Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 05:58 AM GMT

PDB ID	:	2VE6
Title	:	CRYSTAL STRUCTURE OF A MURINE MHC CLASS I H2-DB MOLECULE IN COMPLEX WITH A PHOTOCLEAVABLE PEPTIDE
Authors	:	Grotenbreg, G.M.; Roan, N.R.; Guillen, E.; Meijers, R.; Wang, J.H.; Bell, G.W.; Starnbach, M.N.; Ploegh, H.L.
Deposited on	:	2007-10-17
Resolution	:	2.65 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

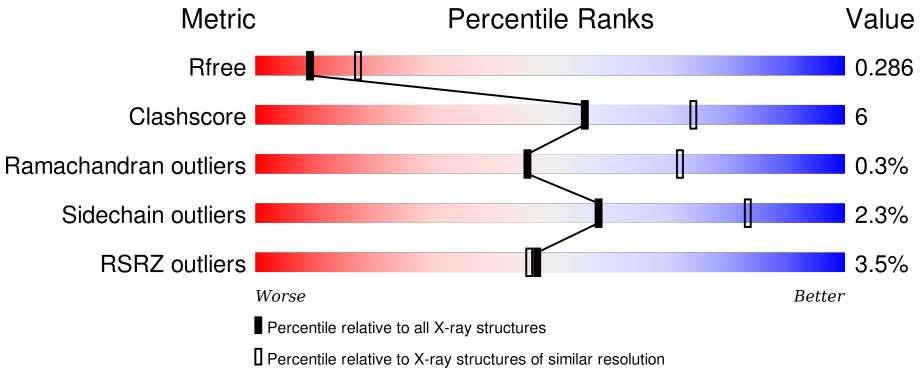
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.65 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}	91344	3152 (2.70-2.62)
Clashscore	102246	3524 (2.70-2.62)
Ramachandran outliers	100387	3469 (2.70-2.62)
Sidechain outliers	100360	3469 (2.70-2.62)
RSRZ outliers	91569	3161 (2.70-2.62)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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	277	86% 14%
1	D	277	87% 13%
1	G	277	8% 82% 16%
1	J	277	4% 87% 12%
2	B	99	89% 11%

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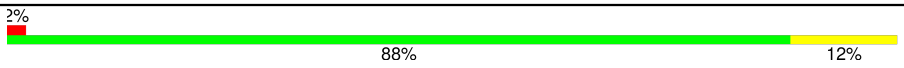
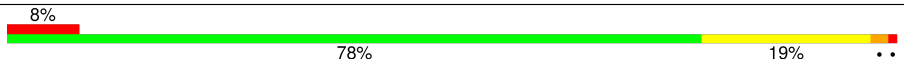
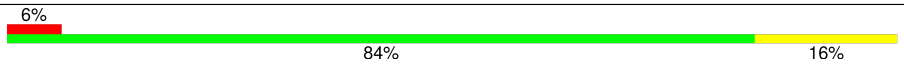
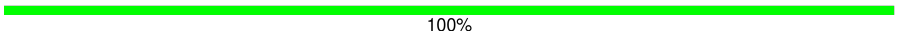
Mol	Chain	Length	Quality of chain
2	E	99	
2	H	99	
2	K	99	
3	C	9	
3	F	9	
3	I	9	
3	L	9	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12856 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	3	0
			2291	1446	407	429	9			
1	D	276	Total	C	N	O	S	0	2	0
			2284	1441	406	428	9			
1	G	276	Total	C	N	O	S	0	0	0
			2264	1430	400	425	9			
1	J	276	Total	C	N	O	S	0	0	0
			2264	1430	400	425	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
			818	522	138	150	8			
2	E	99	Total	C	N	O	S	0	1	0
			826	527	139	151	9			
2	H	99	Total	C	N	O	S	0	0	0
			818	522	138	150	8			
2	K	99	Total	C	N	O	S	0	0	0
			818	522	138	150	8			

- Molecule 3 is a protein called SENDAI VIRUS EPITOPE RESIDUES 324-332 MODIFIED AT P7.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			75	50	11	14			
3	F	9	Total	C	N	O	0	0	0
			75	50	11	14			
3	I	9	Total	C	N	O	0	0	0
			75	50	11	14			

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	L	9	Total	C	N	O	0	0	0
			75	50	11	14			

- Molecule 4 is water.

