



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:49 AM UTC

PDB ID : 6PAG / pdb_00006pag
Title : Killer cell immunoglobulin-like receptor 2DL3 in complex with HLA-C*07:02
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Deposited on : 2019-06-11
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

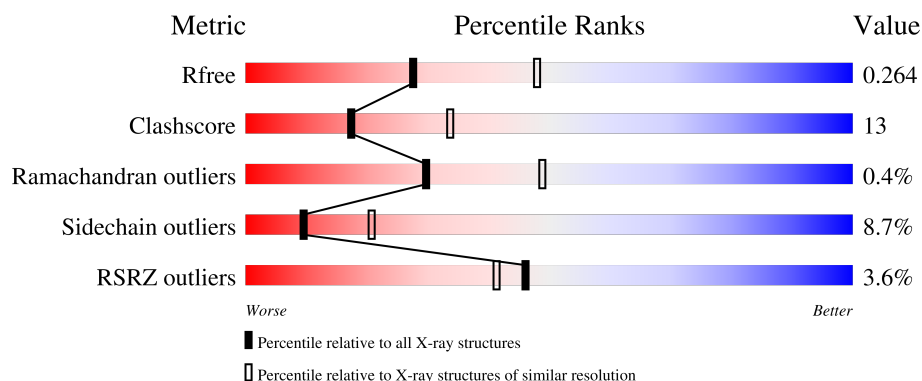
1 Overall quality at a glance

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	278	9% 76% 22% .
2	B	100	78% 19% .
3	C	9	67% 33%
4	D	204	9% 40% 36% 5% 18%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4478 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 HLA class I histocompatibility antigen, Cw-7 alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	277	Total	C	N	O	S	0	1	0
			2246	1387	412	440	7			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	100	Total	C	N	O	S	0	0	0
			837	533	141	159	4			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	initiating methionine	UNP P61769

- Molecule 3 is a protein called ARG-TYR-ARG-PRO-GLY-THR-VAL-ALA-LEU.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	9	Total	C	N	O	0	0	0
			73	46	15	12			

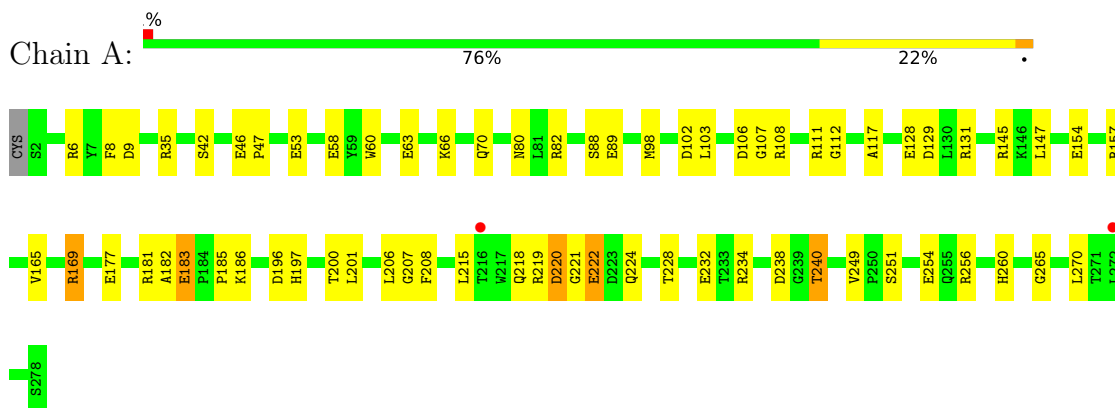
- Molecule 4 is a protein called Killer cell immunoglobulin-like receptor 2DL3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	167	Total	C	N	O	S	0	0	0
			1322	836	231	248	7			

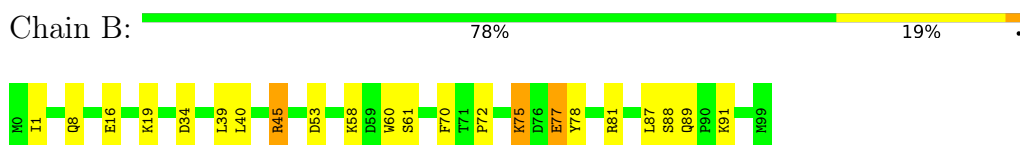
3 Residue-property plots [i](#)

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.

