



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 01:50 PM UTC

PDB ID : 5J6G / pdb_00005j6g
Title : Recognition of the MHC class Ib molecule H2-Q10 by the natural killer cell receptor Ly49C
Authors : Berry, R.; Rossjohn, J.
Deposited on : 2016-04-04
Resolution : 3.30 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	:	4-5-2 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

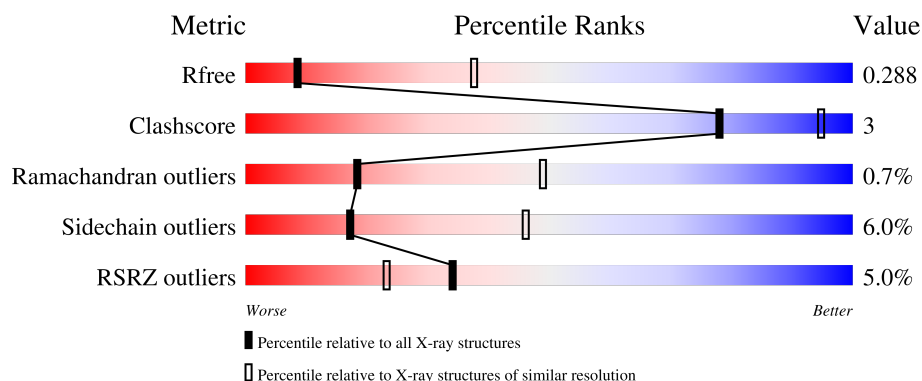
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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}	180053	1169 (3.32-3.28)
Clashscore	190562	1209 (3.32-3.28)
Ramachandran outliers	187476	1188 (3.32-3.28)
Sidechain outliers	187428	1187 (3.32-3.28)
RSRZ outliers	180081	1169 (3.32-3.28)

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	300	4% 79% 11% 9%
1	C	300	6% 80% 12% 8%
2	B	100	3% 88% 10% ..
2	D	100	5% 84% 14% ..
3	E	8	100%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	F	8	100%
4	G	132	2% 83% 9% 8%
4	H	132	7% 80% 11% 8%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7801 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, Q10 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	272	Total	C	N	O	S	0	0	0
			2130	1361	366	394	9			
1	C	276	Total	C	N	O	S	0	0	0
			2154	1376	371	398	9			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	initiating methionine	UNP P01898
A	257	TYR	-	expression tag	UNP P01898
A	258	THR	-	expression tag	UNP P01898
A	259	CYS	-	expression tag	UNP P01898
A	260	HIS	-	expression tag	UNP P01898
A	261	VAL	-	expression tag	UNP P01898
A	262	TYR	-	expression tag	UNP P01898
A	263	HIS	-	expression tag	UNP P01898
A	264	GLU	-	expression tag	UNP P01898
A	265	GLY	-	expression tag	UNP P01898
A	266	LEU	-	expression tag	UNP P01898
A	267	PRO	-	expression tag	UNP P01898
A	268	GLU	-	expression tag	UNP P01898
A	269	PRO	-	expression tag	UNP P01898
A	270	LEU	-	expression tag	UNP P01898
A	271	THR	-	expression tag	UNP P01898
A	272	LEU	-	expression tag	UNP P01898
A	273	ARG	-	expression tag	UNP P01898
A	274	TRP	-	expression tag	UNP P01898
A	275	GLU	-	expression tag	UNP P01898
A	276	PRO	-	expression tag	UNP P01898
A	277	PRO	-	expression tag	UNP P01898
A	278	PRO	-	expression tag	UNP P01898
A	279	SER	-	expression tag	UNP P01898
A	280	ALA	-	expression tag	UNP P01898

