	G	2	Total	O	0	0
			2	2		
4	H	1	Total	O	0	0
			1	1		

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.

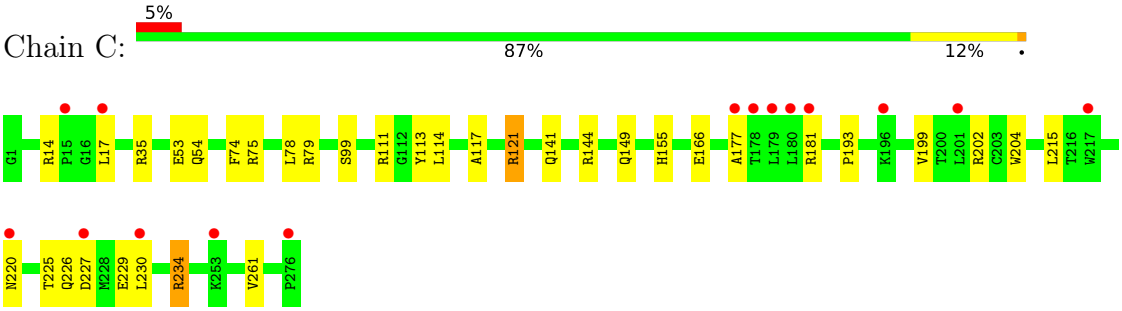
• Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

Chain A:



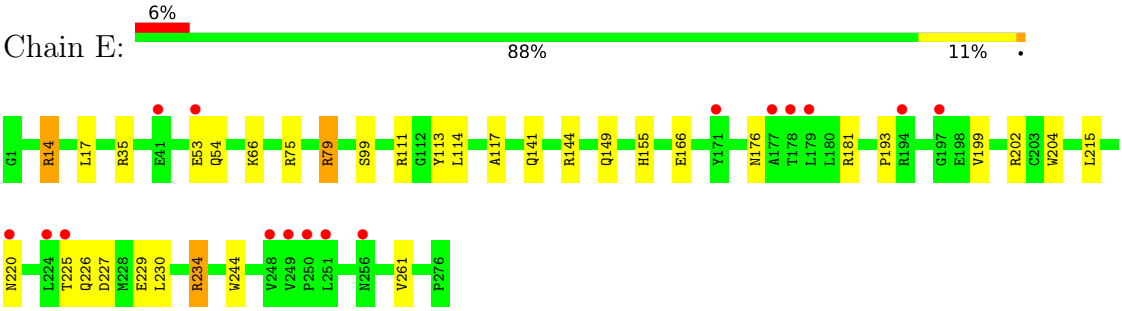
• Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

Chain C:



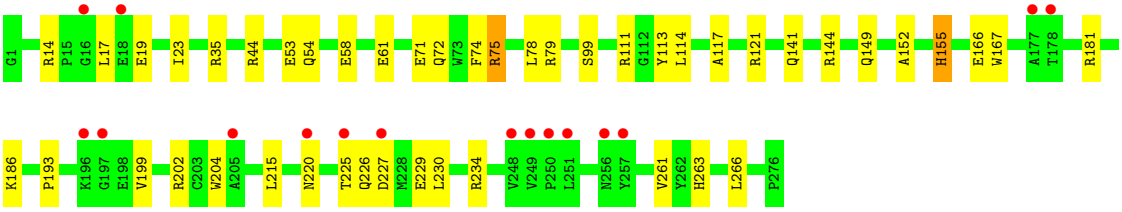
• Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

Chain E:

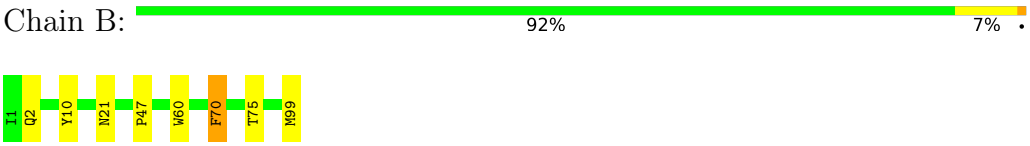


• Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

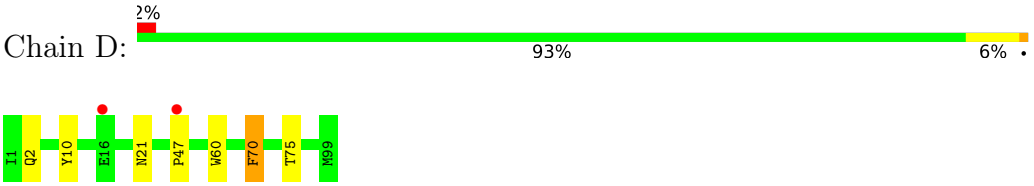
Chain G:



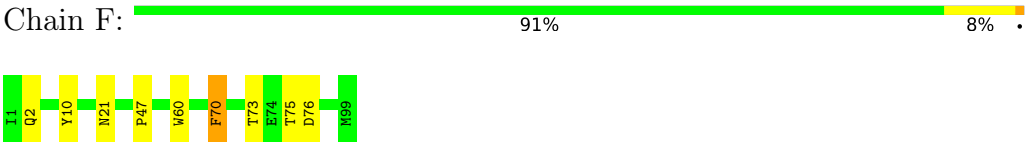
• Molecule 2: Beta-2-microglobulin



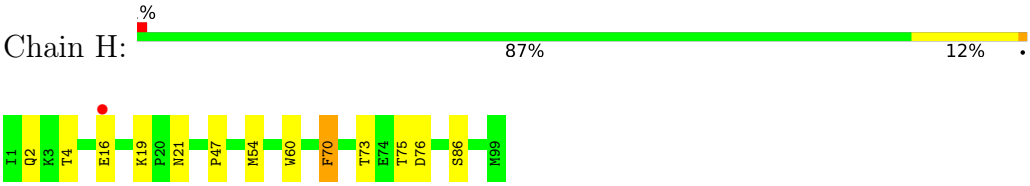
• Molecule 2: Beta-2-microglobulin



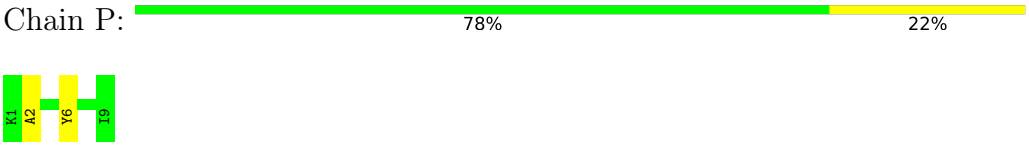
• Molecule 2: Beta-2-microglobulin



• Molecule 2: Beta-2-microglobulin



• Molecule 3: Dopamine beta-hydroxylase

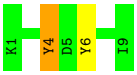


• Molecule 3: Dopamine beta-hydroxylase

There are no outlier residues recorded for this chain.

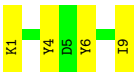
• Molecule 3: Dopamine beta-hydroxylase

Chain J:



• Molecule 3: Dopamine beta-hydroxylase

Chain K:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	92.25Å 123.60Å 99.26Å 90.00° 103.07° 90.00°	Depositor
Resolution (Å)	45.00 – 2.70 44.93 – 2.70	Depositor EDS
% Data completeness (in resolution range)	94.3 (45.00-2.70) 94.3 (44.93-2.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.99 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.234 , 0.264 0.237 , 0.261	Depositor DCC
R_{free} test set	2844 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å^2)	61.6	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.26 , 24.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	12665	wwPDB-VP
Average B, all atoms (Å^2)	82.0	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 50.45 % 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 6.4548e-05. 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	0.58	0/2332	0.81	4/3166 (0.1%)
1	C	0.58	0/2343	0.81	3/3181 (0.1%)
1	E	0.58	0/2343	0.82	4/3181 (0.1%)
1	G	0.59	0/2343	0.82	3/3181 (0.1%)
2	B	0.59	0/845	0.82	1/1146 (0.1%)
2	D	0.59	0/845	0.79	0/1146
2	F	0.58	0/845	0.80	0/1146
2	H	0.58	0/845	0.78	0/1146
3	I	0.61	0/77	0.86	0/104
3	J	0.74	0/77	1.05	1/104 (1.0%)
3	K	0.93	0/77	0.98	0/104
3	P	0.73	0/77	0.89	0/104
All	All	0.59	0/13049	0.82	16/17709 (0.1%)

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	1
1	G	0	1
All	All	0	2

There are no bond length outliers.

