



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:31 PM UTC

PDB ID : 2IPK / pdb_00002ipk
Title : Crystal Structure of the MHC Class II Molecule HLA-DR1 in Complex with the Fluorogenic Peptide, AcPKXVKQNTLKLAT (X=3-[5-(dimethylamino)-1,3-dioxo-1,3-dihydro-2H-isoindol-2-yl]-L-alanine) and the Superantigen, SEC3 Variant 3B2
Authors : Nguyen, T.T.; Stern, L.J.
Deposited on : 2006-10-12
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
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

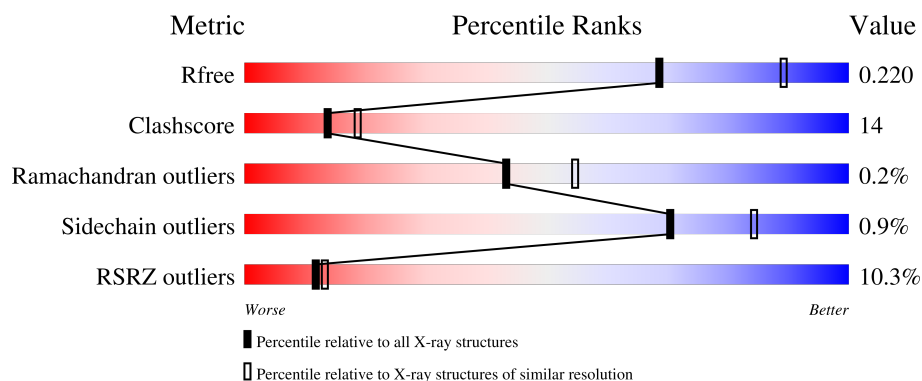
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	183	10% 75% 22% ..
2	B	190	12% 75% 24% .
3	C	14	29% 43% 50% 7%
4	D	240	8% 75% 21% .

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	4DP	C	308	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5464 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 II histocompatibility antigen, DR alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	179	Total	C	N	O	S	0	0	0
			1473	954	239	275	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	MET	-	cloning artifact	UNP P01903

- Molecule 2 is a protein called HLA class II histocompatibility antigen, DRB1-1 beta chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	190	Total	C	N	O	S	0	0	0
			1557	979	279	293	6			

- Molecule 3 is a protein called HA related Fluorogenic Peptide, AcPKXVKQNTLKLAT (X = 3-[5-(dimethylamino)-1,3-dioxo-1,3-dihydro-2H-isoindol-2-yl]-L-alanine).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	14	Total	C	N	O	0	0	0
			116	75	20	21			

- Molecule 4 is a protein called Enterotoxin type C-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	232	Total	C	N	O	S	0	0	0
			1899	1205	309	375	10			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	0	MET	-	cloning artifact	UNP P0A0L3
D	43	SER	LYS	engineered mutation	UNP P0A0L3

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Chain	Residue	Modelled	Actual	Comment	Reference
D	45	PHE	LEU	engineered mutation	UNP P0A0L3
D	46	LYS	ALA	engineered mutation	UNP P0A0L3
D	47	TRP	HIS	engineered mutation	UNP P0A0L3

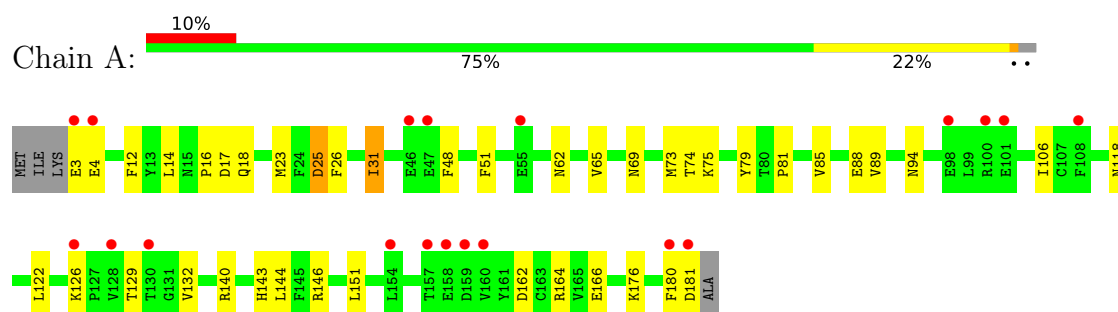
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	133	Total 133	O 133	0	0
5	B	106	Total 106	O 106	0	0
5	C	8	Total 8	O 8	0	0
5	D	172	Total 172	O 172	0	0

