



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:28 PM UTC

PDB ID : 3TBY / pdb_00003tby
Title : CRYSTAL STRUCTURE OF THE MURINE CLASS I MAJOR HISTO-COMPATIBILITY COMPLEX H-2DB IN COMPLEX WITH THE LCMV-DERIVED GP33 ALTERED PEPTIDE ligand (V3P, Y4F)
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Deposited on : 2011-08-08
Resolution : 2.50 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	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

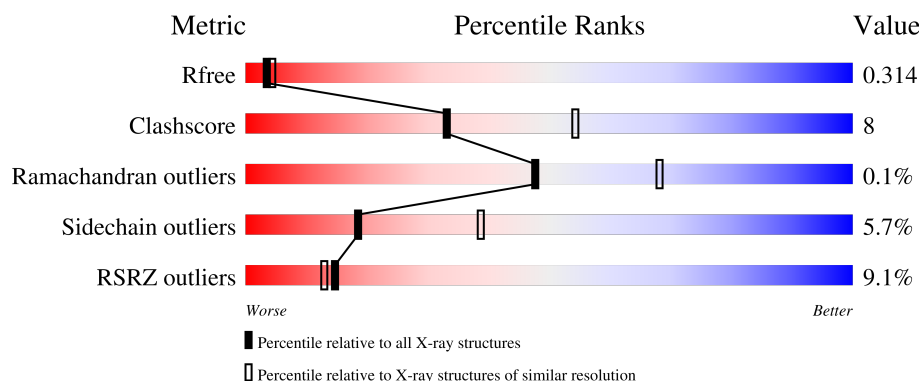
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	180053	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	276	11% 77% 18% • •
1	D	276	11% 80% 15% • •
1	G	276	13% 77% 18% • •
1	J	276	12% 78% 16% • 5%
2	B	99	3% 73% 26% •

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Mol	Chain	Length	Quality of chain
2	E	99	2%67%30%
2	H	99	87%12%
2	K	99	3%80%18%
3	C	9	56%44%
3	F	9	67%33%
3	I	9	56%44%
3	L	9	22%67%11%

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12496 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	266	Total	C	N	O	S	0	0	0
			2187	1383	386	409	9			
1	D	266	Total	C	N	O	S	0	0	0
			2187	1383	386	409	9			
1	G	264	Total	C	N	O	S	0	0	0
			2175	1376	384	406	9			
1	J	262	Total	C	N	O	S	0	0	0
			2159	1366	381	403	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
			817	521	137	152	7			
2	E	99	Total	C	N	O	S	0	0	0
			817	521	137	152	7			
2	H	99	Total	C	N	O	S	0	0	0
			817	521	137	152	7			
2	K	99	Total	C	N	O	S	0	0	0
			817	521	137	152	7			

- Molecule 3 is a protein called GLYCOPROTEIN GPC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	S	0	0	0
			72	48	11	12	1			
3	F	9	Total	C	N	O	S	0	0	0
			72	48	11	12	1			
3	I	9	Total	C	N	O	S	0	0	0
			72	48	11	12	1			
3	L	9	Total	C	N	O	S	0	0	0
			72	48	11	12	1			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	3	PRO	VAL	engineered mutation	UNP P07399
C	4	PHE	TYR	engineered mutation	UNP P07399
C	9	MET	CYS	engineered mutation	UNP P07399
F	3	PRO	VAL	engineered mutation	UNP P07399
F	4	PHE	TYR	engineered mutation	UNP P07399
F	9	MET	CYS	engineered mutation	UNP P07399
I	3	PRO	VAL	engineered mutation	UNP P07399
I	4	PHE	TYR	engineered mutation	UNP P07399
I	9	MET	CYS	engineered mutation	UNP P07399
L	3	PRO	VAL	engineered mutation	UNP P07399
L	4	PHE	TYR	engineered mutation	UNP P07399
L	9	MET	CYS	engineered mutation	UNP P07399

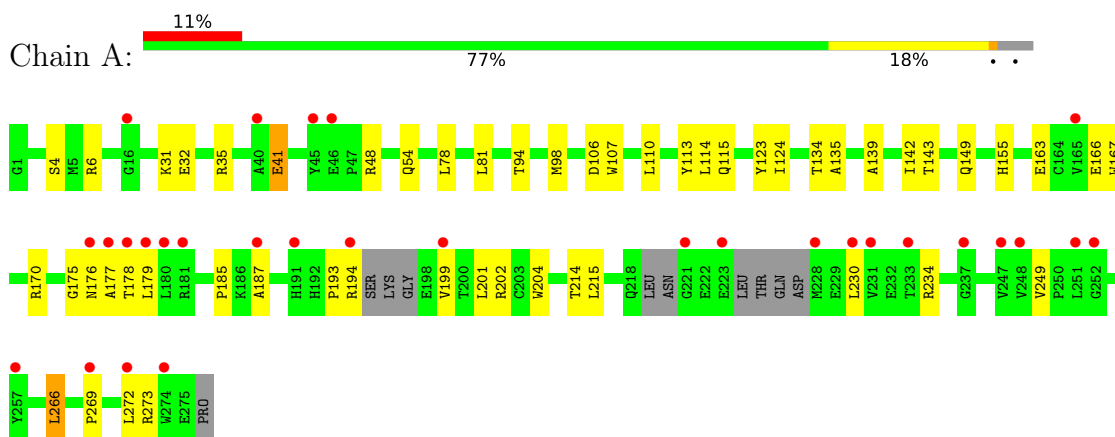
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	38	Total O 38 38	0	0
4	B	26	Total O 26 26	0	0
4	C	2	Total O 2 2	0	0
4	D	35	Total O 35 35	0	0
4	E	24	Total O 24 24	0	0
4	F	1	Total O 1 1	0	0
4	G	49	Total O 49 49	0	0
4	H	19	Total O 19 19	0	0
4	I	2	Total O 2 2	0	0
4	J	22	Total O 22 22	0	0
4	K	13	Total O 13 13	0	0
4	L	1	Total O 1 1	0	0

