



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 14, 2023 – 11:15 PM EDT

PDB ID : 1S7T
Title : Crystal structures of the murine class I major histocompatibility complex H-2Kb in complex with LCMV-derived gp33 index peptide and three of its escape variants
Authors : Velloso, L.M.; Michaelsson, J.; Ljunggren, H.G.; Schneider, G.; Achour, A.
Deposited on : 2004-01-30
Resolution : 2.30 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 : 2.35
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) : 2.35

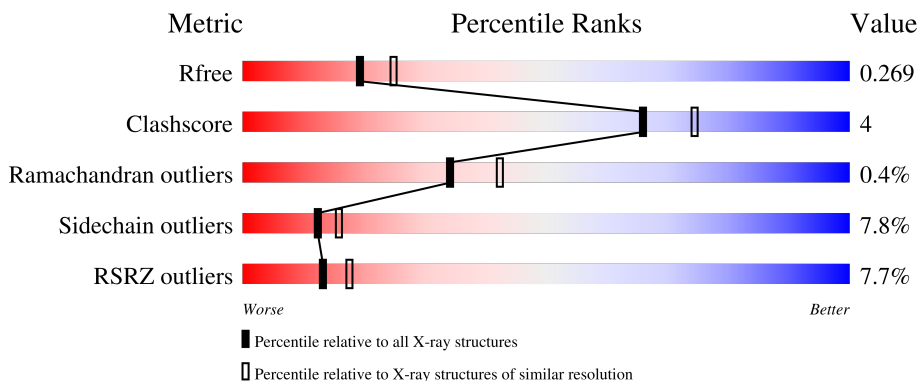
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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.



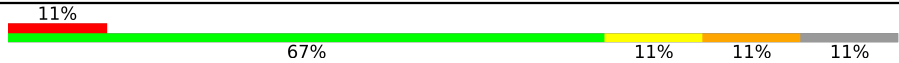
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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 $\leq 5\%$. 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	348	 5% 67% 11% 15% 2%
1	D	348	 6% 66% 12% 16% 2%
2	B	99	 4% 86% 13% 2% 2%
2	E	99	 14% 82% 17% 2% 2%
3	C	9	 78% 11% 11%

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Mol	Chain	Length	Quality of chain
3	F	9	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into five segments: a red segment (11%), a green segment (67%), a yellow segment (11%), an orange segment (11%), and a grey segment (11%). The percentages are labeled below each segment.</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6621 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, K-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	276	2247	1418	395	425	9	0	0	0
1	D	276	2247	1418	395	425	9	0	0	0

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	99	820	524	138	151	7	0	0	0
2	E	99	820	524	138	151	7	0	0	0

- Molecule 3 is a protein called Glycoprotein 9-residue peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	8	62	42	9	10	1	0	0	0
3	F	8	62	42	9	10	1	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	4	PHE	TYR	engineered mutation	UNP P07399
C	9	MET	CYS	SEE REMARK 999	UNP P07399
F	4	PHE	TYR	engineered mutation	UNP P07399
F	9	MET	CYS	SEE REMARK 999	UNP P07399