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	281	SER	-	expression tag	UNP P01898
A	282	GLY	-	expression tag	UNP P01898
A	283	SER	-	expression tag	UNP P01898
A	284	GLY	-	expression tag	UNP P01898
A	285	LEU	-	expression tag	UNP P01898
A	286	HIS	-	expression tag	UNP P01898
A	287	HIS	-	expression tag	UNP P01898
A	288	ILE	-	expression tag	UNP P01898
A	289	LEU	-	expression tag	UNP P01898
A	290	ASP	-	expression tag	UNP P01898
A	291	ALA	-	expression tag	UNP P01898
A	292	GLN	-	expression tag	UNP P01898
A	293	LYS	-	expression tag	UNP P01898
A	294	MET	-	expression tag	UNP P01898
A	295	VAL	-	expression tag	UNP P01898
A	296	TRP	-	expression tag	UNP P01898
A	297	ASN	-	expression tag	UNP P01898
A	298	HIS	-	expression tag	UNP P01898
A	299	ARG	-	expression tag	UNP P01898
C	0	MET	-	initiating methionine	UNP P01898
C	257	TYR	-	expression tag	UNP P01898
C	258	THR	-	expression tag	UNP P01898
C	259	CYS	-	expression tag	UNP P01898
C	260	HIS	-	expression tag	UNP P01898
C	261	VAL	-	expression tag	UNP P01898
C	262	TYR	-	expression tag	UNP P01898
C	263	HIS	-	expression tag	UNP P01898
C	264	GLU	-	expression tag	UNP P01898
C	265	GLY	-	expression tag	UNP P01898
C	266	LEU	-	expression tag	UNP P01898
C	267	PRO	-	expression tag	UNP P01898
C	268	GLU	-	expression tag	UNP P01898
C	269	PRO	-	expression tag	UNP P01898
C	270	LEU	-	expression tag	UNP P01898
C	271	THR	-	expression tag	UNP P01898
C	272	LEU	-	expression tag	UNP P01898
C	273	ARG	-	expression tag	UNP P01898
C	274	TRP	-	expression tag	UNP P01898
C	275	GLU	-	expression tag	UNP P01898
C	276	PRO	-	expression tag	UNP P01898
C	277	PRO	-	expression tag	UNP P01898
C	278	PRO	-	expression tag	UNP P01898

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	279	SER	-	expression tag	UNP P01898
C	280	ALA	-	expression tag	UNP P01898
C	281	SER	-	expression tag	UNP P01898
C	282	GLY	-	expression tag	UNP P01898
C	283	SER	-	expression tag	UNP P01898
C	284	GLY	-	expression tag	UNP P01898
C	285	LEU	-	expression tag	UNP P01898
C	286	HIS	-	expression tag	UNP P01898
C	287	HIS	-	expression tag	UNP P01898
C	288	ILE	-	expression tag	UNP P01898
C	289	LEU	-	expression tag	UNP P01898
C	290	ASP	-	expression tag	UNP P01898
C	291	ALA	-	expression tag	UNP P01898
C	292	GLN	-	expression tag	UNP P01898
C	293	LYS	-	expression tag	UNP P01898
C	294	MET	-	expression tag	UNP P01898
C	295	VAL	-	expression tag	UNP P01898
C	296	TRP	-	expression tag	UNP P01898
C	297	ASN	-	expression tag	UNP P01898
C	298	HIS	-	expression tag	UNP P01898
C	299	ARG	-	expression tag	UNP P01898

- 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
			734	469	121	137	7			
2	D	99	Total	C	N	O	S	0	0	0
			749	479	125	138	7			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P01887
D	0	MET	-	initiating methionine	UNP P01887

- Molecule 3 is a protein called VAL-GLY-ILE-THR-ASN-VAL-ASP-LEU.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	8	Total	C	N	O	0	0	0
			57	36	9	12			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	F	8	Total	C	N	O	0	0	0
			57	36	9	12			

- Molecule 4 is a protein called Killer cell lectin-like receptor 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	G	122	Total	C	N	O	S	0	0	0
			963	631	153	168	11			
4	H	122	Total	C	N	O	S	0	0	0
			957	623	154	170	10			