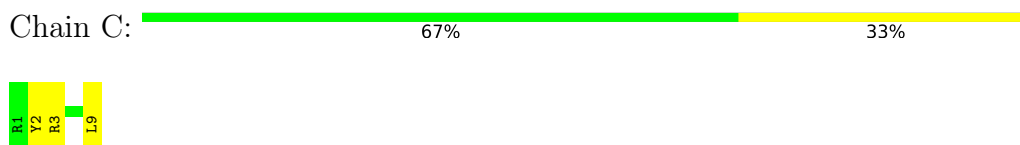
- Molecule 1: HLA class I histocompatibility antigen, Cw-7 alpha chain



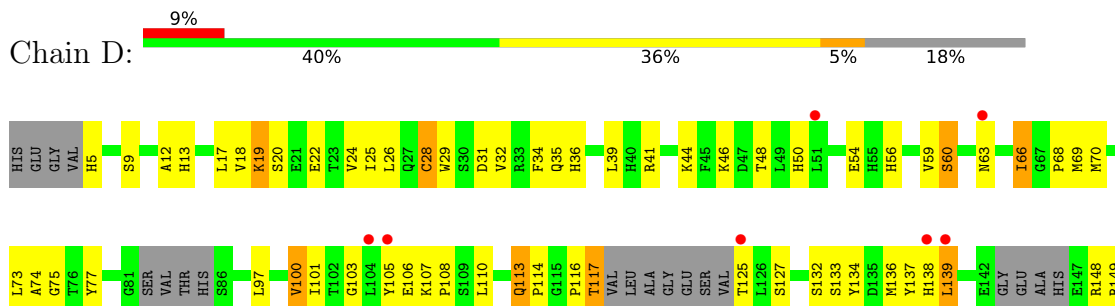
- Molecule 2: Beta-2-microglobulin



- Molecule 3: ARG-TYR-ARG-PRO-GLY-THR-VAL-ALA-LEU



- Molecule 4: Killer cell immunoglobulin-like receptor 2DL3



F150	S151	A152	G153	P154	K155	V156	M157	G158	T159	F160	Q161	A162	D163	F164	F165	L166	GLY	PRO	ALA	THR	HIS	GLY	GLY	THR	TYR	R176	C177	F178	S184	F185	Y186	S189	N190	S191	S192	D193	F194	L195	LEU	VAL	SER	VAL	THR	GLY	ASN	PRO	SER
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	P 64	Depositor
Cell constants a, b, c, α , β , γ	111.86Å 111.86Å 87.99Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.57 – 2.50 32.57 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.6 (32.57-2.50) 98.5 (32.57-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.99 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.8.1 _1168	Depositor
R, R_{free}	0.223 , 0.254 0.217 , 0.264	Depositor DCC
R_{free} test set	1097 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	62.4	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 47.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.048 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4478	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% 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	0.21	0/2303	0.51	2/3126 (0.1%)
2	B	0.17	0/860	0.41	0/1162
3	C	0.14	0/74	0.40	0/98
4	D	0.18	0/1359	0.65	4/1836 (0.2%)
All	All	0.19	0/4596	0.54	6/6222 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
4	D	0	1

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	220	ASP	N-CA-C	-13.71	84.92	108.08
4	D	189	SER	CB-CA-C	-13.03	87.91	110.45
4	D	189	SER	CA-C-N	8.31	134.00	120.94
4	D	189	SER	C-N-CA	8.31	134.00	120.94
1	A	183	GLU	N-CA-C	7.24	125.80	109.81
4	D	189	SER	N-CA-C	-6.41	100.98	110.46

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	D	189	SER	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	2246	0	2097	46	1
2	B	837	0	803	13	0
3	C	73	0	79	1	0
4	D	1322	0	1257	56	0
All	All	4478	0	4236	109	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 13.