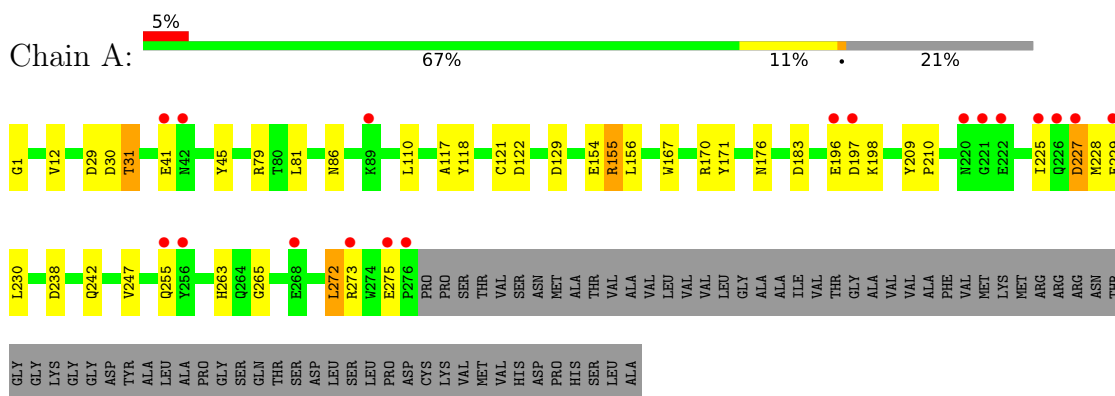
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	124	Total O 124 124	0	0
4	B	70	Total O 70 70	0	0
4	C	7	Total O 7 7	0	0
4	D	111	Total O 111 111	0	0
4	E	42	Total O 42 42	0	0
4	F	9	Total O 9 9	0	0

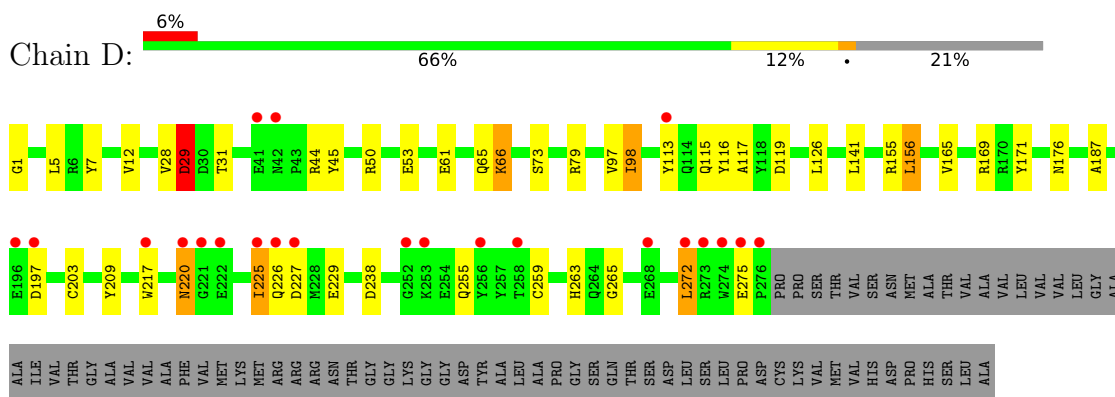
3 Residue-property plots

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.

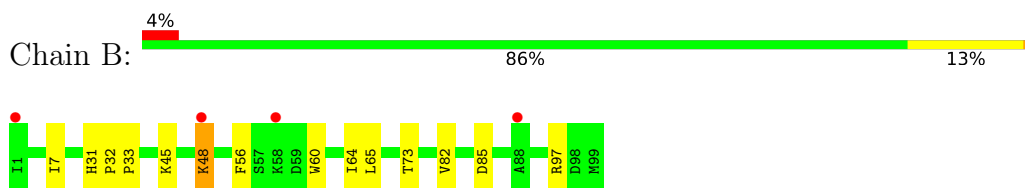
- Molecule 1: H-2 class I histocompatibility antigen, K-B alpha chain



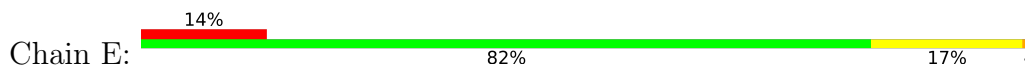
- Molecule 1: H-2 class I histocompatibility antigen, K-B alpha chain



- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin





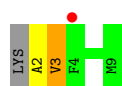
- Molecule 3: Glycoprotein 9-residue peptide