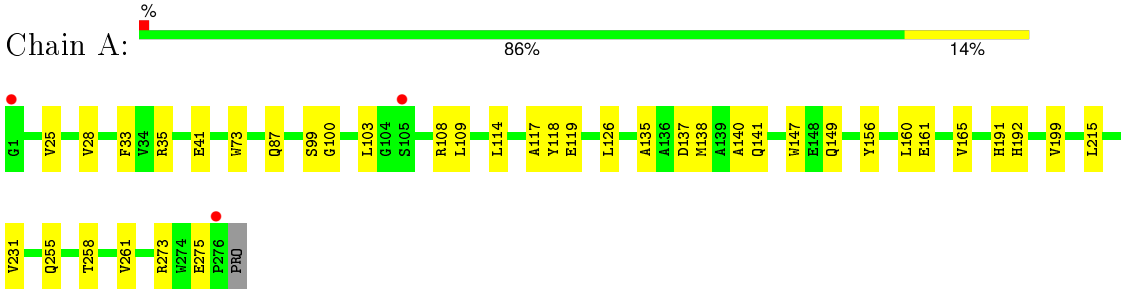
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	49	Total	O	0	0
			49	49		
4	B	27	Total	O	0	0
			27	27		
4	C	1	Total	O	0	0
			1	1		
4	D	38	Total	O	0	0
			38	38		
4	E	11	Total	O	0	0
			11	11		
4	F	1	Total	O	0	0
			1	1		
4	G	21	Total	O	0	0
			21	21		
4	H	4	Total	O	0	0
			4	4		
4	I	1	Total	O	0	0
			1	1		
4	J	15	Total	O	0	0
			15	15		
4	K	5	Total	O	0	0
			5	5		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

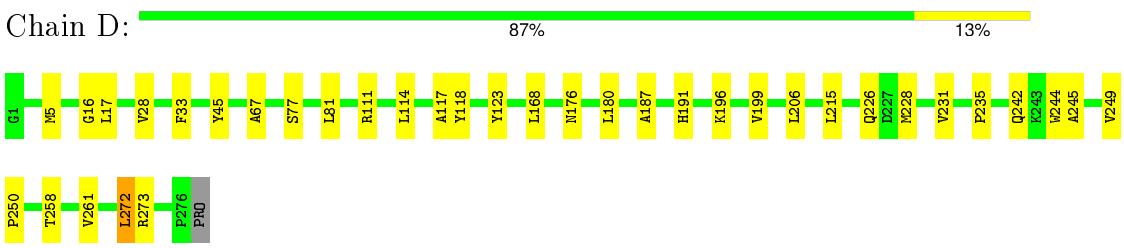
• Molecule 1: H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN D-B ALPHA CHAIN

Chain A:



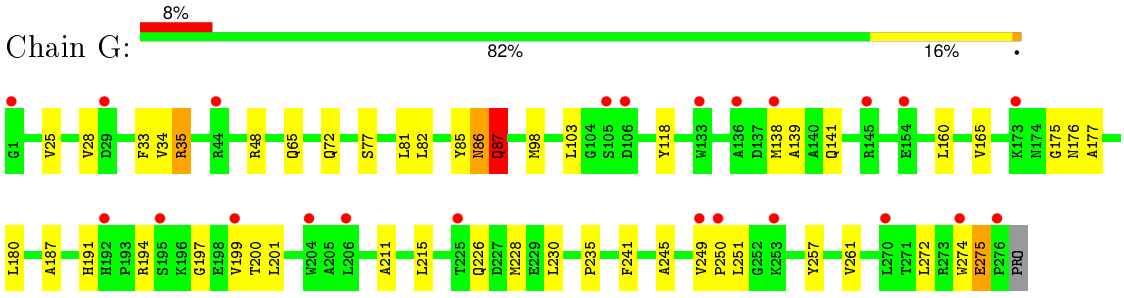
• Molecule 1: H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN D-B ALPHA CHAIN

Chain D:



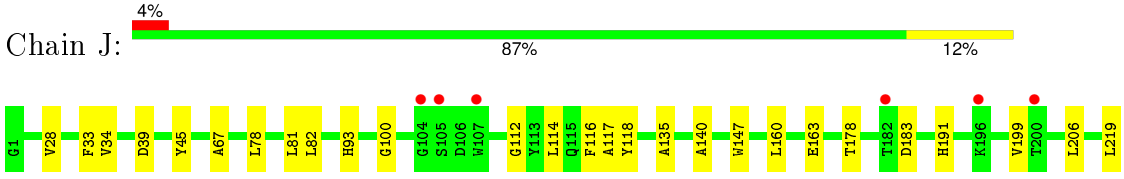
• Molecule 1: H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN D-B ALPHA CHAIN