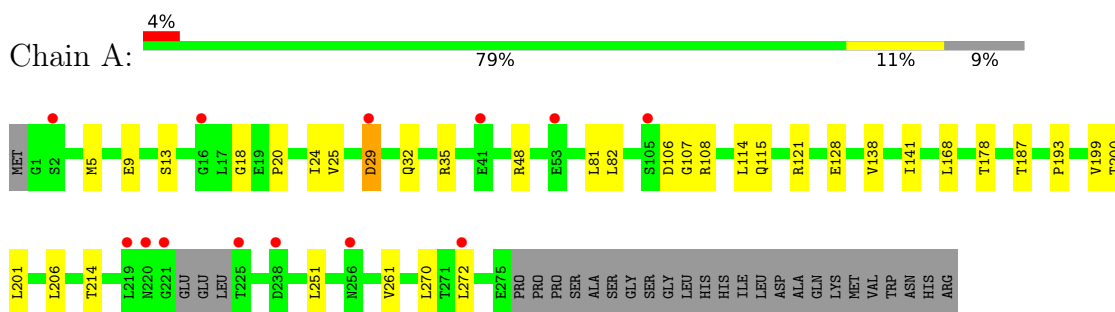
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	135	MET	-	initiating methionine	UNP Q64329
H	135	MET	-	initiating methionine	UNP Q64329

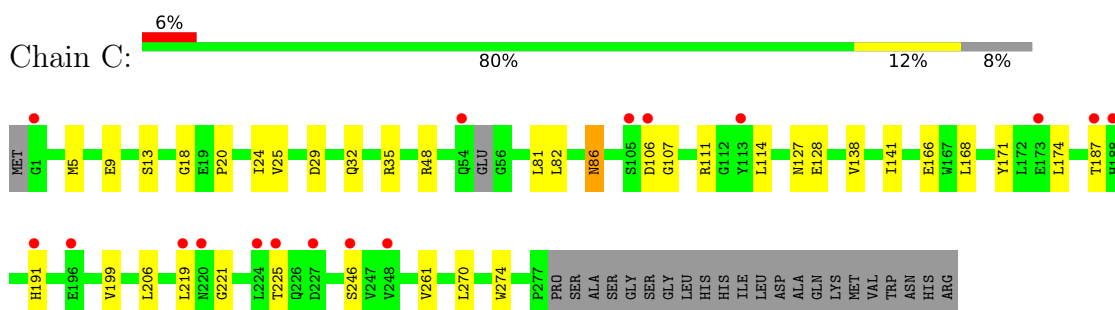
3 Residue-property plots [i](#)

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.

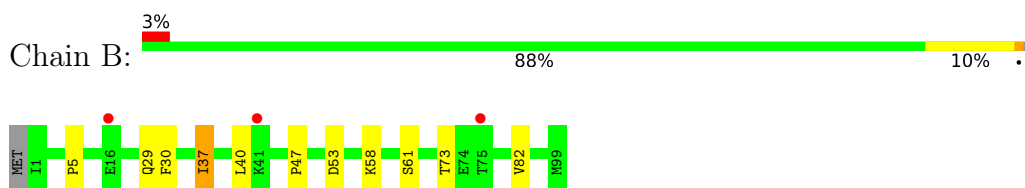
- Molecule 1: H-2 class I histocompatibility antigen, Q10 alpha chain



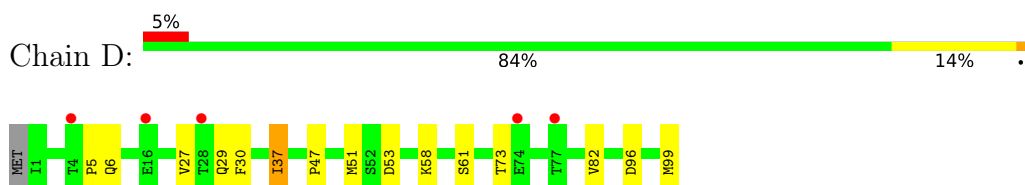
- Molecule 1: H-2 class I histocompatibility antigen, Q10 alpha chain



- Molecule 2: Beta-2-microglobulin



- Molecule 2: Beta-2-microglobulin



- Molecule 3: VAL-GLY-ILE-THR-ASN-VAL-ASP-LEU

Chain E:  100%

There are no outlier residues recorded for this chain.