Chain C: 78% 11% 11%



- Molecule 3: Glycoprotein 9-residue peptide

Chain F: 11% 67% 11% 11% 11%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.30Å 92.69Å 128.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.88 – 2.30 19.88 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.2 (19.88-2.30) 99.2 (19.88-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.59 (at 2.30Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.205 , 0.252 0.225 , 0.269	Depositor DCC
R_{free} test set	1915 reflections (4.06%)	wwPDB-VP
Wilson B-factor (Å ²)	36.2	Xtrriage
Anisotropy	0.126	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	0.000 for k,h,-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6621	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.90 % 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 7.8694e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.47	0/2309	0.75	8/3137 (0.3%)
1	D	0.45	0/2309	0.76	5/3137 (0.2%)
2	B	0.46	0/846	0.73	1/1148 (0.1%)
2	E	0.42	0/846	0.72	3/1148 (0.3%)
3	C	0.66	0/63	0.67	0/84
3	F	0.69	0/63	0.77	0/84
All	All	0.46	0/6436	0.75	17/8738 (0.2%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	85	ASP	CB-CG-OD2	6.31	123.97	118.30
1	D	238	ASP	CB-CG-OD2	6.29	123.96	118.30
1	A	155	ARG	NE-CZ-NH2	-6.05	117.27	120.30
1	D	155	ARG	NE-CZ-NH2	-5.75	117.42	120.30
2	E	59	ASP	CB-CG-OD2	5.61	123.35	118.30
1	A	238	ASP	CB-CG-OD2	5.61	123.34	118.30
2	E	53	ASP	CB-CG-OD2	5.47	123.22	118.30
1	A	227	ASP	CB-CG-OD2	5.41	123.17	118.30
1	A	183	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	197	ASP	CB-CG-OD2	5.27	123.04	118.30
2	B	85	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	155	ARG	NE-CZ-NH1	5.19	122.89	120.30
1	A	129	ASP	CB-CG-OD2	5.12	122.91	118.30
1	D	119	ASP	CB-CG-OD2	5.11	122.90	118.30
1	D	197	ASP	CB-CG-OD2	5.11	122.90	118.30
1	A	122	ASP	CB-CG-OD2	5.08	122.87	118.30
1	D	227	ASP	CB-CG-OD2	5.03	122.83	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	2247	0	2136	15	0
1	D	2247	0	2136	20	0
2	B	820	0	796	7	0
2	E	820	0	796	9	0
3	C	62	0	58	1	0
3	F	62	0	58	5	0
4	A	124	0	0	3	0
4	B	70	0	0	1	0
4	C	7	0	0	0	0
4	D	111	0	0	4	0
4	E	42	0	0	1	0
4	F	9	0	0	0	0
All	All	6621	0	5980	49	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 4.