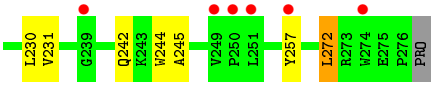
Chain G:



• Molecule 1: H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN D-B ALPHA CHAIN

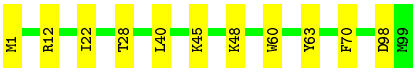
Chain J:





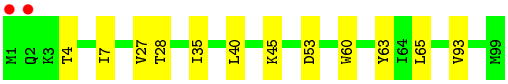
• Molecule 2: BETA-2-MICROGLOBULIN

Chain B:



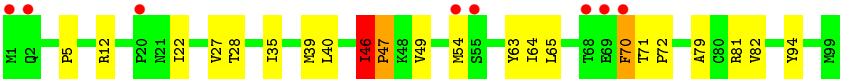
• Molecule 2: BETA-2-MICROGLOBULIN

Chain E:



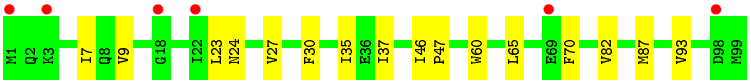
• Molecule 2: BETA-2-MICROGLOBULIN

Chain H:



• Molecule 2: BETA-2-MICROGLOBULIN

Chain K:



• Molecule 3: SENDAI VIRUS EPITOPE RESIDUES 324-332 MODIFIED AT P7

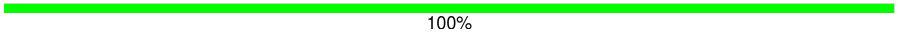
Chain C:

• Molecule 3: SENDAI VIRUS EPITOPE RESIDUES 324-332 MODIFIED AT P7

Chain F:

• Molecule 3: SENDAI VIRUS EPITOPE RESIDUES 324-332 MODIFIED AT P7

Chain I:



There are no outlier residues recorded for this chain.

• Molecule 3: SENDAI VIRUS EPITOPE RESIDUES 324-332 MODIFIED AT P7

Chain L:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	52.24Å 103.87Å 168.81Å 90.00° 90.83° 90.00°	Depositor
Resolution (Å)	19.66 – 2.65 19.66 – 2.65	Depositor EDS
% Data completeness (in resolution range)	96.9 (19.66-2.65) 96.9 (19.66-2.65)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.56 (at 2.67Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.234 , 0.291 0.234 , 0.286	Depositor DCC
R_{free} test set	2558 reflections (5.33%)	DCC
Wilson B-factor (Å^2)	51.6	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 43.8	EDS
Estimated twinning fraction	0.043 for h,-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 50560 reflections	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	12856	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.00% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PRQ

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	0.30	0/2358	0.48	0/3200
1	D	0.30	0/2351	0.49	0/3192
1	G	0.29	0/2331	0.46	0/3166
1	J	0.28	0/2331	0.46	0/3166
2	B	0.28	0/844	0.47	0/1143
2	E	0.30	0/852	0.48	0/1153
2	H	0.30	0/844	0.61	2/1143 (0.2%)
2	K	0.27	0/844	0.43	0/1143
3	C	0.41	0/62	0.43	0/81
3	F	0.40	0/62	0.39	0/81
3	I	0.44	0/62	0.32	0/81
3	L	0.41	0/62	0.34	0/81
All	All	0.29	0/13003	0.48	2/17630 (0.0%)

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
2	H	0	1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	H	46	ILE	C-N-CD	-9.04	100.72	120.60
2	H	46	ILE	C-N-CA	6.64	149.91	122.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	46	ILE	Peptide

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	2291	0	2162	27	0
1	D	2284	0	2155	26	0
1	G	2264	0	2136	43	0
1	J	2264	0	2136	21	0
2	B	818	0	795	7	0
2	E	826	0	803	7	0
2	H	818	0	795	19	0
2	K	818	0	795	8	0
3	C	75	0	63	2	0
3	F	75	0	63	3	0
3	I	75	0	63	0	0
3	L	75	0	63	2	0
4	A	49	0	0	0	0
4	B	27	0	0	1	0
4	C	1	0	0	0	0
4	D	38	0	0	0	0
4	E	11	0	0	0	0
4	F	1	0	0	0	0
4	G	21	0	0	1	0
4	H	4	0	0	0	0
4	I	1	0	0	0	0
4	J	15	0	0	0	0
4	K	5	0	0	0	0
All	All	12856	0	12029	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 6.