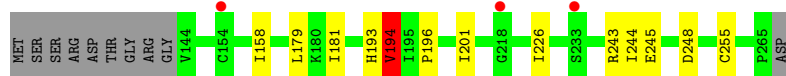
- Molecule 3: VAL-GLY-ILE-THR-ASN-VAL-ASP-LEU

Chain F:  100%

There are no outlier residues recorded for this chain.

- Molecule 4: Killer cell lectin-like receptor 3

Chain G:  2% 83% 9% 8%



- Molecule 4: Killer cell lectin-like receptor 3

Chain H:  7% 80% 11% 8%



4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	101.01Å 57.80Å 210.70Å 90.00° 96.15° 90.00°	Depositor
Resolution (Å)	46.16 – 3.30 46.16 – 3.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.16-3.30) 99.9 (46.16-3.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 3.32Å)	Xtriage
Refinement program	BUSTER 2.10.0	Depositor
R, R_{free}	0.221 , 0.253 0.256 , 0.288	Depositor DCC
R_{free} test set	949 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 58.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	7801	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.12% 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

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	0.69	0/2194	1.11	4/2999 (0.1%)
1	C	0.69	0/2220	1.11	5/3036 (0.2%)
2	B	0.72	0/758	1.01	0/1043
2	D	0.70	0/775	1.01	0/1064
3	E	0.66	0/56	1.18	0/76
3	F	0.66	0/56	1.17	0/76
4	G	0.75	0/994	1.18	0/1353
4	H	0.78	0/988	1.16	0/1348
All	All	0.71	0/8041	1.11	9/10995 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	86	ASN	CA-CB-CG	6.99	119.58	112.60
1	C	18	GLY	CA-C-N	6.18	132.82	121.70
1	C	18	GLY	C-N-CA	6.18	132.82	121.70
1	A	18	GLY	CA-C-N	5.59	131.77	121.70
1	A	18	GLY	C-N-CA	5.59	131.77	121.70
1	A	108	ARG	CA-C-N	5.18	129.63	121.56
1	A	108	ARG	C-N-CA	5.18	129.63	121.56
1	C	127	ASN	CA-C-N	5.00	127.69	120.38
1	C	127	ASN	C-N-CA	5.00	127.69	120.38

There are no chirality outliers.

There are no planarity outliers.

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	2130	0	1942	11	0
1	C	2154	0	1960	12	0
2	B	734	0	630	5	0
2	D	749	0	652	8	0
3	E	57	0	62	0	0
3	F	57	0	62	0	0
4	G	963	0	866	5	0
4	H	957	0	839	6	0
All	All	7801	0	7013	41	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 3.