All (109) 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:155:LYS:HD2	4:D:161:GLN:OE1	1.69	0.92
1:A:98:MET:HE1	2:B:58:LYS:HA	1.55	0.87
4:D:155:LYS:CE	4:D:161:GLN:OE1	2.25	0.84
4:D:155:LYS:NZ	4:D:161:GLN:OE1	2.15	0.79
1:A:183:GLU:O	1:A:183:GLU:HG3	1.81	0.78
4:D:155:LYS:CD	4:D:161:GLN:OE1	2.31	0.78
1:A:196:ASP:O	1:A:197:HIS:ND1	2.20	0.75
4:D:19:LYS:HG3	4:D:22:GLU:HG3	1.71	0.71
4:D:54:GLU:O	4:D:60:SER:HA	1.91	0.70
4:D:105:TYR:O	4:D:190:ASN:ND2	2.25	0.70
1:A:103:LEU:HD11	1:A:165:VAL:HG13	1.75	0.68
4:D:36:HIS:HD2	4:D:50:HIS:HE1	1.42	0.68
1:A:35:ARG:NH2	1:A:46:GLU:OE1	2.27	0.68
1:A:107:GLY:O	1:A:169:ARG:NH1	2.29	0.65
4:D:25:ILE:HD11	4:D:63:ASN:HB3	1.78	0.65
4:D:13:HIS:HB2	4:D:25:ILE:HG23	1.79	0.64
4:D:18:VAL:HG21	4:D:24:VAL:HG11	1.79	0.64
4:D:36:HIS:CD2	4:D:50:HIS:HE1	2.16	0.64
4:D:103:GLY:HA2	4:D:190:ASN:OD1	1.98	0.64
1:A:182:ALA:HB1	1:A:265:GLY:HA2	1.80	0.63
4:D:106:GLU:O	4:D:134:TYR:OH	2.16	0.63
2:B:45:ARG:NH1	2:B:81:ARG:HH12	1.96	0.63
4:D:153:GLY:N	4:D:161:GLN:O	2.26	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:110:LEU:HA	4:D:127:SER:O	1.99	0.61
4:D:9:SER:O	4:D:28:CYS:HA	2.01	0.61
4:D:32:VAL:O	4:D:60:SER:OG	2.18	0.60
1:A:177:GLU:O	1:A:181:ARG:HB2	2.01	0.60
4:D:176:ARG:NH2	4:D:191:SER:OG	2.35	0.60
1:A:218:GLN:NE2	1:A:221:GLY:O	2.27	0.60
1:A:8:PHE:HE2	1:A:98:MET:HE2	1.67	0.60
4:D:157:ASN:OD1	4:D:157:ASN:N	2.33	0.60
4:D:12:ALA:HB2	4:D:97:LEU:HD21	1.84	0.60
1:A:220:ASP:N	1:A:256:ARG:O	2.35	0.59
1:A:219:ARG:O	1:A:220:ASP:C	2.44	0.58
4:D:110:LEU:HD22	4:D:195:LEU:HD23	1.84	0.58
4:D:137:TYR:HA	4:D:178:PHE:O	2.03	0.58
4:D:138:HIS:O	4:D:177:CYS:HA	2.04	0.57
1:A:201:LEU:HD11	1:A:254:GLU:HB3	1.85	0.57
4:D:5:HIS:O	4:D:5:HIS:ND1	2.38	0.56
1:A:82:ARG:HD2	1:A:89:GLU:HA	1.88	0.55
2:B:45:ARG:HH11	2:B:45:ARG:HG3	1.71	0.55
4:D:150:PHE:HB2	4:D:164:PHE:CE1	2.42	0.54
4:D:26:LEU:HD22	4:D:39:LEU:HD21	1.90	0.54
1:A:63:GLU:OE2	1:A:66:LYS:NZ	2.39	0.54
1:A:8:PHE:CE2	1:A:98:MET:HE2	2.44	0.52
1:A:6:ARG:HH21	1:A:102:ASP:CG	2.18	0.52
4:D:44:LYS:NZ	4:D:184:SER:OG	2.41	0.52
4:D:154:PRO:HA	4:D:160:PHE:HA	1.91	0.52
4:D:152:ALA:HA	4:D:162:ALA:HB2	1.92	0.51
4:D:117:THR:O	4:D:117:THR:OG1	2.27	0.50
4:D:125:THR:OG1	4:D:125:THR:O	2.28	0.50
1:A:128:GLU:OE1	1:A:128:GLU:N	2.34	0.49
4:D:137:TYR:HD2	4:D:162:ALA:HB3	1.76	0.48
1:A:106:ASP:OD1	1:A:108:ARG:HG2	2.12	0.48