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:D:228:MET:HE2	1:D:245:ALA:HB1	1.43	1.00
2:H:46:ILE:HG22	2:H:47:PRO:C	1.87	0.92
1:D:215:LEU:HD22	1:D:261:VAL:HG22	1.56	0.87
1:G:187:ALA:HB3	1:G:272:LEU:HD11	1.64	0.79
1:D:228:MET:CE	1:D:245:ALA:HB1	2.14	0.77
2:H:46:ILE:HG22	2:H:47:PRO:O	1.91	0.71
1:G:199:VAL:HG23	1:G:251:LEU:HD12	1.71	0.70
2:H:46:ILE:CG2	2:H:47:PRO:C	2.60	0.69
1:G:201:LEU:HD12	1:G:249:VAL:HG21	1.75	0.69
1:D:187:ALA:HB3	1:D:272:LEU:HD21	1.75	0.67
1:G:191:HIS:CE1	1:G:199:VAL:HG13	2.29	0.67
1:A:25:VAL:HG21	4:B:2016:HOH:O	1.93	0.67
1:G:187:ALA:CB	1:G:272:LEU:HD11	2.24	0.67
1:D:77:SER:HB3	3:F:9:LEU:HD12	1.78	0.66
1:A:103:LEU:HD21	1:A:165:VAL:HG13	1.79	0.64
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.32	0.63
1:G:215:LEU:HD22	1:G:261:VAL:HG22	1.80	0.63
1:G:274:TRP:CD1	1:G:275:GLU:O	2.51	0.63
1:G:103:LEU:HD21	1:G:165:VAL:HG13	1.81	0.63
1:G:199:VAL:HG23	1:G:251:LEU:CD1	2.28	0.62
1:D:191:HIS:NE2	1:D:199:VAL:HG11	2.14	0.61
1:G:141:GLN:NE2	4:G:2014:HOH:O	2.33	0.61
1:D:231:VAL:HG13	1:D:244:TRP:CZ2	2.36	0.60
1:J:33:PHE:CD2	1:J:34:VAL:HG13	2.36	0.60
1:J:219:LEU:HD13	1:J:257:TYR:CE2	2.37	0.60
1:A:28:VAL:HG23	1:A:33:PHE:CE1	2.37	0.60
2:B:12:ARG:NH1	2:B:22:ILE:HD12	2.18	0.59
1:G:230:LEU:HD13	1:G:245:ALA:HB2	1.84	0.58
2:K:46:ILE:HG23	2:K:47:PRO:HD2	1.86	0.58
1:J:81:LEU:HD13	1:J:118:TYR:CD1	2.39	0.58
1:G:86:ASN:HA	1:G:87:GLN:HB3	1.86	0.58
1:J:28:VAL:HG23	1:J:33:PHE:CE1	2.39	0.57
1:A:28:VAL:HG23	1:A:33:PHE:CD1	2.40	0.56
1:A:147:TRP:CZ2	3:C:9:LEU:HD12	2.41	0.56
1:G:249:VAL:HG13	1:G:257:TYR:CE1	2.40	0.56
1:A:114:LEU:HD22	1:A:156:TYR:CG	2.41	0.56
1:G:274:TRP:CG	1:G:275:GLU:O	2.59	0.56
2:B:28:THR:HG22	2:B:63:TYR:HB2	1.88	0.56
2:H:12:ARG:NH2	2:H:22:ILE:HD12	2.22	0.55
1:A:258:THR:HG22	1:A:273:ARG:HB3	1.89	0.55
2:B:40:LEU:HD23	2:B:45:LYS:HA	1.89	0.55
1:J:117:ALA:HB2	2:K:60:TRP:CE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:28:VAL:HG23	1:J:33:PHE:CD1	2.42	0.54
1:G:28:VAL:HG23	1:G:33:PHE:CD1	2.42	0.54
1:D:81:LEU:HD13	1:D:118:TYR:CD1	2.42	0.54
1:A:191:HIS:NE2	1:A:199:VAL:HG11	2.23	0.54
1:G:33:PHE:CD2	1:G:34:VAL:HG13	2.43	0.53
2:H:28:THR:HG22	2:H:63:TYR:HB2	1.90	0.53
2:E:28:THR:HG22	2:E:63:TYR:HB2	1.90	0.53
2:K:24:ASN:HB3	2:K:65:LEU:HD11	1.91	0.53
1:A:255:GLN:HE22	1:A:273:ARG:HD3	1.74	0.52
1:G:235:PRO:HG2	2:H:65:LEU:HD22	1.92	0.52
1:A:138:MET:HE3	1:A:141:GLN:HB2	1.90	0.52
1:D:16:GLY:C	1:D:17:LEU:HD22	2.30	0.52