All (41) 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:C:5:MET:HB2	1:C:168:LEU:HD13	1.85	0.58
2:B:29:GLN:HA	2:B:61:SER:HB2	1.85	0.57
1:A:193:PRO:HA	1:A:199:VAL:HG12	1.87	0.57
2:D:29:GLN:HA	2:D:61:SER:HB2	1.86	0.56
2:D:37:ILE:HB	2:D:51:MET:HE1	1.89	0.54
1:A:5:MET:HB2	1:A:168:LEU:HD13	1.89	0.54
1:A:121:ARG:HD2	4:G:196:PRO:HB2	1.89	0.54
2:D:58:LYS:HB2	4:H:247:ILE:HD12	1.90	0.54
1:C:106:ASP:N	1:C:107:GLY:HA2	2.24	0.53
1:A:106:ASP:N	1:A:107:GLY:HA2	2.24	0.53
1:A:138:VAL:HA	1:A:141:ILE:HD12	1.93	0.50
4:G:158:ILE:HB	4:G:255:CYS:HB3	1.94	0.50
4:H:158:ILE:HB	4:H:255:CYS:HB3	1.94	0.49
1:A:13:SER:HA	1:A:20:PRO:HB3	1.95	0.49
1:C:138:VAL:HA	1:C:141:ILE:HD12	1.93	0.49
1:A:25:VAL:HG13	1:A:32:GLN:HE21	1.79	0.48
1:C:13:SER:HA	1:C:20:PRO:HB3	1.96	0.48
1:C:35:ARG:HD2	1:C:48:ARG:HD3	1.96	0.48
1:A:35:ARG:HD2	1:A:48:ARG:HD3	1.96	0.47
1:C:32:GLN:HE22	2:D:53:ASP:HB2	1.80	0.46
1:C:191:HIS:HB2	1:C:274:TRP:NE1	2.31	0.46
1:C:25:VAL:HG13	1:C:32:GLN:HE21	1.81	0.46
1:A:187:THR:HG21	1:A:261:VAL:HG21	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:5:PRO:HB3	2:D:30:PHE:HB3	1.98	0.46
1:C:187:THR:HG21	1:C:261:VAL:HG21	1.98	0.45
2:B:5:PRO:HB3	2:B:30:PHE:HB3	1.98	0.44
4:H:179:LEU:HD23	4:H:201:ILE:HG22	2.01	0.42
1:C:111:ARG:HD2	4:H:229:MET:O	2.20	0.42
1:A:32:GLN:HE22	2:B:53:ASP:HB2	1.85	0.42
1:C:9:GLU:HG2	1:C:24:ILE:HG12	2.02	0.41
2:B:58:LYS:O	4:G:243:ARG:NH2	2.54	0.41
4:G:179:LEU:HD23	4:G:201:ILE:HG22	2.01	0.41
2:B:37:ILE:HG23	2:B:82:VAL:HG22	2.02	0.41
1:C:171:TYR:HA	1:C:174:LEU:HD12	2.02	0.41
4:H:181:ILE:HB	4:H:222:LEU:HD22	2.03	0.41
4:H:229:MET:HE1	4:H:244:ILE:HG13	2.02	0.41
2:D:37:ILE:HG23	2:D:82:VAL:HG22	2.02	0.40
2:D:96:ASP:HB3	2:D:99:MET:HB2	2.03	0.40
4:G:193:HIS:O	4:G:194:VAL:HG13	2.21	0.40
1:A:9:GLU:HG2	1:A:24:ILE:HG12	2.03	0.40
2:D:27:VAL:HG21	2:D:37:ILE:HG12	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	268/300 (89%)	252 (94%)	15 (6%)	1 (0%)	30	60
1	C	272/300 (91%)	256 (94%)	14 (5%)	2 (1%)	18	49
2	B	97/100 (97%)	92 (95%)	4 (4%)	1 (1%)	12	40
2	D	97/100 (97%)	92 (95%)	4 (4%)	1 (1%)	12	40
3	E	6/8 (75%)	6 (100%)	0	0	100	100
3	F	6/8 (75%)	6 (100%)	0	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	G	120/132 (91%)	109 (91%)	10 (8%)	1 (1%)	16	45
4	H	120/132 (91%)	111 (92%)	8 (7%)	1 (1%)	16	45
All	All	986/1080 (91%)	924 (94%)	55 (6%)	7 (1%)	18	49

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	29	ASP
2	B	47	PRO
1	C	29	ASP
1	C	221	GLY
2	D	47	PRO
4	H	234	ARG
4	G	194	VAL

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	206/255 (81%)	192 (93%)	14 (7%)	14	42
1	C	209/255 (82%)	197 (94%)	12 (6%)	18	47
2	B	72/94 (77%)	69 (96%)	3 (4%)	26	55
2	D	75/94 (80%)	72 (96%)	3 (4%)	28	56
3	E	7/7 (100%)	7 (100%)	0	100	100
3	F	7/7 (100%)	7 (100%)	0	100	100
4	G	96/122 (79%)	90 (94%)	6 (6%)	16	44
4	H	94/122 (77%)	86 (92%)	8 (8%)	10	33
All	All	766/956 (80%)	720 (94%)	46 (6%)	17	46