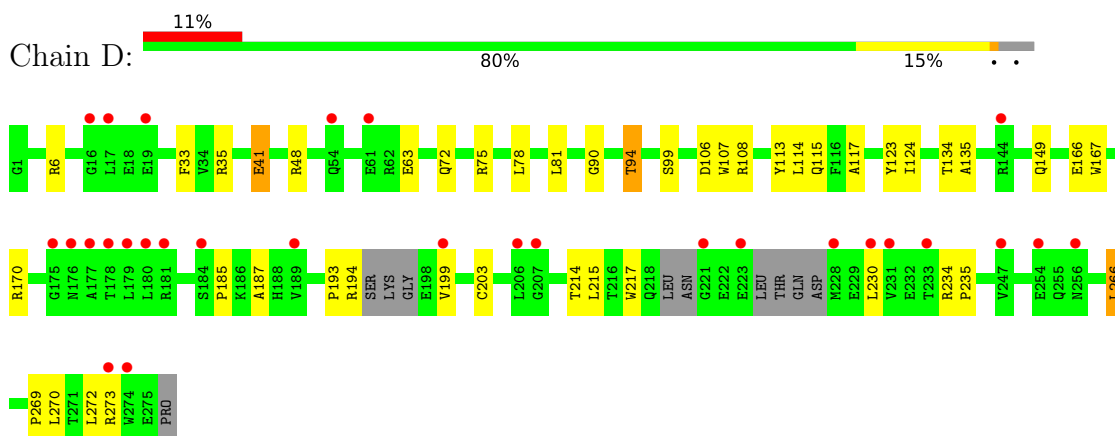
3 Residue-property plots [i](#)

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.

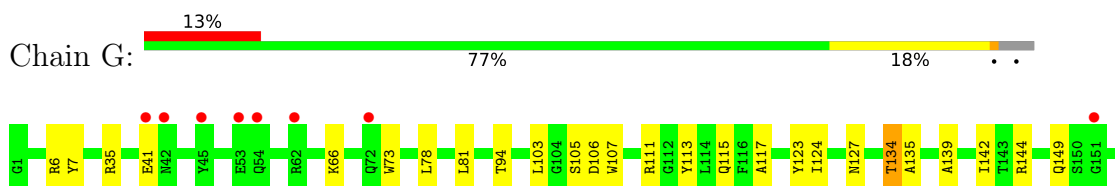
- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

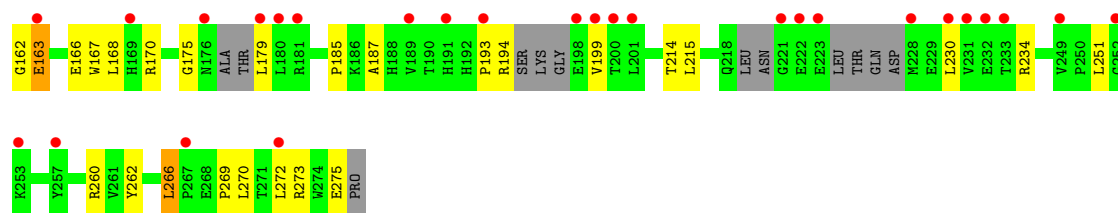


- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

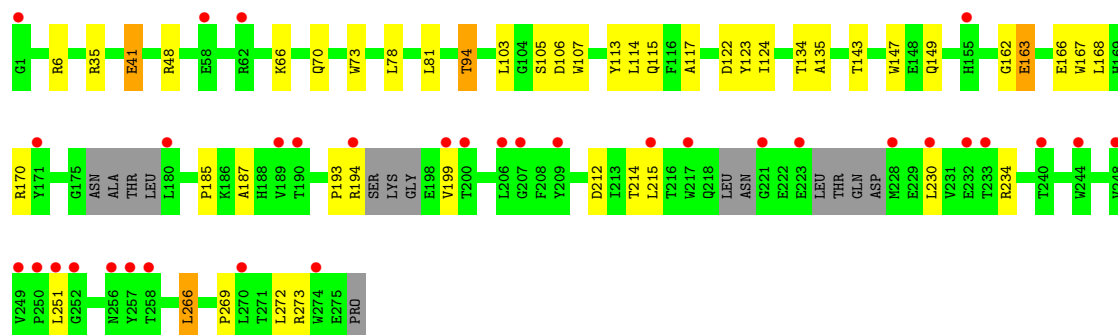
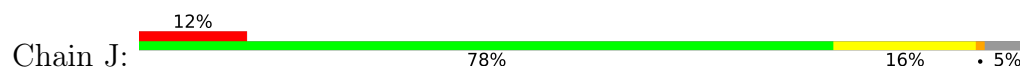


- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

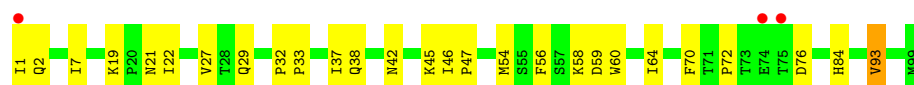
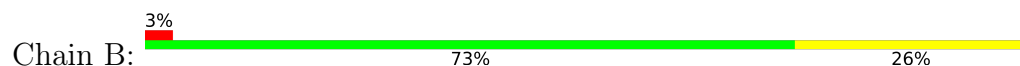




- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain



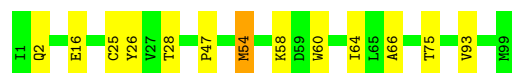
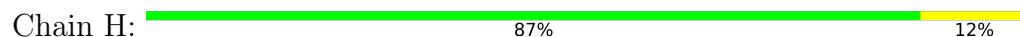
- Molecule 2: Beta-2-microglobulin



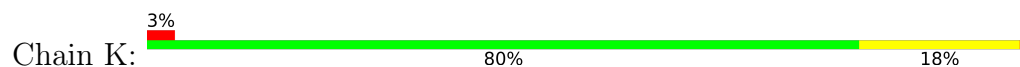
- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



● Molecule 3: GLYCOPROTEIN GPC

Chain C:  56% 44%

● Molecule 3: GLYCOPROTEIN GPC

Chain F:  67% 33%

● Molecule 3: GLYCOPROTEIN GPC

Chain I:  56% 44%

● Molecule 3: GLYCOPROTEIN GPC

Chain L:  22% 67% 11%

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.82Å 124.27Å 99.65Å 90.00° 103.29° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.9 (20.00-2.50) 97.7 (20.00-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 2.50Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.284 , 0.315 0.284 , 0.314	Depositor DCC
R_{free} test set	3747 reflections (4.93%)	wwPDB-VP
Wilson B-factor (Å ²)	40.2	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 34.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	12496	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.22% of the height of the origin peak. No significant pseudotranslation is detected.*

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	0.61	0/2250	0.71	0/3052
1	D	0.58	0/2250	0.72	0/3052
1	G	0.60	0/2237	0.70	0/3032
1	J	0.61	0/2221	0.72	0/3010
2	B	0.67	0/843	0.82	1/1144 (0.1%)
2	E	0.71	0/843	0.94	2/1144 (0.2%)
2	H	0.76	0/843	0.92	0/1144
2	K	0.76	0/843	0.98	2/1144 (0.2%)
3	C	0.85	0/74	0.92	0/97
3	F	0.77	0/74	1.01	0/97
3	I	0.84	0/74	1.13	0/97
3	L	0.87	0/74	0.87	0/97
All	All	0.64	0/12626	0.78	5/17110 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	47	PRO	N-CA-C	9.11	131.25	112.47
2	E	47	PRO	CB-CA-C	-8.12	98.16	111.56
2	K	46	ILE	CA-C-N	5.16	126.29	119.84
2	K	46	ILE	C-N-CA	5.16	126.29	119.84
2	B	56	PHE	N-CA-C	5.03	117.02	109.23

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	2187	0	2049	33	0
1	D	2187	0	2049	34	0
1	G	2175	0	2036	30	0
1	J	2159	0	2019	31	0
2	B	817	0	785	20	0
2	E	817	0	785	23	0
2	H	817	0	785	8	0
2	K	817	0	785	18	0
3	C	72	0	72	6	0
3	F	72	0	72	3	0
3	I	72	0	72	4	0
3	L	72	0	72	8	0
4	A	38	0	0	2	0
4	B	26	0	0	1	0
4	C	2	0	0	0	0
4	D	35	0	0	6	0
4	E	24	0	0	1	0
4	F	1	0	0	0	0
4	G	49	0	0	3	0
4	H	19	0	0	0	0
4	I	2	0	0	0	0
4	J	22	0	0	1	0
4	K	13	0	0	0	0
4	L	1	0	0	0	0
All	All	12496	0	11581	186	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 8.