1:G:228:MET:CE	1:G:245:ALA:HB1	2.39	0.52
2:H:46:ILE:CG2	2:H:49:VAL:HG23	2.40	0.51
1:J:78:LEU:O	1:J:82:LEU:HD13	2.11	0.51
1:J:230:LEU:HD13	1:J:245:ALA:HB2	1.93	0.51
2:H:70:PHE:HA	2:H:71:THR:HB	1.94	0.50
1:D:123:TYR:CE2	3:F:9:LEU:HD22	2.47	0.49
1:J:45:TYR:CE2	1:J:67:ALA:HB2	2.46	0.49
1:A:109:LEU:HD22	1:A:161:GLU:HG2	1.93	0.49
1:D:176:ASN:HB2	1:D:180:LEU:HD12	1.93	0.49
2:H:70:PHE:HA	2:H:71:THR:CB	2.42	0.49
2:H:35:ILE:HD11	2:H:82:VAL:CG1	2.42	0.49
1:J:114:LEU:HD11	1:J:116:PHE:CZ	2.48	0.49
2:K:7:ILE:HB	2:K:93:VAL:HG21	1.95	0.49
1:A:215:LEU:HD22	1:A:261:VAL:HG22	1.95	0.49
2:H:54:MET:HG3	2:H:64:ILE:HD12	1.94	0.48
3:L:5:ASN:N	3:L:5:ASN:HD22	2.11	0.48
2:K:35:ILE:HD13	2:K:37:ILE:HD11	1.94	0.48
2:E:7:ILE:HB	2:E:93:VAL:HG21	1.95	0.48
1:D:258:THR:HG22	1:D:273[A]:ARG:HG3	1.96	0.48
2:H:46:ILE:HG23	2:H:47:PRO:HB2	1.95	0.48
1:G:25:VAL:HG22	1:G:35:ARG:HD2	1.96	0.48
1:J:163:GLU:OE2	1:J:163:GLU:N	2.47	0.48
1:G:82:LEU:HA	1:G:87:GLN:HG2	1.96	0.47
1:G:86:ASN:CA	1:G:87:GLN:CB	2.92	0.47
1:G:175:GLY:O	1:G:177:ALA:N	2.47	0.47
1:D:231:VAL:CG1	1:D:244:TRP:CZ2	2.96	0.47
1:A:135:ALA:HB1	1:A:140:ALA:HB3	1.96	0.47
1:J:191:HIS:NE2	1:J:199:VAL:HG11	2.29	0.47
1:D:45:TYR:CE2	1:D:67:ALA:HB2	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.50	0.47
1:J:219:LEU:HD13	1:J:257:TYR:CZ	2.50	0.47
1:A:114:LEU:HD23	1:A:126:LEU:HB2	1.96	0.47
1:D:258:THR:HG22	1:D:273[A]:ARG:CG	2.45	0.47
1:A:191:HIS:CD2	1:A:199:VAL:HG11	2.50	0.46
2:E:27:VAL:HG11	2:E:35:ILE:CD1	2.45	0.46
1:J:147:TRP:CZ2	3:L:9:LEU:HD12	2.50	0.46
2:H:40:LEU:HD21	2:H:81:ARG:NH2	2.29	0.46
1:G:211:ALA:HB2	1:G:241:PHE:CE1	2.51	0.46
1:G:249:VAL:HG12	1:G:250:PRO:O	2.15	0.46
1:G:228:MET:HE2	1:G:245:ALA:HB1	1.98	0.46
1:D:28:VAL:HG23	1:D:33:PHE:CE1	2.50	0.46
1:A:100:GLY:O	1:A:160:LEU:HD22	2.15	0.46
1:G:86:ASN:N	1:G:87:GLN:HB2	2.30	0.46
1:D:228:MET:CE	1:D:245:ALA:CB	2.90	0.45
1:A:87:GLN:NE2	1:A:118:TYR:OH	2.48	0.45
1:D:272:LEU:N	1:D:272:LEU:HD12	2.31	0.45
1:D:191:HIS:CD2	1:D:199:VAL:HG11	2.52	0.45
1:A:114:LEU:HD22	1:A:156:TYR:CB	2.47	0.45
2:E:40:LEU:HD23	2:E:45:LYS:HA	1.99	0.45
1:J:135:ALA:HB1	1:J:140:ALA:HB3	1.98	0.45
1:J:272:LEU:N	1:J:272:LEU:HD23	2.31	0.45
2:E:27:VAL:HG11	2:E:35:ILE:HD11	1.98	0.45
1:G:77:SER:O	1:G:81:LEU:HB2	2.17	0.45
1:G:197:GLY:C	1:G:251:LEU:HD13	2.37	0.45
2:B:12:ARG:CZ	2:B:22:ILE:HD12	2.47	0.45
1:A:25:VAL:HG22	1:A:35:ARG:HG3	1.98	0.45
1:A:73:TRP:CH2	3:C:9:LEU:HD13	2.52	0.45
1:G:81:LEU:HD22	1:G:118:TYR:CE1	2.51	0.45