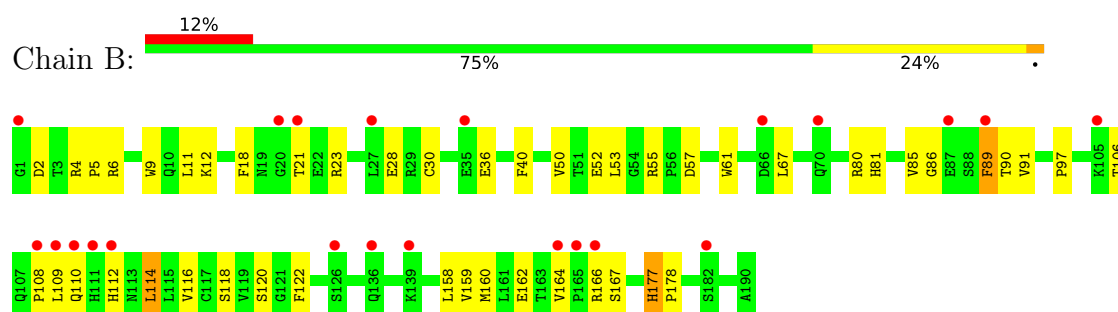
3 Residue-property plots [i](#)

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.

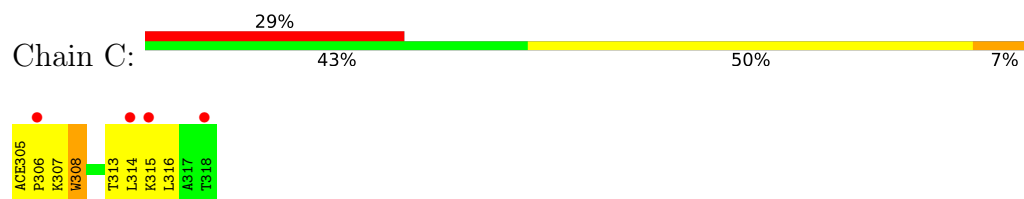
- Molecule 1: HLA class II histocompatibility antigen, DR alpha chain



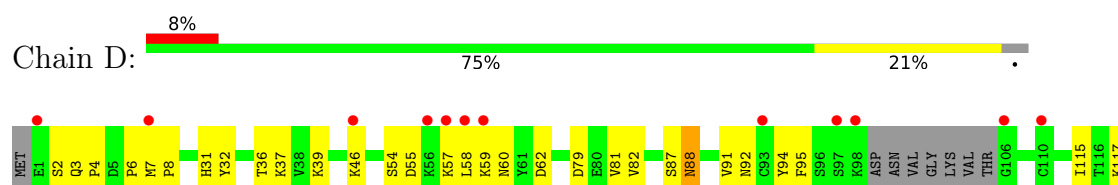
- Molecule 2: HLA class II histocompatibility antigen, DRB1-1 beta chain

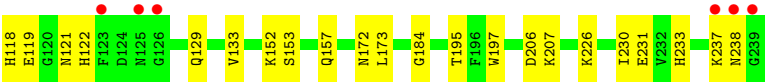


- Molecule 3: HA related Fluorogenic Peptide, AcPKXVKQNTLKLAT (X=3-[5-(dimethylamino)-1,3-dioxo-1,3-dihydro-2H-isoindol-2-yl]-L-alanine)



- Molecule 4: Enterotoxin type C-3





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	171.98Å 171.98Å 121.13Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	32.50 – 2.30 32.50 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.6 (32.50-2.30) 99.6 (32.50-2.30)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.96 (at 2.20Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.203 , 0.224 0.198 , 0.220	Depositor DCC
R_{free} test set	3438 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	40.6	Xtriage
Anisotropy	0.078	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 44.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.021 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5464	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 3.48% 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

Bond lengths and bond angles in the following residue types are not validated in this section: 4DP, ACE

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	0.46	0/1518	0.99	7/2070 (0.3%)
2	B	0.41	0/1597	0.94	5/2168 (0.2%)
3	C	1.02	1/94 (1.1%)	0.71	0/123
4	D	0.42	0/1941	0.88	4/2611 (0.2%)
All	All	0.45	1/5150 (0.0%)	0.93	16/6972 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	305	ACE	C-N	-9.07	1.34	1.43