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	35	ARG	NE-CZ-NH1	7.61	124.11	120.30
1	C	35	ARG	NE-CZ-NH2	-7.38	116.61	120.30
2	B	99	MET	CA-CB-CG	7.23	125.59	113.30
1	C	35	ARG	NE-CZ-NH1	7.20	123.90	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	35	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	A	35	ARG	NE-CZ-NH2	-6.89	116.85	120.30
1	G	35	ARG	NE-CZ-NH2	-6.39	117.10	120.30
1	A	35	ARG	NE-CZ-NH1	5.97	123.29	120.30
1	G	35	ARG	NE-CZ-NH1	5.90	123.25	120.30
3	J	4	TYR	CA-CB-CG	5.74	124.31	113.40
1	C	53	GLU	CB-CA-C	-5.65	99.09	110.40
1	E	53	GLU	CB-CA-C	-5.64	99.12	110.40
1	A	53	GLU	CB-CA-C	-5.42	99.57	110.40
1	G	53	GLU	CB-CA-C	-5.33	99.74	110.40
1	A	79	ARG	NE-CZ-NH1	5.26	122.93	120.30
1	E	79	ARG	NE-CZ-NH1	5.03	122.82	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	14	ARG	Peptide
1	G	75	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	2265	0	2136	19	1
1	C	2275	0	2142	20	1
1	E	2272	0	2143	22	0
1	G	2272	0	2143	32	0
2	B	819	0	791	4	0
2	D	819	0	791	4	0
2	F	819	0	791	5	0
2	H	819	0	791	23	0
3	I	74	0	72	0	0
3	J	74	0	72	1	0
3	K	74	0	72	4	0
3	P	74	0	72	1	0
4	A	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
4	G	2	0	0	1	0
4	H	1	0	0	0	0
All	All	12665	0	12016	113	1

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 5.