2:H:5:PRO:HB2	2:H:27:VAL:HG13	1.98	0.45
1:D:235:PRO:HG2	2:E:65:LEU:HD22	2.00	0.44
1:G:82:LEU:O	1:G:87:GLN:HB3	2.17	0.44
2:H:71:THR:N	2:H:72:PRO:HD3	2.33	0.44
1:G:191:HIS:HE1	1:G:199:VAL:HG22	1.82	0.44
1:A:135:ALA:HB1	1:A:140:ALA:CB	2.48	0.43
1:G:138:MET:O	1:G:139:ALA:HB3	2.18	0.43
1:G:103:LEU:CD2	1:G:165:VAL:HG13	2.46	0.43
1:A:137:ASP:O	1:A:141:GLN:HG2	2.19	0.43
1:A:109:LEU:HD22	1:A:161:GLU:CG	2.48	0.43
2:H:46:ILE:HG21	2:H:49:VAL:HG23	2.01	0.43
1:G:86:ASN:HA	1:G:87:GLN:CB	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:GLU:O	2:B:1:MET:HE2	2.19	0.43
2:K:27:VAL:HG12	2:K:30:PHE:CE1	2.54	0.43
1:J:82:LEU:HD11	1:J:93:HIS:CD2	2.54	0.42
1:D:28:VAL:HG23	1:D:33:PHE:CD1	2.55	0.42
1:J:206:LEU:HD22	1:J:242:GLN:NE2	2.35	0.42
2:H:39:MET:C	2:H:40:LEU:HD12	2.40	0.42
1:J:112:GLY:HA3	1:J:160:LEU:HD13	2.01	0.42
1:D:5:MET:HB2	1:D:168:LEU:HD13	2.02	0.42
1:D:187:ALA:CB	1:D:272:LEU:HD21	2.45	0.42
1:G:199:VAL:N	1:G:249:VAL:O	2.53	0.42
1:G:85:TYR:CE2	1:G:139:ALA:CB	3.03	0.42
2:K:9:VAL:HG12	2:K:23:LEU:HD11	2.02	0.42
1:G:81:LEU:HD23	1:G:81:LEU:O	2.20	0.41
1:A:118:TYR:CD2	1:A:119:GLU:HG2	2.55	0.41
1:G:191:HIS:ND1	1:G:199:VAL:HG13	2.35	0.41
1:G:81:LEU:HD22	1:G:118:TYR:CZ	2.55	0.41
3:F:7:PRQ:HAM	3:F:7:PRQ:OAD	2.20	0.41
1:G:160:LEU:O	1:G:165:VAL:HG23	2.21	0.41
1:D:206:LEU:HD22	1:D:242:GLN:HG3	2.03	0.41
1:G:194:ARG:HB2	1:G:200:THR:HG23	2.03	0.41
1:D:249:VAL:HG13	1:D:250:PRO:HD2	2.03	0.41
1:G:187:ALA:CB	1:G:272:LEU:CD1	2.97	0.40
2:K:35:ILE:HD11	2:K:82:VAL:CG1	2.50	0.40
1:J:100:GLY:O	1:J:160:LEU:HD22	2.21	0.40
2:H:79:ALA:HB2	2:H:94:TYR:CD2	2.55	0.40
1:A:192:HIS:NE2	2:B:98:ASP:O	2.54	0.40
1:J:231:VAL:HG11	1:J:244:TRP:CD1	2.56	0.40
2:H:46:ILE:HG22	2:H:47:PRO:CA	2.50	0.40
1:G:85:TYR:C	1:G:87:GLN:HB2	2.42	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	276/277 (100%)	264 (96%)	12 (4%)	0	100	100
1	D	276/277 (100%)	270 (98%)	6 (2%)	0	100	100
1	G	274/277 (99%)	254 (93%)	16 (6%)	4 (2%)	13	28
1	J	274/277 (99%)	263 (96%)	11 (4%)	0	100	100
2	B	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
2	E	98/99 (99%)	95 (97%)	3 (3%)	0	100	100
2	H	97/99 (98%)	94 (97%)	2 (2%)	1 (1%)	19	41
2	K	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
3	C	4/9 (44%)	3 (75%)	1 (25%)	0	100	100
3	F	4/9 (44%)	4 (100%)	0	0	100	100
3	I	4/9 (44%)	4 (100%)	0	0	100	100
3	L	4/9 (44%)	4 (100%)	0	0	100	100
All	All	1505/1540 (98%)	1444 (96%)	56 (4%)	5 (0%)	46	72