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	164	VAL	CA-C-N	8.85	128.87	119.76
2	B	164	VAL	C-N-CA	8.85	128.87	119.76
1	A	85	VAL	CA-C-N	7.58	125.19	119.66
1	A	85	VAL	C-N-CA	7.58	125.19	119.66
1	A	88	GLU	N-CA-C	-7.25	97.42	109.46
1	A	31	ILE	N-CA-C	-6.74	105.19	111.45
4	D	82	VAL	N-CA-C	6.44	116.67	108.82
1	A	126	LYS	CA-C-N	6.03	125.97	119.76
1	A	126	LYS	C-N-CA	6.03	125.97	119.76
2	B	120	SER	N-CA-C	5.96	118.47	109.41
4	D	7	MET	N-CA-C	-5.91	101.95	110.40
4	D	115	ILE	N-CA-C	5.83	116.33	108.17
2	B	177	HIS	CA-C-N	5.41	125.12	119.82
2	B	177	HIS	C-N-CA	5.41	125.12	119.82
4	D	81	VAL	N-CA-C	-5.36	100.03	108.23
1	A	144	LEU	N-CA-C	-5.04	102.05	109.86

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	1473	0	1407	37	0
2	B	1557	0	1488	75	0
3	C	116	0	126	29	0
4	D	1899	0	1829	42	0
5	A	133	0	0	3	0
5	B	106	0	0	1	0
5	C	8	0	0	0	0
5	D	172	0	0	3	0
All	All	5464	0	4850	143	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 14.