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	29	ASP
1	A	81	LEU
1	A	82	LEU
1	A	114	LEU
1	A	115	GLN
1	A	128	GLU
1	A	178	THR
1	A	200	THR
1	A	201	LEU
1	A	206	LEU
1	A	214	THR
1	A	251	LEU
1	A	270	LEU
1	A	272	LEU
2	B	37	ILE
2	B	40	LEU
2	B	73	THR
1	C	81	LEU
1	C	82	LEU
1	C	86	ASN
1	C	114	LEU
1	C	128	GLU
1	C	166	GLU
1	C	199	VAL
1	C	206	LEU
1	C	219	LEU
1	C	225	THR
1	C	246	SER
1	C	270	LEU
2	D	6	GLN
2	D	37	ILE
2	D	73	THR
4	G	181	ILE
4	G	194	VAL
4	G	226	ILE
4	G	244	ILE
4	G	245	GLU
4	G	248	ASP
4	H	173	HIS
4	H	181	ILE
4	H	194	VAL
4	H	206	ASP
4	H	211	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
4	H	223	ASP
4	H	244	ILE
4	H	248	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	3	HIS
1	A	32	GLN
1	A	75	HIS
1	A	87	GLN
1	A	115	GLN
1	A	127	ASN
1	A	218	GLN
2	B	8	GLN
1	C	32	GLN
1	C	75	HIS
1	C	87	GLN
1	C	115	GLN
1	C	127	ASN
4	G	160	ASN
4	G	198	ASN
4	H	160	ASN
4	H	172	GLN
4	H	198	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	272/300 (90%)	0.68	13 (4%) 35 24	20, 44, 89, 138	0
1	C	276/300 (92%)	0.75	17 (6%) 26 18	26, 50, 78, 113	0
2	B	99/100 (99%)	0.60	3 (3%) 52 35	23, 49, 63, 71	0
2	D	99/100 (99%)	0.79	5 (5%) 33 22	30, 56, 72, 78	0
3	E	8/8 (100%)	0.14	0 100 100	31, 34, 38, 52	0
3	F	8/8 (100%)	0.56	0 100 100	29, 32, 38, 60	0
4	G	122/132 (92%)	0.55	3 (2%) 58 39	17, 38, 58, 71	0
4	H	122/132 (92%)	0.74	9 (7%) 20 15	21, 41, 64, 110	0
All	All	1006/1080 (93%)	0.69	50 (4%) 34 23	17, 47, 77, 138	0

All (50) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	H	266	ASP	4.0
1	C	196	GLU	3.9
4	H	233	SER	3.7
1	C	220	ASN	3.5
4	H	248	ASP	3.4
1	A	105	SER	3.4
1	A	221	GLY	3.4
1	C	54	GLN	3.1
2	D	77	THR	2.8
1	C	225	THR	2.8
1	C	188	HIS	2.8
4	H	211	GLU	2.8
1	A	41	GLU	2.8
2	B	75	THR	2.7
1	C	1	GLY	2.7
1	A	219	LEU	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	219	LEU	2.6
4	G	233	SER	2.6
4	H	175	SER	2.5
1	A	29	ASP	2.5
2	D	4	THR	2.5
1	C	106	ASP	2.4
1	A	220	ASN	2.4
1	A	53	GLU	2.4
1	A	238	ASP	2.4
1	C	227	ASP	2.4
1	A	16	GLY	2.3
2	B	16	GLU	2.3
4	H	156	TYR	2.2
1	C	246	SER	2.2
2	D	74	GLU	2.1
4	G	218	GLY	2.1
1	A	256	ASN	2.1
2	D	28	THR	2.1
1	A	2	SER	2.1
1	C	173	GLU	2.1
1	C	187	THR	2.1
2	B	41	LYS	2.1
1	C	248	VAL	2.1
1	A	272	LEU	2.1
1	C	191	HIS	2.1
1	C	113	TYR	2.1
1	A	225	THR	2.1
4	H	258	GLY	2.1
4	H	265	PRO	2.0
1	C	105	SER	2.0
4	H	262	ASP	2.0
4	G	154	CYS	2.0
2	D	16	GLU	2.0
1	C	224	LEU	2.0

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

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.