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	G	176	ASN
2	H	47	PRO
1	G	86	ASN
1	G	87	GLN
1	G	275	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	237/235 (101%)	230 (97%)	7 (3%)	48	77
1	D	236/235 (100%)	231 (98%)	5 (2%)	61	85
1	G	234/235 (100%)	226 (97%)	8 (3%)	44	72
1	J	234/235 (100%)	230 (98%)	4 (2%)	68	88

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
2	B	93/93 (100%)	91 (98%)	2 (2%)	60 84
2	E	94/93 (101%)	92 (98%)	2 (2%)	61 85
2	H	93/93 (100%)	92 (99%)	1 (1%)	80 93
2	K	93/93 (100%)	91 (98%)	2 (2%)	60 84
3	C	5/5 (100%)	4 (80%)	1 (20%)	1 3
3	F	5/5 (100%)	5 (100%)	0	100 100
3	I	5/5 (100%)	5 (100%)	0	100 100
3	L	5/5 (100%)	5 (100%)	0	100 100
All	All	1334/1332 (100%)	1302 (98%)	32 (2%)	58 82

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

Mol	Chain	Res	Type
1	A	41	GLU
1	A	99	SER
1	A	108	ARG
1	A	149[A]	GLN
1	A	149[B]	GLN
1	A	231	VAL
1	A	275	GLU
2	B	48	LYS
2	B	70	PHE
3	C	9	LEU
1	D	111	ARG
1	D	114	LEU
1	D	196	LYS
1	D	226	GLN
1	D	272	LEU
2	E	4	THR
2	E	53	ASP
1	G	35	ARG
1	G	48	ARG
1	G	65	GLN
1	G	72	GLN
1	G	87	GLN
1	G	98	MET
1	G	180	LEU
1	G	226	GLN
2	H	70	PHE

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Mol	Chain	Res	Type
1	J	39	ASP
1	J	178	THR
1	J	183	ASP
1	J	272	LEU
2	K	70	PHE
2	K	87	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (23) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	GLN
1	A	87	GLN
1	A	97	GLN
2	B	29	GLN
3	C	5	ASN
1	D	54	GLN
1	D	87	GLN
1	D	97	GLN
1	D	226	GLN
1	D	255	GLN
2	E	8	GLN
2	E	29	GLN
3	F	5	ASN
1	G	72	GLN
1	G	97	GLN
1	G	127	ASN
1	G	191	HIS
1	G	226	GLN
3	I	5	ASN
1	J	72	GLN
1	J	97	GLN
1	J	242	GLN
3	L	5	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
3	PRQ	C	7	3	12,14,15	2.02	1 (8%)	10,18,20	1.35	2 (20%)
3	PRQ	F	7	3	12,14,15	2.15	1 (8%)	10,18,20	1.12	1 (10%)
3	PRQ	I	7	3	12,14,15	2.11	1 (8%)	10,18,20	1.27	2 (20%)
3	PRQ	L	7	3	12,14,15	2.15	1 (8%)	10,18,20	1.09	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	PRQ	C	7	3	-	0/10/11/12	0/1/1/1
3	PRQ	F	7	3	-	0/10/11/12	0/1/1/1
3	PRQ	I	7	3	-	0/10/11/12	0/1/1/1
3	PRQ	L	7	3	-	0/10/11/12	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	7	PRQ	OAC-NAN	6.63	1.35	1.22
3	I	7	PRQ	OAC-NAN	6.93	1.36	1.22
3	L	7	PRQ	OAC-NAN	7.02	1.36	1.22
3	F	7	PRQ	OAC-NAN	7.03	1.36	1.22