All (143) 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:B:116:VAL:HG13	2:B:160:MET:HE2	1.41	1.02
2:B:158:LEU:HB3	2:B:160:MET:HE1	1.46	0.98
1:A:73:MET:HE1	2:B:53:LEU:HG	1.49	0.94
2:B:85:VAL:HG13	3:C:306:PRO:HB2	1.56	0.88
2:B:21:THR:HG23	2:B:80:ARG:HD3	1.55	0.86
4:D:88:ASN:H	4:D:88:ASN:HD22	1.23	0.86
2:B:89:PHE:HD1	2:B:89:PHE:H	1.24	0.85
2:B:89:PHE:HD1	2:B:89:PHE:N	1.75	0.83
4:D:121:ASN:HD21	4:D:153:SER:H	1.25	0.83
2:B:52:GLU:H	2:B:52:GLU:CD	1.87	0.82
2:B:11:LEU:HD23	3:C:313:THR:HG22	1.61	0.81
2:B:67:LEU:HD11	3:C:314:LEU:HD11	1.60	0.80
2:B:11:LEU:CD2	3:C:313:THR:HG22	2.10	0.80
2:B:89:PHE:N	2:B:89:PHE:CD1	2.48	0.80
4:D:117:LYS:HE2	4:D:119:GLU:HB3	1.65	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:67:LEU:HD21	3:C:314:LEU:HD13	1.67	0.77
2:B:89:PHE:CE2	3:C:308:4DP:CAC	2.72	0.73
4:D:122:HIS:O	4:D:152:LYS:HE3	1.89	0.72
4:D:122:HIS:NE2	5:D:407:HOH:O	2.21	0.72
1:A:62:ASN:ND2	3:C:313:THR:HG23	2.05	0.71
2:B:2:ASP:OD1	2:B:4:ARG:HD3	1.91	0.70
2:B:159:VAL:C	2:B:160:MET:HE3	2.14	0.70
2:B:114:LEU:HD21	2:B:160:MET:HB3	1.74	0.68
4:D:118:HIS:CD2	5:D:407:HOH:O	2.49	0.65
4:D:88:ASN:H	4:D:88:ASN:ND2	1.94	0.65
1:A:81:PRO:HB3	2:B:5:PRO:HB2	1.78	0.64
1:A:16:PRO:HD2	2:B:6:ARG:HD3	1.79	0.64
2:B:160:MET:HE3	2:B:160:MET:N	2.13	0.64
2:B:21:THR:CG2	2:B:80:ARG:HD3	2.26	0.63
4:D:206:ASP:OD1	4:D:207:LYS:HG3	1.98	0.63
2:B:11:LEU:HD23	3:C:313:THR:CG2	2.28	0.62
4:D:55:ASP:HB3	4:D:59:LYS:HA	1.81	0.62
2:B:23:ARG:HH11	2:B:23:ARG:HG2	1.64	0.61
2:B:109:LEU:HD13	2:B:112:HIS:ND1	2.15	0.61
2:B:89:PHE:CE2	3:C:308:4DP:HAC3	2.34	0.61
1:A:51:PHE:HB2	2:B:89:PHE:CE2	2.35	0.61
4:D:121:ASN:ND2	4:D:153:SER:H	1.99	0.60
4:D:39:LYS:HZ2	4:D:79:ASP:HA	1.67	0.59
1:A:180:PHE:O	1:A:181:ASP:HB2	2.03	0.59
2:B:86:GLY:HA2	2:B:89:PHE:CE1	2.36	0.59
4:D:88:ASN:HD22	4:D:88:ASN:N	1.99	0.59
1:A:17:ASP:O	4:D:46:LYS:HE3	2.02	0.59
1:A:73:MET:HG3	2:B:9:TRP:CZ3	2.37	0.59
4:D:39:LYS:NZ	4:D:79:ASP:HA	2.18	0.58
1:A:143:HIS:HD2	2:B:12:LYS:NZ	2.02	0.57
4:D:2:SER:HB2	4:D:195:THR:H	1.69	0.57
2:B:108:PRO:O	2:B:109:LEU:HG	2.05	0.57
2:B:61:TRP:CZ2	3:C:316:LEU:HD23	2.39	0.57
2:B:21:THR:O	2:B:80:ARG:NH1	2.38	0.57
2:B:67:LEU:CD2	3:C:314:LEU:HD13	2.35	0.56
1:A:14:LEU:HD11	2:B:6:ARG:HB3	1.87	0.56
2:B:97:PRO:HB3	2:B:122:PHE:HB3	1.88	0.56
2:B:90:THR:HG23	3:C:308:4DP:CAD	2.36	0.56
4:D:121:ASN:HD21	4:D:153:SER:N	2.01	0.56
1:A:65:VAL:HG13	3:C:315:LYS:HD2	1.88	0.55
4:D:36:THR:HG22	4:D:37:LYS:HG3	1.88	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:62:ASN:CG	3:C:313:THR:HG23	2.32	0.55
2:B:57:ASP:CG	3:C:316:LEU:HD22	2.32	0.54
2:B:116:VAL:HG13	2:B:160:MET:CE	2.26	0.54
4:D:58:LEU:HD23	4:D:58:LEU:H	1.73	0.53
2:B:158:LEU:CB	2:B:160:MET:HE1	2.31	0.53
4:D:231:GLU:OE1	4:D:233:HIS:HE1	1.90	0.52
2:B:90:THR:CG2	3:C:308:4DP:HAD3	2.40	0.52
2:B:36:GLU:HG2	2:B:50:VAL:HG21	1.92	0.51
2:B:109:LEU:HD12	2:B:162:GLU:CD	2.36	0.51
2:B:21:THR:HG23	2:B:80:ARG:CD	2.33	0.51
2:B:106:THR:HG22	2:B:108:PRO:HD3	1.93	0.51
2:B:89:PHE:HE2	3:C:308:4DP:HAC3	1.74	0.50
1:A:129:THR:HG22	1:A:129:THR:O	2.11	0.50
2:B:11:LEU:HD21	3:C:313:THR:HG22	1.92	0.50
2:B:86:GLY:HA3	5:B:296:HOH:O	2.12	0.49
2:B:11:LEU:CD2	3:C:313:THR:CG2	2.86	0.49
4:D:94:TYR:O	4:D:95:PHE:HB3	2.12	0.49