All (186) 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:K:33:PRO:O	2:K:54:MET:HE1	1.80	0.82
2:E:22:ILE:HD13	2:E:69:GLU:HA	1.68	0.74
1:J:66:LYS:HG2	3:L:4:PHE:CE1	2.26	0.70
2:E:81:ARG:HD3	2:E:90:PRO:HB2	1.74	0.69
1:G:35:ARG:NH2	2:H:54:MET:O	2.25	0.68
3:L:2:ALA:HB1	3:L:3:PRO:HD2	1.74	0.68
2:B:42:ASN:ND2	2:B:76:ASP:OD1	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:54:MET:HE3	2:H:64:ILE:HD12	1.75	0.67
2:H:54:MET:HE2	2:H:64:ILE:HB	1.75	0.67
1:A:185:PRO:HD2	1:A:266:LEU:HD13	1.78	0.66
1:J:185:PRO:HD2	1:J:266:LEU:HD13	1.78	0.65
1:A:31:LYS:HZ1	1:A:179:LEU:HD12	1.61	0.65
1:D:185:PRO:HD2	1:D:266:LEU:HD13	1.79	0.64
1:G:185:PRO:HD2	1:G:266:LEU:HD13	1.81	0.61
1:J:117:ALA:HB2	2:K:60:TRP:CE2	2.36	0.61
2:B:7:ILE:HB	2:B:93:VAL:HG11	1.84	0.60
2:B:21:ASN:HB3	2:B:70:PHE:CE1	2.37	0.59
1:A:54:GLN:HG3	4:A:369:HOH:O	2.02	0.59
1:J:70:GLN:HE22	3:L:5:ASN:ND2	2.01	0.58
1:D:187:ALA:HB3	1:D:272:LEU:HD12	1.84	0.58
1:J:187:ALA:HB3	1:J:272:LEU:HD12	1.85	0.58
1:G:7:TYR:CE2	3:I:2:ALA:HB2	2.40	0.57
1:A:31:LYS:NZ	1:A:179:LEU:HD12	2.20	0.57
1:D:124:ILE:HG13	1:D:135:ALA:HB2	1.87	0.57
2:H:54:MET:CE	2:H:64:ILE:HD12	2.35	0.56
2:K:7:ILE:CD1	2:K:82:VAL:HG21	2.35	0.56
1:G:187:ALA:HB3	1:G:272:LEU:HD12	1.87	0.55
2:B:27:VAL:HG21	2:B:37:ILE:HD13	1.89	0.55
2:E:2:GLN:HE22	2:E:85:ASP:HB3	1.71	0.55
1:D:75:ARG:NH2	4:D:356:HOH:O	2.38	0.54
2:K:22:ILE:HD13	2:K:69:GLU:HA	1.89	0.54
1:D:235:PRO:HG2	2:E:65:LEU:HD13	1.90	0.54
2:K:21:ASN:OD1	2:K:22:ILE:N	2.34	0.53
2:K:40:LEU:HB2	2:K:79:ALA:HB3	1.91	0.52
1:G:117:ALA:HB2	2:H:60:TRP:CE2	2.45	0.52
1:A:187:ALA:HB3	1:A:272:LEU:HD12	1.92	0.52
2:E:59:ASP:O	2:E:60:TRP:HB2	2.10	0.52
1:A:214:THR:C	1:A:215:LEU:HD12	2.35	0.52
2:B:38:GLN:NE2	2:B:45:LYS:HG3	2.25	0.51
1:G:214:THR:C	1:G:215:LEU:HD12	2.36	0.51
1:A:139:ALA:O	1:A:142:ILE:HD12	2.11	0.51
1:D:94:THR:HG21	2:E:31:HIS:CE1	2.45	0.51
1:A:167:TRP:CE3	1:A:170:ARG:HD3	2.45	0.51
2:E:81:ARG:HD3	2:E:90:PRO:CB	2.40	0.51
1:G:167:TRP:CE3	1:G:170:ARG:HD3	2.46	0.51
1:D:81:LEU:HD21	1:D:123:TYR:CZ	2.45	0.51
1:J:230:LEU:C	1:J:230:LEU:HD12	2.36	0.51
1:J:103:LEU:HD11	1:J:168:LEU:HD23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:167:TRP:CE3	1:J:170:ARG:HD3	2.46	0.50
2:K:7:ILE:HD13	2:K:82:VAL:HG21	1.92	0.50
1:G:81:LEU:HD21	1:G:123:TYR:CZ	2.45	0.50
1:D:167:TRP:CE3	1:D:170:ARG:HD3	2.46	0.50
1:A:81:LEU:HD21	1:A:123:TYR:CZ	2.47	0.50
1:J:214:THR:C	1:J:215:LEU:HD12	2.36	0.50
1:A:31:LYS:HZ1	1:A:178:THR:HG22	1.77	0.50
1:A:175:GLY:C	1:A:177:ALA:H	2.20	0.50
1:A:230:LEU:HD12	1:A:230:LEU:C	2.36	0.50
1:D:230:LEU:C	1:D:230:LEU:HD12	2.37	0.50
2:E:21:ASN:OD1	2:E:22:ILE:N	2.42	0.50
2:B:54:MET:HE2	2:B:64:ILE:HD12	1.94	0.49
1:D:35:ARG:NH2	2:E:54:MET:O	2.43	0.49
1:G:139:ALA:O	1:G:142:ILE:HD12	2.13	0.49
1:G:106:ASP:O	1:G:107:TRP:HB2	2.13	0.48
1:D:94:THR:HG21	2:E:31:HIS:HE1	1.78	0.48
2:K:35:ILE:O	2:K:35:ILE:HG23	2.12	0.48