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	I	7	PRQ	CAI-CAL-NAN	2.07	119.27	116.59
3	F	7	PRQ	CAH-CAK-CAL	2.21	119.44	117.00
3	C	7	PRQ	CAI-CAL-NAN	2.27	119.53	116.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	C	7	PRQ	CAH-CAK-CAL	2.42	119.67	117.00
3	I	7	PRQ	CAH-CAK-CAL	2.48	119.74	117.00

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	7	PRQ	1	0

5.5 Carbohydrates (i)

There are no carbohydrates 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	276/277 (99%)	-0.11	3 (1%) 82 82	46, 54, 61, 64	0
1	D	276/277 (99%)	-0.17	0 100 100	47, 53, 59, 61	0
1	G	276/277 (99%)	0.52	23 (8%) 14 11	49, 57, 63, 64	0
1	J	276/277 (99%)	0.37	12 (4%) 39 37	51, 58, 63, 66	0
2	B	99/99 (100%)	-0.20	0 100 100	48, 52, 57, 62	0
2	E	99/99 (100%)	-0.07	2 (2%) 68 67	46, 52, 57, 59	0
2	H	99/99 (100%)	0.64	8 (8%) 15 12	56, 59, 62, 63	0
2	K	99/99 (100%)	0.52	6 (6%) 25 22	52, 55, 63, 64	0
3	C	8/9 (88%)	-0.11	0 100 100	40, 41, 41, 41	0
3	F	8/9 (88%)	0.26	0 100 100	37, 41, 41, 41	0
3	I	8/9 (88%)	0.19	0 100 100	66, 66, 67, 67	0
3	L	8/9 (88%)	0.33	0 100 100	68, 68, 70, 71	0
All	All	1532/1540 (99%)	0.17	54 (3%) 48 46	37, 55, 62, 71	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	105	SER	7.9
2	K	1	MET	6.0
1	G	105	SER	5.0
1	J	250	PRO	4.2
2	H	54	MET	4.0
1	G	199	VAL	3.4
1	G	250	PRO	3.3
2	E	1	MET	3.2
1	G	274	TRP	3.1
1	G	192	HIS	3.0
2	H	68	THR	3.0

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Mol	Chain	Res	Type	RSRZ
1	J	196	LYS	3.0
2	H	1	MET	3.0
1	J	107	TRP	2.9
1	G	249	VAL	2.9
1	G	106	ASP	2.9
2	H	69	GLU	2.9
1	J	239	GLY	2.8
1	G	145	ARG	2.7
2	K	18	GLY	2.7
2	K	22	ILE	2.7
1	G	270	LEU	2.6
1	J	249	VAL	2.6
1	J	182	THR	2.5
1	G	133	TRP	2.5
1	J	257	TYR	2.5
1	G	1	GLY	2.5
1	G	154	GLU	2.5
1	J	104	GLY	2.4
1	J	200	THR	2.4
1	A	1	GLY	2.4
2	H	55	SER	2.4
1	A	105	SER	2.4
2	H	20	PRO	2.4
1	J	251	LEU	2.3
1	G	253	LYS	2.3
1	G	276	PRO	2.3
2	H	2	GLN	2.3
2	H	70	PHE	2.2
1	G	173	LYS	2.2
1	G	195	SER	2.1
1	J	274	TRP	2.1
2	K	69	GLU	2.1
2	K	98	ASP	2.1
1	G	225	THR	2.1
1	G	44	ARG	2.1
1	G	136	ALA	2.1
2	E	2	GLN	2.0
1	A	276[A]	PRO	2.0
1	G	138	MET	2.0
1	G	204	TRP	2.0
1	G	29	ASP	2.0
2	K	3	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	G	206	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
3	PRQ	I	7	14/15	0.88	0.20	-	66,67,67,67	0
3	PRQ	F	7	14/15	0.93	0.19	-	37,40,41,41	0
3	PRQ	L	7	14/15	0.91	0.22	-	68,70,70,70	0
3	PRQ	C	7	14/15	0.95	0.17	-	41,43,45,46	0

6.3 Carbohydrates (i)

There are no carbohydrates 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.