1:A:180:PHE:O	1:A:181:ASP:CB	2.61	0.48
2:B:67:LEU:HD11	3:C:314:LEU:CD1	2.39	0.48
4:D:129:GLN:NE2	4:D:226:LYS:HB3	2.29	0.48
2:B:52:GLU:HA	2:B:55:ARG:NH1	2.28	0.48
2:B:110:GLN:O	2:B:110:GLN:HG3	2.14	0.47
1:A:122:LEU:HB2	1:A:162:ASP:HB2	1.96	0.47
4:D:39:LYS:NZ	4:D:79:ASP:C	2.73	0.47
1:A:3:GLU:HA	2:B:18:PHE:CD2	2.50	0.47
1:A:51:PHE:O	3:C:306:PRO:HD2	2.15	0.47
1:A:17:ASP:O	1:A:18:GLN:HB2	2.15	0.47
2:B:109:LEU:CB	2:B:112:HIS:HB2	2.45	0.47
2:B:114:LEU:CD2	2:B:160:MET:HB3	2.44	0.46
1:A:25:ASP:OD1	1:A:25:ASP:C	2.58	0.46
4:D:6:PRO:HB3	4:D:197:TRP:CZ2	2.50	0.46
2:B:9:TRP:CH2	2:B:30:CYS:HB3	2.49	0.46
1:A:69:ASN:CG	3:C:316:LEU:HG	2.40	0.46
1:A:48:PHE:HB3	3:C:308:4DP:CAC	2.45	0.46
1:A:75:LYS:HE3	5:A:257:HOH:O	2.16	0.46
1:A:140:ARG:HG3	1:A:146:ARG:HG3	1.96	0.46
4:D:87:SER:H	4:D:157:GLN:NE2	2.13	0.46
4:D:129:GLN:HE21	4:D:226:LYS:HB3	1.80	0.46
2:B:18:PHE:CD1	2:B:23:ARG:HD3	2.50	0.45
2:B:18:PHE:HB2	2:B:23:ARG:HB3	1.98	0.45
1:A:94:ASN:HB3	1:A:106:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:3:GLN:HA	4:D:4:PRO:HD3	1.84	0.45
2:B:21:THR:CG2	2:B:21:THR:O	2.64	0.45
4:D:233:HIS:HD2	5:D:294:HOH:O	2.00	0.45
5:A:312:HOH:O	3:C:315:LYS:HE3	2.16	0.45
1:A:143:HIS:HD2	2:B:12:LYS:HZ1	1.65	0.45
2:B:21:THR:O	2:B:21:THR:HG22	2.16	0.45
1:A:17:ASP:CG	2:B:6:ARG:HH11	2.25	0.45
1:A:164:ARG:NH1	1:A:166:GLU:OE1	2.50	0.45
1:A:23:MET:HE1	1:A:25:ASP:HB2	1.98	0.44
2:B:2:ASP:CG	2:B:6:ARG:HH22	2.24	0.44
1:A:74:THR:HG22	1:A:79:TYR:CD2	2.52	0.44
2:B:86:GLY:HA3	3:C:308:4DP:CAE	2.48	0.44
4:D:237:LYS:C	4:D:238:ASN:HD22	2.26	0.44
2:B:23:ARG:HG2	2:B:23:ARG:NH1	2.31	0.44
4:D:55:ASP:O	4:D:59:LYS:HD2	2.18	0.44
4:D:91:VAL:O	4:D:92:ASN:HB2	2.18	0.44
2:B:166:ARG:O	2:B:167:SER:C	2.59	0.43
4:D:55:ASP:CB	4:D:60:ASN:H	2.30	0.43
1:A:89:VAL:HG12	1:A:176:LYS:HG3	2.00	0.43
1:A:12:PHE:C	1:A:12:PHE:CD1	2.97	0.43
1:A:118:ASN:HB3	1:A:166:GLU:HB2	2.00	0.43
2:B:109:LEU:HB3	2:B:112:HIS:HB2	2.01	0.43
4:D:172:ASN:O	4:D:173:LEU:C	2.62	0.43
2:B:81:HIS:HE1	3:C:307:LYS:O	2.02	0.43
1:A:73:MET:CE	2:B:53:LEU:HG	2.34	0.43
1:A:132:VAL:HG12	1:A:151:LEU:HD13	2.01	0.42
2:B:89:PHE:CE2	3:C:308:4DP:HAC1	2.53	0.42
2:B:118:SER:HA	2:B:158:LEU:HD23	2.01	0.42
2:B:177:HIS:HA	2:B:178:PRO:HD3	1.90	0.42
4:D:58:LEU:HD23	4:D:58:LEU:N	2.34	0.42
4:D:39:LYS:NZ	4:D:79:ASP:O	2.53	0.42
4:D:231:GLU:OE1	4:D:233:HIS:CE1	2.72	0.42
1:A:73:MET:HG2	3:C:316:LEU:CD1	2.50	0.42
4:D:39:LYS:NZ	4:D:79:ASP:CA	2.82	0.42
2:B:28:GLU:HB3	2:B:40:PHE:HB3	2.02	0.42
2:B:90:THR:OG1	2:B:91:VAL:N	2.52	0.41
1:A:26:PHE:HB2	1:A:31:ILE:HD11	2.02	0.41
2:B:90:THR:HG23	3:C:308:4DP:HAD2	2.01	0.41
4:D:184:GLY:HA2	4:D:233:HIS:O	2.21	0.41
4:D:31:HIS:O	4:D:32:TYR:HB3	2.19	0.41
4:D:54:SER:HA	4:D:62:ASP:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:110:GLN:C	2:B:112:HIS:N	2.78	0.41
1:A:4:GLU:HB2	5:A:193:HOH:O	2.21	0.40
4:D:37:LYS:HG2	4:D:118:HIS:CD2	2.56	0.40
4:D:118:HIS:ND1	4:D:118:HIS:C	2.79	0.40
4:D:133:VAL:HG22	4:D:230:ILE:HB	2.02	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	177/183 (97%)	172 (97%)	5 (3%)	0	100	100
2	B	188/190 (99%)	181 (96%)	7 (4%)	0	100	100
3	C	11/14 (79%)	11 (100%)	0	0	100	100
4	D	228/240 (95%)	220 (96%)	7 (3%)	1 (0%)	30	38
All	All	604/627 (96%)	584 (97%)	19 (3%)	1 (0%)	43	55