1:G:230:LEU:C	1:G:230:LEU:HD12	2.38	0.48
1:D:117:ALA:HB2	2:E:60:TRP:CE2	2.49	0.48
2:E:50:GLU:HB2	2:E:67:HIS:CE1	2.49	0.48
1:A:155:HIS:HB3	3:C:6:PHE:CZ	2.48	0.48
1:D:193:PRO:O	1:D:194:ARG:C	2.57	0.48
1:J:94:THR:HG21	2:K:31:HIS:CE1	2.48	0.48
2:K:7:ILE:HD13	2:K:82:VAL:CG2	2.43	0.48
1:A:31:LYS:NZ	1:A:179:LEU:CD1	2.77	0.47
1:G:124:ILE:HG13	1:G:135:ALA:HB2	1.95	0.47
1:D:75:ARG:NH1	4:D:344:HOH:O	2.46	0.47
2:E:42:ASN:ND2	2:E:76:ASP:OD1	2.38	0.47
1:G:6:ARG:NH2	1:G:113:TYR:CE1	2.83	0.47
1:G:260:ARG:HD2	4:G:382:HOH:O	2.14	0.47
1:G:66:LYS:NZ	3:I:2:ALA:O	2.39	0.47
1:J:48:ARG:NH1	2:K:53:ASP:OD2	2.46	0.47
1:A:31:LYS:NZ	1:A:178:THR:HG22	2.30	0.47
2:B:32:PRO:HD2	2:B:84:HIS:CE1	2.50	0.47
2:B:38:GLN:HE21	2:B:45:LYS:CG	2.27	0.47
1:G:193:PRO:O	1:G:194:ARG:C	2.57	0.47
1:J:106:ASP:O	1:J:107:TRP:HB2	2.14	0.47
2:B:27:VAL:HG21	2:B:37:ILE:CD1	2.44	0.46
1:D:214:THR:C	1:D:215:LEU:HD12	2.40	0.46
1:A:230:LEU:HD12	1:A:230:LEU:O	2.16	0.46
1:G:199:VAL:HG13	1:G:251:LEU:HG	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:66:LYS:HZ1	3:L:1:LYS:HB3	1.80	0.46
1:A:41:GLU:CD	1:A:41:GLU:N	2.74	0.46
2:E:5:PRO:HB3	2:E:30:PHE:HB3	1.97	0.46
1:A:124:ILE:HG13	1:A:135:ALA:HB2	1.98	0.46
3:C:5:ASN:N	3:C:5:ASN:HD22	2.12	0.46
1:D:6:ARG:NH2	1:D:113:TYR:CE1	2.84	0.46
2:H:26:TYR:CE2	2:H:28:THR:HG21	2.50	0.46
1:A:35:ARG:NH2	2:B:54:MET:O	2.48	0.45
1:A:98:MET:HG3	2:B:60:TRP:CZ3	2.52	0.45
1:J:212:ASP:HB3	4:J:357:HOH:O	2.16	0.45
1:J:81:LEU:HD21	1:J:123:TYR:CZ	2.51	0.45
1:A:155:HIS:HB3	3:C:6:PHE:CE1	2.52	0.45
2:B:46:ILE:HG23	2:B:47:PRO:HD2	1.99	0.45
1:D:230:LEU:HD12	1:D:230:LEU:O	2.17	0.45
2:E:35:ILE:HG22	2:E:54:MET:HE1	1.98	0.45
2:B:54:MET:CE	2:B:64:ILE:HD12	2.47	0.44
1:G:266:LEU:HD21	1:G:270:LEU:HG	1.98	0.44
1:J:124:ILE:HG13	1:J:135:ALA:HB2	1.98	0.44
1:A:6:ARG:NH2	1:A:113:TYR:CE1	2.86	0.44
2:H:25:CYS:HB3	2:H:66:ALA:HB3	1.98	0.44
1:J:193:PRO:O	1:J:194:ARG:C	2.60	0.44
1:A:193:PRO:O	1:A:194:ARG:C	2.61	0.44
2:B:38:GLN:HE21	2:B:45:LYS:HG3	1.82	0.44
3:C:4:PHE:C	3:C:5:ASN:HD22	2.25	0.44
1:D:108:ARG:NE	4:D:349:HOH:O	2.49	0.44
2:E:84:HIS:HB3	2:E:87:MET:HE2	1.98	0.44
1:D:72:GLN:HG2	4:D:344:HOH:O	2.17	0.44
1:G:266:LEU:HD23	1:G:269:PRO:HA	1.99	0.44
1:J:122:ASP:OD1	2:K:60:TRP:NE1	2.49	0.44
1:G:162:GLY:O	1:G:163:GLU:C	2.61	0.44
1:J:230:LEU:HD12	1:J:230:LEU:O	2.18	0.43
2:K:2:GLN:HE21	2:K:86:SER:HA	1.82	0.43
1:J:6:ARG:NH2	1:J:113:TYR:CE1	2.86	0.43
1:J:147:TRP:CD1	3:L:7:ALA:HB3	2.53	0.43
1:J:162:GLY:O	1:J:163:GLU:C	2.61	0.43
1:J:266:LEU:HD23	1:J:269:PRO:HA	2.01	0.43
1:G:73:TRP:CD1	3:I:8:THR:HG22	2.53	0.43
1:G:111:ARG:HA	4:G:352:HOH:O	2.18	0.43
1:J:117:ALA:HB2	2:K:60:TRP:CD2	2.53	0.43
1:A:193:PRO:HA	1:A:199:VAL:HG12	2.01	0.43
1:A:185:PRO:HD2	1:A:266:LEU:CD1	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:63:GLU:OE2	3:F:1:LYS:HG3	2.18	0.43
2:E:9:VAL:HG23	2:E:93:VAL:HG22	2.00	0.43
1:A:266:LEU:HD23	1:A:269:PRO:HA	2.01	0.43