All (113) 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:H:16:GLU:HG3	2:H:19:LYS:NZ	1.33	1.39
2:H:16:GLU:CB	2:H:19:LYS:HD2	1.74	1.18
1:A:14:ARG:HB2	1:A:17:LEU:HD13	1.26	1.17
1:G:14:ARG:HB2	1:G:17:LEU:HD13	1.28	1.15
2:H:16:GLU:HG3	2:H:19:LYS:CE	1.81	1.11
1:C:14:ARG:HB2	1:C:17:LEU:HD13	1.24	1.11
2:H:16:GLU:HB2	2:H:19:LYS:CD	1.80	1.11
1:E:14:ARG:HB2	1:E:17:LEU:HD13	1.29	1.10
2:H:16:GLU:CG	2:H:19:LYS:NZ	2.25	0.99
2:H:16:GLU:HB2	2:H:19:LYS:HD2	1.02	0.98
1:G:19:GLU:HB3	1:G:75:ARG:HH22	1.32	0.92
2:H:4:THR:HG22	2:H:86:SER:HB2	1.49	0.92
2:H:16:GLU:HG3	2:H:19:LYS:HZ1	1.14	0.89
1:C:14:ARG:CB	1:C:17:LEU:HD13	2.07	0.85
2:H:16:GLU:CG	2:H:19:LYS:HD2	2.07	0.84
1:C:14:ARG:HB2	1:C:17:LEU:CD1	2.08	0.84
2:H:16:GLU:HG3	2:H:19:LYS:HZ2	1.39	0.82
1:G:14:ARG:CB	1:G:17:LEU:HD13	2.10	0.81
1:E:14:ARG:CB	1:E:17:LEU:HD13	2.11	0.81
1:E:176:ASN:HB3	1:G:186:LYS:NZ	1.95	0.80
1:A:14:ARG:CB	1:A:17:LEU:HD13	2.08	0.80
1:G:14:ARG:HB2	1:G:17:LEU:CD1	2.11	0.78
1:E:14:ARG:HB2	1:E:17:LEU:CD1	2.12	0.78
1:A:14:ARG:HB2	1:A:17:LEU:CD1	2.10	0.78
1:G:19:GLU:HB3	1:G:75:ARG:NH2	2.00	0.77
2:H:16:GLU:CG	2:H:19:LYS:CE	2.62	0.77
2:H:16:GLU:CB	2:H:19:LYS:CD	2.52	0.76
1:G:155[B]:HIS:HD2	3:K:6:TYR:HB2	1.58	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:14:ARG:HH11	1:C:17:LEU:HD11	1.59	0.68
2:H:16:GLU:CG	2:H:19:LYS:CD	2.71	0.68
1:E:176:ASN:HB3	1:G:186:LYS:HZ1	1.60	0.67
1:G:14:ARG:HH11	1:G:17:LEU:HD11	1.60	0.67
1:A:14:ARG:HH11	1:A:17:LEU:HD11	1.59	0.66
1:E:14:ARG:HH11	1:E:17:LEU:HD11	1.61	0.65
2:H:16:GLU:CG	2:H:19:LYS:HZ1	1.98	0.64
1:A:181:ARG:HG3	1:C:177:ALA:HB2	1.81	0.61
1:E:225:THR:HG22	1:E:225:THR:O	2.01	0.61
1:E:141:GLN:OE1	1:E:144:ARG:NH1	2.35	0.60
1:C:141:GLN:OE1	1:C:144:ARG:NH1	2.35	0.60
2:H:4:THR:HG22	2:H:86:SER:CB	2.30	0.58
1:A:141:GLN:OE1	1:A:144:ARG:NH1	2.36	0.57
1:G:225:THR:O	1:G:225:THR:HG22	2.04	0.57
1:C:225:THR:O	1:C:225:THR:HG22	2.04	0.57
1:G:141:GLN:OE1	1:G:144:ARG:NH1	2.37	0.57
2:H:16:GLU:HB2	2:H:19:LYS:CG	2.34	0.57
1:G:72:GLN:OE1	1:G:75:ARG:HD2	2.04	0.57
1:C:14:ARG:NH1	1:C:17:LEU:HD11	2.20	0.56
1:A:14:ARG:NH1	1:A:17:LEU:HD11	2.20	0.56
1:C:215:LEU:CD2	1:C:261:VAL:HG22	2.37	0.55
1:G:23:ILE:HD12	2:H:54:MET:SD	2.46	0.55
1:A:215:LEU:CD2	1:A:261:VAL:HG22	2.36	0.55
1:A:181:ARG:HG3	1:C:177:ALA:CB	2.38	0.54
1:A:234:ARG:HD3	2:B:10:TYR:CE2	2.43	0.54
1:E:14:ARG:NH1	1:E:17:LEU:HD11	2.22	0.54
2:H:16:GLU:CG	2:H:19:LYS:HZ2	2.06	0.54
1:E:215:LEU:CD2	1:E:261:VAL:HG22	2.39	0.53
1:G:14:ARG:NH1	1:G:17:LEU:HD11	2.21	0.53
1:E:176:ASN:HB3	1:G:186:LYS:HZ2	1.71	0.53