4:D:69:MET:HE3	4:D:101:ILE:HB	1.95	0.48
1:A:224:GLN:O	1:A:228:THR:N	2.47	0.48
2:B:39:LEU:C	2:B:40:LEU:HD23	2.38	0.48
1:A:111:ARG:NH1	1:A:112:GLY:O	2.43	0.48
1:A:145:ARG:HD2	4:D:133:SER:OG	2.14	0.48
1:A:219:ARG:O	1:A:220:ASP:HB2	2.12	0.48
4:D:66:ILE:O	4:D:66:ILE:HG13	2.14	0.47
4:D:29:TRP:HA	4:D:60:SER:O	2.14	0.47
2:B:87:LEU:HD13	2:B:91:LYS:HG3	1.96	0.47
1:A:80:ASN:OD1	4:D:44:LYS:HE3	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:185:PRO:HB3	1:A:208:PHE:HB3	1.96	0.46
1:A:254:GLU:OE1	1:A:254:GLU:N	2.42	0.46
4:D:39:LEU:O	4:D:48:THR:HA	2.16	0.46
4:D:74:ALA:HB1	4:D:186:TYR:HB3	1.98	0.46
1:A:117:ALA:HB2	2:B:60:TRP:CE2	2.51	0.45
2:B:75:LYS:HE2	2:B:75:LYS:HB3	1.76	0.45
1:A:186:LYS:HG3	1:A:206:LEU:HB2	1.98	0.45
1:A:222:GLU:HG3	1:A:224:GLN:HE22	1.82	0.45
4:D:107:LYS:HB2	4:D:192:SER:HA	1.97	0.45
1:A:129:ASP:O	1:A:157:ARG:NH1	2.50	0.45
1:A:181:ARG:HE	1:A:181:ARG:HB3	1.53	0.45
4:D:18:VAL:HB	4:D:69:MET:HG2	1.99	0.45
1:A:35:ARG:HG3	2:B:53:ASP:CG	2.42	0.45
1:A:9:ASP:OD2	3:C:2:TYR:OH	2.30	0.44
4:D:137:TYR:CE2	4:D:152:ALA:HB2	2.51	0.44
2:B:77:GLU:N	2:B:77:GLU:CD	2.75	0.44
4:D:75:GLY:HA2	4:D:186:TYR:CD2	2.53	0.44
1:A:219:ARG:O	1:A:222:GLU:HG2	2.19	0.43
1:A:238:ASP:OD1	1:A:240:THR:HG22	2.18	0.43
2:B:19:LYS:O	2:B:72:PRO:HD2	2.19	0.43
4:D:113:GLN:HA	4:D:114:PRO:HA	1.64	0.43
4:D:193:ASP:OD1	4:D:193:ASP:N	2.51	0.42
1:A:218:GLN:HA	1:A:222:GLU:O	2.20	0.42
4:D:41:ARG:O	4:D:46:LYS:HA	2.19	0.42
1:A:207:GLY:HA2	1:A:240:THR:HG21	2.01	0.42
1:A:219:ARG:HE	1:A:222:GLU:HG3	1.83	0.42
2:B:40:LEU:O	2:B:78:TYR:HA	2.20	0.42
1:A:234:ARG:HD2	2:B:8:GLN:OE1	2.20	0.42
4:D:73:LEU:O	4:D:77:TYR:OH	2.32	0.42
4:D:138:HIS:HB2	4:D:178:PHE:HB2	2.01	0.42
4:D:35:GLN:HG3	4:D:36:HIS:ND1	2.34	0.42
4:D:136:MET:HA	4:D:151:SER:HA	2.01	0.42
1:A:183:GLU:O	1:A:183:GLU:CG	2.52	0.42
1:A:249:VAL:HG21	1:A:254:GLU:HG3	2.01	0.42
4:D:178:PHE:HD2	4:D:189:SER:O	2.03	0.41
1:A:270:LEU:HD12	1:A:270:LEU:HA	1.93	0.41
4:D:17:LEU:HD22	4:D:100:VAL:HG22	2.02	0.41
1:A:218:GLN:OE1	1:A:260:HIS:HD2	2.03	0.41
4:D:56:HIS:O	4:D:59:VAL:HG22	2.21	0.41
4:D:108:PRO:O	4:D:192:SER:HB2	2.19	0.41
4:D:139:LEU:HB2	4:D:148:ARG:HG3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:GLU:N	1:A:154:GLU:OE1	2.53	0.41
1:A:219:ARG:O	1:A:221:GLY:N	2.54	0.41
2:B:16:GLU:HB2	2:B:19:LYS:HG3	2.03	0.41
1:A:47:PRO:HB3	1:A:60:TRP:CZ2	2.56	0.41