1:G:230:LEU:HD12	1:G:230:LEU:O	2.19	0.43
1:J:35:ARG:NH2	2:K:54:MET:O	2.43	0.43
1:A:4:SER:OG	4:A:360:HOH:O	2.04	0.43
1:D:266:LEU:HD23	1:D:269:PRO:HA	2.01	0.43
1:A:143:THR:HG23	3:C:9:MET:HA	2.01	0.43
1:D:99:SER:HB2	3:F:3:PRO:HG3	2.01	0.43
2:H:54:MET:CE	2:H:64:ILE:CD1	2.96	0.42
1:D:106:ASP:O	1:D:107:TRP:HB2	2.18	0.42
1:D:185:PRO:HD2	1:D:266:LEU:CD1	2.47	0.42
2:B:38:GLN:NE2	2:B:45:LYS:CG	2.83	0.42
2:B:19:LYS:O	2:B:72:PRO:HD2	2.19	0.42
2:E:32:PRO:HB2	2:E:33:PRO:HD2	2.01	0.42
2:E:38:GLN:CD	2:E:81:ARG:HH12	2.27	0.42
1:G:187:ALA:HB3	1:G:272:LEU:CD1	2.50	0.42
1:D:266:LEU:HD21	1:D:270:LEU:HG	2.02	0.42
1:J:41:GLU:N	1:J:41:GLU:CD	2.77	0.42
1:J:66:LYS:NZ	3:L:1:LYS:HB3	2.33	0.42
1:D:193:PRO:HA	1:D:199:VAL:HG12	2.00	0.42
1:D:33:PHE:C	1:D:48:ARG:HB2	2.45	0.42
2:K:7:ILE:CG2	2:K:93:VAL:HG11	2.49	0.42
1:D:90:GLY:N	4:D:339:HOH:O	2.53	0.41
2:B:59:ASP:O	2:B:60:TRP:HB2	2.20	0.41
2:E:38:GLN:NE2	2:E:81:ARG:HH12	2.19	0.41
1:D:41:GLU:CD	1:D:41:GLU:N	2.78	0.41
1:D:72:GLN:CG	4:D:344:HOH:O	2.68	0.41
1:D:203:CYS:HB2	1:D:217:TRP:CZ2	2.56	0.41
1:G:175:GLY:O	1:G:179:LEU:HD12	2.21	0.41
1:J:73:TRP:CE2	3:L:5:ASN:HB3	2.56	0.41
1:J:193:PRO:HA	1:J:199:VAL:HG12	2.03	0.41
2:K:35:ILE:O	2:K:35:ILE:CG2	2.68	0.41
1:A:106:ASP:O	1:A:107:TRP:HB2	2.20	0.41
1:A:201:LEU:HD12	1:A:249:VAL:HG21	2.02	0.41
2:B:32:PRO:HD3	4:B:106:HOH:O	2.20	0.41
1:J:199:VAL:HG13	1:J:251:LEU:HG	2.03	0.41
3:C:5:ASN:N	3:C:5:ASN:ND2	2.69	0.41
1:D:108:ARG:HD3	1:G:262:TYR:CG	2.56	0.41
2:E:67:HIS:CG	4:E:105:HOH:O	2.74	0.41
3:F:5:ASN:N	3:F:5:ASN:HD22	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:66:LYS:HD3	3:I:4:PHE:CE1	2.55	0.41
2:K:9:VAL:HG23	2:K:93:VAL:HG22	2.03	0.41
2:B:32:PRO:HB2	2:B:33:PRO:HD2	2.03	0.41
1:G:144:ARG:HD2	4:G:345:HOH:O	2.20	0.40
1:A:202:ARG:HG2	1:A:204:TRP:NE1	2.37	0.40
1:D:187:ALA:HB3	1:D:272:LEU:CD1	2.51	0.40
1:D:187:ALA:CB	1:D:272:LEU:HD12	2.51	0.40
1:G:103:LEU:HD11	1:G:168:LEU:HD23	2.02	0.40
1:J:143:THR:OG1	3:L:9:MET:O	2.35	0.40
2:B:21:ASN:HB3	2:B:70:PHE:HE1	1.86	0.40
1:G:127:ASN:OD1	1:G:134:THR:HG22	2.21	0.40
1:A:32:GLU:OE2	1:A:48:ARG:HD2	2.21	0.40
1:A:110:LEU:HD12	1:A:110:LEU:HA	1.97	0.40
2:E:46:ILE:HA	2:E:47:PRO:HD2	1.94	0.40
2:E:51:MET:SD	2:E:66:ALA:HB2	2.61	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	258/276 (94%)	242 (94%)	16 (6%)	0	100	100
1	D	258/276 (94%)	242 (94%)	16 (6%)	0	100	100
1	G	254/276 (92%)	237 (93%)	17 (7%)	0	100	100
1	J	252/276 (91%)	236 (94%)	16 (6%)	0	100	100
2	B	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
2	E	97/99 (98%)	93 (96%)	4 (4%)	0	100	100
2	H	97/99 (98%)	93 (96%)	3 (3%)	1 (1%)	12	24
2	K	97/99 (98%)	94 (97%)	3 (3%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	F	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	I	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	L	7/9 (78%)	5 (71%)	2 (29%)	0	100	100
All	All	1438/1536 (94%)	1354 (94%)	83 (6%)	1 (0%)	48	68