1:A:225:THR:HG22	1:A:225:THR:O	2.09	0.52
1:A:234:ARG:HD3	2:B:10:TYR:CZ	2.44	0.52
1:C:117:ALA:HB2	2:D:60:TRP:CE2	2.45	0.51
1:G:215:LEU:CD2	1:G:261:VAL:HG22	2.39	0.51
1:C:234:ARG:HD3	2:D:10:TYR:CZ	2.46	0.51
1:G:117:ALA:HB2	2:H:60:TRP:CE2	2.47	0.50
1:A:215:LEU:HD23	1:A:261:VAL:HG22	1.93	0.49
2:H:16:GLU:CB	2:H:19:LYS:CE	2.90	0.48
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.49	0.48
1:E:215:LEU:HD23	1:E:261:VAL:HG22	1.96	0.48
2:H:21:ASN:HB3	2:H:70:PHE:CE1	2.49	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:234:ARG:HD3	2:D:10:TYR:CE2	2.48	0.48
1:G:19:GLU:HG3	1:G:75:ARG:HH12	1.77	0.47
1:C:215:LEU:HD23	1:C:261:VAL:HG22	1.95	0.47
1:G:155[B]:HIS:CD2	3:K:6:TYR:HB2	2.45	0.47
1:E:234:ARG:HD3	2:F:10:TYR:CE2	2.50	0.46
2:D:21:ASN:HB3	2:D:70:PHE:CE1	2.50	0.46
2:F:21:ASN:HB3	2:F:70:PHE:CE1	2.50	0.46
2:H:4:THR:CG2	2:H:86:SER:HB2	2.34	0.45
1:G:74:PHE:O	1:G:78:LEU:HG	2.15	0.45
1:G:215:LEU:HD23	1:G:261:VAL:HG22	1.98	0.45
2:B:21:ASN:HB3	2:B:70:PHE:CE1	2.52	0.45
1:G:202:ARG:HG2	1:G:204:TRP:NE1	2.32	0.45
1:E:202:ARG:HG2	1:E:204:TRP:NE1	2.32	0.44
1:E:117:ALA:HB2	2:F:60:TRP:CE2	2.53	0.44
1:G:111:ARG:HD3	1:G:113:TYR:CZ	2.52	0.44
1:G:167:TRP:CH2	3:K:1:LYS:HE3	2.52	0.44
1:A:202:ARG:HG2	1:A:204:TRP:NE1	2.32	0.44
1:C:155[A]:HIS:CD2	1:C:155[A]:HIS:C	2.90	0.44
1:C:202:ARG:HG2	1:C:204:TRP:NE1	2.32	0.44
1:E:193:PRO:HA	1:E:199:VAL:HG12	2.00	0.43
1:E:155[A]:HIS:HB3	3:J:6:TYR:CE1	2.53	0.43
1:A:111:ARG:HD3	1:A:113:TYR:CZ	2.53	0.43
1:C:111:ARG:HD3	1:C:113:TYR:CZ	2.54	0.43
1:G:111:ARG:HD3	1:G:113:TYR:OH	2.18	0.43
1:E:111:ARG:HD3	1:E:113:TYR:CZ	2.54	0.43
2:H:73:THR:HG1	2:H:76:ASP:CG	2.23	0.42
1:G:71:GLU:O	1:G:75:ARG:HG3	2.19	0.42
1:C:193:PRO:HA	1:C:199:VAL:HG12	2.01	0.42
1:A:66:LYS:NZ	3:P:2:ALA:O	2.46	0.42
1:G:193:PRO:HA	1:G:199:VAL:HG12	2.01	0.42
1:A:111:ARG:HD3	1:A:113:TYR:OH	2.20	0.41
1:C:74:PHE:O	1:C:78:LEU:HG	2.20	0.41
1:E:234:ARG:HD3	2:F:10:TYR:CZ	2.55	0.41
1:G:44:ARG:HH22	1:G:61:GLU:HG3	1.86	0.41
1:A:193:PRO:HA	1:A:199:VAL:HG12	2.01	0.41
1:C:111:ARG:HD3	1:C:113:TYR:OH	2.20	0.41
1:E:111:ARG:HD3	1:E:113:TYR:OH	2.20	0.41
1:E:202:ARG:HD3	1:E:244:TRP:CE3	2.55	0.41
2:F:73:THR:HG1	2:F:76:ASP:CG	2.24	0.41
1:G:72:GLN:HE22	1:G:75:ARG:HE	1.69	0.41
1:G:152:ALA:HA	3:K:6:TYR:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:263:HIS:N	1:G:266:LEU:HD12	2.36	0.41
1:E:225:THR:O	1:E:225:THR:CG2	2.68	0.40
1:G:225:THR:N	4:G:301:HOH:O	2.47	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:TYR:O	1:C:121:ARG:NH2[1_455]	2.14	0.06