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:GLU:OE2	1:A:131:ARG:NH2[5_555]	2.18	0.02

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	276/278 (99%)	264 (96%)	12 (4%)	0	100	100
2	B	98/100 (98%)	97 (99%)	1 (1%)	0	100	100
3	C	7/9 (78%)	7 (100%)	0	0	100	100
4	D	157/204 (77%)	142 (90%)	13 (8%)	2 (1%)	9	18
All	All	538/591 (91%)	510 (95%)	26 (5%)	2 (0%)	30	49

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	68	PRO
4	D	116	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	234/234 (100%)	222 (95%)	12 (5%)	21	43
2	B	95/95 (100%)	86 (90%)	9 (10%)	8	17
3	C	7/7 (100%)	5 (71%)	2 (29%)	0	0
4	D	148/175 (85%)	129 (87%)	19 (13%)	4	9
All	All	484/511 (95%)	442 (91%)	42 (9%)	9	21

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	42	SER
1	A	58	GLU
1	A	70	GLN
1	A	88	SER
1	A	147	LEU
1	A	169	ARG
1	A	200	THR
1	A	215	LEU
1	A	222	GLU
1	A	232	GLU
1	A	240	THR
1	A	251	SER
2	B	1	ILE
2	B	34	ASP
2	B	45	ARG
2	B	61	SER
2	B	70	PHE
2	B	75	LYS
2	B	77	GLU
2	B	88	SER
2	B	89	GLN
3	C	3	ARG
3	C	9	LEU
4	D	19	LYS

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Mol	Chain	Res	Type
4	D	20	SER
4	D	28	CYS
4	D	31	ASP
4	D	34	PHE
4	D	60	SER
4	D	66	ILE
4	D	70	MET
4	D	100	VAL
4	D	113	GLN
4	D	117	THR
4	D	132	SER
4	D	139	LEU
4	D	149	ARG
4	D	150	PHE
4	D	157	ASN
4	D	159	THR
4	D	163	ASP
4	D	195	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	87	GLN
1	A	260	HIS
2	B	17	ASN
4	D	50	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no 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	277/278 (99%)	-0.05	2 (0%) 84 81	27, 68, 111, 182	1 (0%)
2	B	100/100 (100%)	-0.02	0 100 100	42, 76, 118, 143	0
3	C	9/9 (100%)	-0.24	0 100 100	54, 63, 72, 73	0
4	D	167/204 (81%)	0.70	18 (10%) 11 9	66, 101, 147, 178	0
All	All	553/591 (93%)	0.18	20 (3%) 46 41	27, 79, 138, 182	1 (0%)

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	162	ALA	3.6
4	D	150	PHE	3.3
4	D	189	SER	3.1
4	D	125	THR	2.8
4	D	63	ASN	2.8
4	D	160	PHE	2.7
4	D	164	PHE	2.7
4	D	155	LYS	2.6
4	D	190	ASN	2.6
4	D	152	ALA	2.4
4	D	51	LEU	2.4
4	D	178	PHE	2.4
1	A	272	LEU	2.4
4	D	138	HIS	2.3
4	D	104	LEU	2.2
4	D	105	TYR	2.2
4	D	161	GLN	2.2
1	A	216	THR	2.1
4	D	139	LEU	2.1
4	D	166	LEU	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.