All (49) 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)
4:D:378:HOH:O	2:E:22:ILE:HD12	0.79	0.97
4:D:360:HOH:O	2:E:1:ILE:HD11	1.89	0.72
1:D:61:GLU:OE2	1:D:65:GLN:NE2	2.23	0.71
1:A:86:ASN:HB3	4:A:468:HOH:O	1.96	0.66
1:A:29:ASP:O	1:A:30:ASP:HB2	1.97	0.65
1:D:171:TYR:OH	3:F:2:ALA:HB2	2.02	0.59
1:A:1:GLY:N	4:A:471:HOH:O	2.35	0.59
1:D:187:ALA:HB3	1:D:272:LEU:HD21	1.84	0.59
1:A:263:HIS:CD2	1:A:265:GLY:H	2.21	0.59
1:A:171:TYR:OH	3:C:2:ALA:HB2	2.04	0.57
1:D:98:ILE:HG23	1:D:115:GLN:HG3	1.86	0.56
2:B:48:LYS:O	2:B:48:LYS:HE3	2.06	0.56
1:D:7:TYR:OH	3:F:2:ALA:HB3	2.09	0.52
1:D:66:LYS:HD3	3:F:3:VAL:HG12	1.90	0.52
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:220:ASN:HD22	1:D:220:ASN:N	2.08	0.52
1:D:29:ASP:O	1:D:209:TYR:OH	2.22	0.51
1:D:126:LEU:HD22	1:D:156:LEU:HD13	1.94	0.49
2:B:73:THR:CG2	4:B:162:HOH:O	2.61	0.49
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.48	0.48
1:D:1:GLY:N	4:D:416:HOH:O	2.47	0.47
2:B:31:HIS:ND1	2:B:32:PRO:HA	2.29	0.46
4:D:378:HOH:O	2:E:22:ILE:CD1	1.69	0.46
1:D:5:LEU:HD21	3:F:2:ALA:HB1	1.98	0.45
1:A:29:ASP:O	1:A:30:ASP:CB	2.58	0.45
1:A:272:LEU:HD12	1:A:272:LEU:N	2.30	0.45
1:D:263:HIS:HD2	1:D:265:GLY:H	1.65	0.45
1:A:225:ILE:HG22	1:A:225:ILE:O	2.17	0.45
2:B:32:PRO:HB2	2:B:33:PRO:HD2	1.99	0.45
2:E:32:PRO:HB2	2:E:33:PRO:HD2	2.00	0.44
1:D:203:CYS:HB2	1:D:217:TRP:CZ2	2.53	0.44
2:E:12:ARG:HD2	2:E:12:ARG:C	2.37	0.44
2:E:87:MET:HE1	2:E:91:LYS:HD3	2.01	0.43
1:A:227:ASP:O	1:A:247:VAL:HG23	2.19	0.42
1:D:7:TYR:CG	3:F:3:VAL:HG23	2.55	0.42
1:D:97:VAL:HG22	1:D:116:TYR:CD2	2.55	0.42
2:B:7:ILE:HD11	2:B:82:VAL:HB	2.01	0.42
1:D:50:ARG:O	1:D:53:GLU:HB2	2.19	0.42
1:D:98:ILE:HG23	1:D:115:GLN:CG	2.48	0.42
1:A:31:THR:HG22	1:A:209:TYR:OH	2.19	0.42
2:E:7:ILE:HB	2:E:93:VAL:HG21	2.02	0.42
1:A:81:LEU:HD23	1:A:118:TYR:CD1	2.55	0.41
1:A:121:CYS:SG	4:A:465:HOH:O	2.33	0.41
1:A:167:TRP:CZ3	1:A:170:ARG:HD3	2.55	0.41
2:E:91:LYS:NZ	4:E:141:HOH:O	2.53	0.41
2:B:64:ILE:HG13	2:B:65:LEU:N	2.35	0.40
1:D:225:ILE:O	1:D:225:ILE:HG22	2.21	0.40
1:A:210:PRO:O	1:A:263:HIS:HE1	2.03	0.40
1:D:28:VAL:O	1:D:29:ASP:C	2.60	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	274/348 (79%)	265 (97%)	8 (3%)	1 (0%)	34	42
1	D	274/348 (79%)	264 (96%)	8 (3%)	2 (1%)	22	26
2	B	97/99 (98%)	96 (99%)	1 (1%)	0	100	100
2	E	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
3	C	6/9 (67%)	6 (100%)	0	0	100	100
3	F	6/9 (67%)	6 (100%)	0	0	100	100
All	All	754/912 (83%)	732 (97%)	19 (2%)	3 (0%)	34	42

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	29	ASP
1	D	225	ILE
1	A	196	GLU

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	234/290 (81%)	215 (92%)	19 (8%)	11	15
1	D	234/290 (81%)	212 (91%)	22 (9%)	8	10
2	B	94/94 (100%)	90 (96%)	4 (4%)	29	40
2	E	94/94 (100%)	88 (94%)	6 (6%)	17	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	C	6/7 (86%)	6 (100%)	0	100	100
3	F	6/7 (86%)	5 (83%)	1 (17%)	2	2
All	All	668/782 (85%)	616 (92%)	52 (8%)	12	16