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	274/276 (99%)	254 (93%)	18 (7%)	2 (1%)	22 46
1	C	275/276 (100%)	255 (93%)	19 (7%)	1 (0%)	34 60
1	E	275/276 (100%)	255 (93%)	19 (7%)	1 (0%)	34 60
1	G	275/276 (100%)	253 (92%)	21 (8%)	1 (0%)	34 60
2	B	97/99 (98%)	93 (96%)	3 (3%)	1 (1%)	15 37
2	D	97/99 (98%)	93 (96%)	3 (3%)	1 (1%)	15 37
2	F	97/99 (98%)	93 (96%)	3 (3%)	1 (1%)	15 37
2	H	97/99 (98%)	93 (96%)	3 (3%)	1 (1%)	15 37
3	I	7/9 (78%)	6 (86%)	1 (14%)	0	100 100
3	J	7/9 (78%)	6 (86%)	1 (14%)	0	100 100
3	K	7/9 (78%)	5 (71%)	2 (29%)	0	100 100
3	P	7/9 (78%)	5 (71%)	1 (14%)	1 (14%)	0 0
All	All	1515/1536 (99%)	1411 (93%)	94 (6%)	10 (1%)	22 46

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	54	GLN
1	C	54	GLN
1	G	54	GLN
3	P	6	TYR
1	A	226	GLN
1	E	54	GLN
2	B	47	PRO
2	D	47	PRO
2	F	47	PRO
2	H	47	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	234/234 (100%)	221 (94%)	13 (6%)	21 45
1	C	235/234 (100%)	221 (94%)	14 (6%)	19 42
1	E	235/234 (100%)	221 (94%)	14 (6%)	19 42
1	G	235/234 (100%)	219 (93%)	16 (7%)	16 36
2	B	93/94 (99%)	90 (97%)	3 (3%)	39 68
2	D	93/94 (99%)	90 (97%)	3 (3%)	39 68
2	F	93/94 (99%)	90 (97%)	3 (3%)	39 68
2	H	93/94 (99%)	90 (97%)	3 (3%)	39 68
3	I	7/7 (100%)	7 (100%)	0	100 100
3	J	7/7 (100%)	6 (86%)	1 (14%)	3 8
3	K	7/7 (100%)	5 (71%)	2 (29%)	0 1
3	P	7/7 (100%)	7 (100%)	0	100 100
All	All	1339/1340 (100%)	1267 (95%)	72 (5%)	22 47

All (72) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	ARG
1	A	99	SER
1	A	114	LEU
1	A	121	ARG
1	A	149	GLN
1	A	166	GLU
1	A	181	ARG
1	A	220	ASN
1	A	226	GLN
1	A	227	ASP
1	A	229	GLU
1	A	230	LEU
1	A	234	ARG
2	B	2	GLN
2	B	70	PHE
2	B	75	THR
1	C	75	ARG
1	C	79	ARG
1	C	99	SER
1	C	114	LEU
1	C	121	ARG
1	C	149	GLN
1	C	166	GLU
1	C	181	ARG
1	C	220	ASN
1	C	226	GLN
1	C	227	ASP
1	C	229	GLU
1	C	230	LEU
1	C	234	ARG
2	D	2	GLN
2	D	70	PHE
2	D	75	THR
1	E	66	LYS
1	E	75	ARG
1	E	79	ARG
1	E	99	SER
1	E	114	LEU
1	E	149	GLN
1	E	166	GLU
1	E	181	ARG
1	E	220	ASN
1	E	226	GLN