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	H	47	PRO

5.3.2 Protein sidechains ⓘ

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	224/234 (96%)	211 (94%)	13 (6%)	18	38
1	D	224/234 (96%)	213 (95%)	11 (5%)	22	45
1	G	223/234 (95%)	210 (94%)	13 (6%)	18	38
1	J	221/234 (94%)	208 (94%)	13 (6%)	18	37
2	B	93/94 (99%)	87 (94%)	6 (6%)	15	32
2	E	93/94 (99%)	88 (95%)	5 (5%)	20	41
2	H	93/94 (99%)	87 (94%)	6 (6%)	15	32
2	K	93/94 (99%)	89 (96%)	4 (4%)	26	51
3	C	7/7 (100%)	7 (100%)	0	100	100
3	F	7/7 (100%)	7 (100%)	0	100	100
3	I	7/7 (100%)	6 (86%)	1 (14%)	3	6
3	L	7/7 (100%)	6 (86%)	1 (14%)	3	6
All	All	1292/1340 (96%)	1219 (94%)	73 (6%)	18	39

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	GLU
1	A	78	LEU
1	A	94	THR
1	A	114	LEU
1	A	115	GLN
1	A	134	THR
1	A	149	GLN
1	A	163	GLU
1	A	166	GLU
1	A	176	ASN
1	A	234	ARG
1	A	266	LEU
1	A	273	ARG
2	B	1	ILE
2	B	2	GLN
2	B	22	ILE
2	B	29	GLN
2	B	58	LYS
2	B	93	VAL
1	D	41	GLU
1	D	78	LEU
1	D	94	THR
1	D	114	LEU
1	D	115	GLN
1	D	134	THR
1	D	149	GLN
1	D	166	GLU
1	D	234	ARG
1	D	266	LEU
1	D	273	ARG
2	E	1	ILE
2	E	2	GLN
2	E	58	LYS
2	E	91	LYS
2	E	93	VAL
1	G	41	GLU
1	G	78	LEU
1	G	94	THR
1	G	105	SER
1	G	115	GLN
1	G	134	THR
1	G	149	GLN
1	G	163	GLU

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Mol	Chain	Res	Type
1	G	166	GLU
1	G	234	ARG
1	G	266	LEU
1	G	273	ARG
1	G	275	GLU
2	H	2	GLN
2	H	16	GLU
2	H	54	MET
2	H	58	LYS
2	H	75	THR
2	H	93	VAL
3	I	9	MET
1	J	41	GLU
1	J	78	LEU
1	J	94	THR
1	J	105	SER
1	J	114	LEU
1	J	115	GLN
1	J	134	THR
1	J	149	GLN
1	J	163	GLU
1	J	166	GLU
1	J	234	ARG
1	J	266	LEU
1	J	273	ARG
2	K	2	GLN
2	K	58	LYS
2	K	91	LYS
2	K	93	VAL
3	L	9	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (31) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	96	GLN
1	A	97	GLN
1	A	155	HIS
1	A	176	ASN
1	A	255	GLN
2	B	31	HIS
2	B	38	GLN
3	C	5	ASN

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Mol	Chain	Res	Type
1	D	30	ASN
1	D	97	GLN
1	D	255	GLN
2	E	2	GLN
2	E	13	HIS
2	E	38	GLN
3	F	5	ASN
1	G	42	ASN
1	G	97	GLN
1	G	176	ASN
1	G	192	HIS
1	G	255	GLN
2	H	31	HIS
2	H	34	HIS
2	H	38	GLN
3	I	5	ASN
1	J	42	ASN
1	J	97	GLN
1	J	155	HIS
1	J	255	GLN
2	K	2	GLN
2	K	38	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 ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides 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, 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	266/276 (96%)	0.84	30 (11%) 10 8	18, 38, 73, 109	0
1	D	266/276 (96%)	0.76	29 (10%) 10 9	17, 38, 68, 124	0
1	G	264/276 (95%)	0.92	35 (13%) 7 6	17, 37, 76, 101	0
1	J	262/276 (94%)	0.90	34 (12%) 7 6	16, 41, 77, 110	0
2	B	99/99 (100%)	0.35	3 (3%) 52 48	19, 33, 44, 53	0
2	E	99/99 (100%)	0.38	2 (2%) 65 61	21, 33, 46, 48	0
2	H	99/99 (100%)	0.25	0 100 100	17, 32, 43, 51	0
2	K	99/99 (100%)	0.56	3 (3%) 52 48	22, 37, 46, 51	0
3	C	9/9 (100%)	0.12	0 100 100	18, 25, 30, 33	0
3	F	9/9 (100%)	-0.02	0 100 100	18, 21, 26, 30	0
3	I	9/9 (100%)	0.38	0 100 100	21, 23, 30, 34	0
3	L	9/9 (100%)	0.20	0 100 100	22, 24, 26, 26	0
All	All	1490/1536 (97%)	0.71	136 (9%) 15 13	16, 36, 70, 124	0