All (52) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	VAL
1	A	31	THR
1	A	41	GLU
1	A	45	TYR
1	A	79	ARG
1	A	110	LEU
1	A	154	GLU
1	A	155	ARG
1	A	156	LEU
1	A	176	ASN
1	A	198	LYS
1	A	228	MET
1	A	229	GLU
1	A	230	LEU
1	A	242	GLN
1	A	255	GLN
1	A	272	LEU
1	A	273	ARG
1	A	275	GLU
2	B	45	LYS
2	B	48	LYS
2	B	56	PHE
2	B	97	ARG
1	D	12	VAL
1	D	29	ASP
1	D	31	THR
1	D	44	ARG
1	D	45	TYR
1	D	66	LYS
1	D	73	SER
1	D	79	ARG
1	D	98	ILE
1	D	113	TYR
1	D	141	LEU

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Mol	Chain	Res	Type
1	D	156	LEU
1	D	165	VAL
1	D	169	ARG
1	D	176	ASN
1	D	220	ASN
1	D	226	GLN
1	D	229	GLU
1	D	255	GLN
1	D	259	CYS
1	D	272	LEU
1	D	275	GLU
2	E	12	ARG
2	E	45	LYS
2	E	50	GLU
2	E	56	PHE
2	E	67	HIS
2	E	70	PHE
3	F	3	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	176	ASN
1	A	263	HIS
2	B	17	ASN
1	D	115	GLN
1	D	220	ASN
2	E	29	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 [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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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, 95th 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	276/348 (79%)	0.34	18 (6%) 18 24	17, 27, 45, 57	0
1	D	276/348 (79%)	0.54	22 (7%) 12 16	18, 29, 55, 65	0
2	B	99/99 (100%)	0.18	4 (4%) 38 45	16, 23, 33, 35	0
2	E	99/99 (100%)	0.90	14 (14%) 2 3	17, 31, 44, 45	0
3	C	8/9 (88%)	0.56	0 100 100	31, 32, 33, 34	0
3	F	8/9 (88%)	0.11	1 (12%) 3 5	23, 25, 29, 31	0
All	All	766/912 (83%)	0.46	59 (7%) 13 17	16, 27, 50, 65	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	225	ILE	8.7
1	D	220	ASN	7.7
1	D	226	GLN	7.2
2	E	1	ILE	6.4
1	A	227	ASP	6.0
1	A	220	ASN	5.9
1	A	225	ILE	5.8
1	D	256	TYR	5.8
1	A	226	GLN	5.0
1	D	276	PRO	4.4
1	D	42	ASN	4.4
2	E	20	PRO	4.3
1	D	222	GLU	4.2
1	A	256	TYR	4.0
1	A	41	GLU	4.0
2	E	22	ILE	3.9
1	A	42	ASN	3.8
2	E	14	PRO	3.7
1	A	196	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	227	ASP	3.5
2	E	71	THR	3.4
2	E	69	GLU	3.4
1	D	41	GLU	3.4
1	D	273	ARG	3.3
2	E	47	PRO	3.2
1	D	275	GLU	3.1
2	E	16	GLU	3.1
2	E	48	LYS	3.1
1	D	221	GLY	3.0
1	A	276	PRO	3.0
2	E	19	LYS	2.9
1	A	197	ASP	2.9
2	E	18	GLY	2.8
1	D	268	GLU	2.8
1	D	196	GLU	2.7
2	E	13	HIS	2.7
1	D	274	TRP	2.6
1	D	252	GLY	2.6
2	B	58	LYS	2.5
1	A	275	GLU	2.5
1	A	255	GLN	2.4
1	A	273	ARG	2.4
1	D	253	LYS	2.3
1	A	222	GLU	2.3
2	B	48	LYS	2.3
2	E	27	VAL	2.2
1	A	89	LYS	2.2
1	D	258	THR	2.2
3	F	4	PHE	2.2
2	B	88	ALA	2.2
1	A	268	GLU	2.2
2	E	58	LYS	2.1
2	B	1	ILE	2.1
1	D	272	LEU	2.1
1	D	113	TYR	2.1
1	A	221	GLY	2.1
1	D	217	TRP	2.1
1	A	229	GLU	2.0
1	D	197	ASP	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.