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Mol	Chain	Res	Type
1	E	227	ASP
1	E	229	GLU
1	E	230	LEU
1	E	234	ARG
2	F	2	GLN
2	F	70	PHE
2	F	75	THR
1	G	58	GLU
1	G	79	ARG
1	G	99	SER
1	G	114	LEU
1	G	121	ARG
1	G	149	GLN
1	G	155[A]	HIS
1	G	155[B]	HIS
1	G	166	GLU
1	G	181	ARG
1	G	220	ASN
1	G	226	GLN
1	G	227	ASP
1	G	229	GLU
1	G	230	LEU
1	G	234	ARG
2	H	2	GLN
2	H	70	PHE
2	H	75	THR
3	J	4	TYR
3	K	4	TYR
3	K	9	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	29	GLN
2	B	31	HIS
2	D	6	GLN
2	D	29	GLN
2	D	31	HIS
2	F	29	GLN
2	F	31	HIS
1	G	72	GLN
2	H	31	HIS

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	276/276 (100%)	-0.03	11 (3%) 38 37	44, 76, 139, 215	0
1	C	276/276 (100%)	0.02	15 (5%) 25 24	44, 77, 146, 206	0
1	E	276/276 (100%)	0.17	16 (5%) 23 22	38, 75, 155, 228	0
1	G	276/276 (100%)	0.20	16 (5%) 23 22	40, 78, 160, 247	0
2	B	99/99 (100%)	-0.07	0 100 100	45, 69, 104, 115	0
2	D	99/99 (100%)	-0.11	2 (2%) 65 67	46, 68, 99, 138	0
2	F	99/99 (100%)	-0.13	0 100 100	51, 72, 98, 119	0
2	H	99/99 (100%)	0.01	1 (1%) 82 83	45, 78, 107, 125	0
3	I	9/9 (100%)	-0.24	0 100 100	55, 66, 88, 96	0
3	J	9/9 (100%)	-0.16	0 100 100	50, 55, 92, 99	0
3	K	9/9 (100%)	-0.10	0 100 100	50, 57, 71, 80	0
3	P	9/9 (100%)	-0.29	0 100 100	55, 64, 77, 81	0
All	All	1536/1536 (100%)	0.04	61 (3%) 38 37	38, 75, 146, 247	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	178	THR	13.8
1	E	178	THR	12.9
1	E	177	ALA	9.9
1	C	177	ALA	9.6
1	G	177	ALA	7.6
1	C	178	THR	7.5
1	A	178	THR	6.7
1	E	179	LEU	6.3
1	G	250	PRO	6.1
1	A	227	ASP	5.8
1	A	179	LEU	5.6

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Mol	Chain	Res	Type	RSRZ
1	G	251	LEU	4.4
1	G	220	ASN	4.4
1	G	249	VAL	4.1
1	E	251	LEU	4.1
1	C	253	LYS	4.1
2	H	16	GLU	4.0
1	E	53	GLU	3.7
1	G	256	ASN	3.7
1	E	250	PRO	3.7
1	C	196	LYS	3.5
1	E	197	GLY	3.4
1	C	17	LEU	3.4
1	E	249	VAL	3.3
1	C	181	ARG	3.1
1	G	248	VAL	3.1
1	G	196	LYS	3.0
1	C	227	ASP	3.0
1	A	181	ARG	3.0
1	C	217	TRP	3.0
1	E	225	THR	2.9
1	G	225	THR	2.9
1	C	220	ASN	2.9
1	E	220	ASN	2.8
1	G	197	GLY	2.8
1	C	179	LEU	2.6
1	G	18	GLU	2.6
1	G	257	TYR	2.6
1	E	194	ARG	2.5
1	C	180	LEU	2.5
1	A	177	ALA	2.5
1	E	248	VAL	2.5
1	E	41	GLU	2.5
1	A	197	GLY	2.5
1	C	201	LEU	2.4
1	G	227	ASP	2.3
1	A	15	PRO	2.3
2	D	16	GLU	2.2
1	E	171	TYR	2.2
1	A	18	GLU	2.2
1	E	256	ASN	2.2
1	A	201	LEU	2.2
1	C	15	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	G	16	GLY	2.2
1	A	75	ARG	2.2
1	A	217	TRP	2.1
1	C	276	PRO	2.1
1	E	224	LEU	2.1
1	G	205	ALA	2.1
1	C	230	LEU	2.0
2	D	47	PRO	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.