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	177	ALA	6.8
1	D	178	THR	6.0
1	G	221	GLY	4.6
1	J	221	GLY	4.6
1	J	233	THR	4.6
1	G	54	GLN	4.5
1	G	180	LEU	4.5
1	D	221	GLY	4.5
1	A	251	LEU	4.5
1	G	179	LEU	4.1
1	D	177	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	D	175	GLY	4.0
1	D	233	THR	4.0
1	J	189	VAL	4.0
2	K	18	GLY	3.8
1	A	180	LEU	3.8
1	G	233	THR	3.7
1	A	194	ARG	3.7
1	J	217	TRP	3.7
1	A	16	GLY	3.7
1	A	179	LEU	3.7
1	J	248	VAL	3.5
1	J	180	LEU	3.4
1	D	180	LEU	3.3
1	J	251	LEU	3.3
1	D	231	VAL	3.3
1	J	199	VAL	3.3
1	A	221	GLY	3.3
1	D	179	LEU	3.3
1	D	17	LEU	3.2
1	G	222	GLU	3.0
1	A	40	ALA	3.0
1	G	252	GLY	3.0
1	A	248	VAL	2.9
2	E	47	PRO	2.9
1	A	45	TYR	2.9
1	G	169	HIS	2.9
1	G	231	VAL	2.9
1	J	1	GLY	2.9
1	G	230	LEU	2.8
1	J	252	GLY	2.8
1	J	228	MET	2.8
1	G	41	GLU	2.8
1	G	72	GLN	2.8
1	G	45	TYR	2.8
1	J	257	TYR	2.8
1	G	193	PRO	2.7
1	J	190	THR	2.7
1	G	191	HIS	2.7
1	G	199	VAL	2.7
1	A	178	THR	2.7
1	G	53	GLU	2.7
1	D	230	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	61	GLU	2.6
1	J	200	THR	2.6
1	G	181	ARG	2.6
1	A	228	MET	2.6
1	D	256	ASN	2.6
1	A	257	TYR	2.6
1	A	237	GLY	2.5
1	G	223	GLU	2.5
1	J	270	LEU	2.5
1	J	209	TYR	2.5
1	A	165	VAL	2.5
1	A	187	ALA	2.5
1	G	200	THR	2.5
1	A	252	GLY	2.5
1	J	274	TRP	2.4
1	D	176	ASN	2.4
1	G	249	VAL	2.4
1	J	215	LEU	2.4
1	D	181	ARG	2.4
1	A	176	ASN	2.4
1	G	267	PRO	2.4
2	B	1	ILE	2.4
1	J	155	HIS	2.4
1	G	198	GLU	2.4
1	J	250	PRO	2.4
1	D	54	GLN	2.4
1	D	247	VAL	2.4
1	G	253	LYS	2.4
1	A	230	LEU	2.3
1	G	228	MET	2.3
1	A	231	VAL	2.3
1	A	247	VAL	2.3
1	G	163	GLU	2.3
1	A	274	TRP	2.3
1	G	62	ARG	2.3
1	D	228	MET	2.3
2	B	74	GLU	2.3
1	A	199	VAL	2.3
1	A	181	ARG	2.3
1	G	176	ASN	2.2
1	G	257	TYR	2.3
1	A	191	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	16	GLY	2.2
1	A	46	GLU	2.2
1	G	42	ASN	2.2
1	D	207	GLY	2.2
1	J	206	LEU	2.2
1	G	189	VAL	2.2
1	D	19	GLU	2.2
1	D	273	ARG	2.2
1	D	274	TRP	2.2
1	J	194	ARG	2.2
1	J	256	ASN	2.2
1	G	151	GLY	2.2
1	J	171	TYR	2.2
1	J	62	ARG	2.2
1	J	244	TRP	2.2
1	J	249	VAL	2.1
1	D	189	VAL	2.1
1	A	223	GLU	2.1
1	J	58	GLU	2.1
1	D	184	SER	2.1
1	D	206	LEU	2.1
1	J	207	GLY	2.1
1	J	240	THR	2.1
1	J	258	THR	2.1
1	D	223	GLU	2.1
2	K	93	VAL	2.1
1	D	144	ARG	2.1
1	G	272	LEU	2.1
1	J	230	LEU	2.1
1	A	233	THR	2.1
1	J	223	GLU	2.1
1	A	272	LEU	2.0
1	G	201	LEU	2.0
1	J	232	GLU	2.0
2	B	75	THR	2.0
2	K	1	ILE	2.0
1	A	269	PRO	2.0
1	D	199	VAL	2.0
1	D	254	GLU	2.0
1	G	232	GLU	2.0
2	E	1	ILE	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 oligosaccharides 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.