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	57	LYS

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	164/167 (98%)	163 (99%)	1 (1%)	78	89
2	B	171/171 (100%)	169 (99%)	2 (1%)	63	79
3	C	11/11 (100%)	11 (100%)	0	100	100
4	D	214/221 (97%)	212 (99%)	2 (1%)	70	84
All	All	560/570 (98%)	555 (99%)	5 (1%)	70	84

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	ASP
2	B	89	PHE
2	B	114	LEU
4	D	8	PRO
4	D	88	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	143	HIS
1	A	149	HIS
2	B	81	HIS
2	B	113	ASN
2	B	156	GLN
3	C	311	GLN
4	D	60	ASN
4	D	88	ASN
4	D	92	ASN
4	D	118	HIS
4	D	121	ASN
4	D	125	ASN
4	D	127	ASN
4	D	129	GLN
4	D	157	GLN
4	D	177	ASN
4	D	194	ASN
4	D	233	HIS
4	D	238	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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	4DP	C	308	3	19,20,21	2.60	4 (21%)	25,29,31	2.03	8 (32%)

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	4DP	C	308	3	-	0/8/26/28	0/2/2/2

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	308	4DP	CAL-CAJ	-5.90	1.39	1.48
3	C	308	4DP	CAK-CAI	-5.81	1.39	1.48
3	C	308	4DP	CAI-NAN	-5.23	1.33	1.39
3	C	308	4DP	CAJ-NAN	-5.18	1.33	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	308	4DP	CAK-CAI-NAN	4.92	109.52	105.88
3	C	308	4DP	CAL-CAJ-NAN	4.40	109.13	105.88
3	C	308	4DP	CAI-NAN-CAJ	-3.62	108.93	112.02
3	C	308	4DP	CAL-CAK-CAI	-2.73	105.87	108.26
3	C	308	4DP	CAF-CAK-CAI	2.71	134.14	129.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	308	4DP	CAG-CAH-NAM	-2.30	118.80	121.33
3	C	308	4DP	CA-CB-NAN	2.15	114.06	111.13
3	C	308	4DP	CAG-CAL-CAJ	2.12	133.02	129.39

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	308	4DP	9	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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, 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	179/183 (97%)	0.28	19 (10%)	11 12	24, 37, 88, 138	0
2	B	190/190 (100%)	0.54	22 (11%)	9 10	25, 47, 98, 165	0
3	C	12/14 (85%)	1.48	4 (33%)	1 1	36, 45, 76, 82	0
4	D	232/240 (96%)	0.26	18 (7%)	19 21	25, 41, 89, 133	0
All	All	613/627 (97%)	0.38	63 (10%)	12 13	24, 42, 90, 165	0

All (63) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	98	LYS	7.2
1	A	108	PHE	5.4
4	D	106	GLY	5.1
4	D	93	CYS	5.0
4	D	110	CYS	4.6
4	D	97	SER	4.5
2	B	111	HIS	4.2
2	B	89	PHE	4.2
4	D	126	GLY	4.1
1	A	181	ASP	4.0
4	D	57	LYS	3.9
2	B	1	GLY	3.7
1	A	3	GLU	3.7
4	D	239	GLY	3.7
2	B	139	LYS	3.7
2	B	70	GLN	3.5
4	D	7	MET	3.4
1	A	101	GLU	3.3
4	D	58	LEU	3.3
4	D	238	ASN	3.2
2	B	108	PRO	3.1

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Mol	Chain	Res	Type	RSRZ
3	C	318	THR	3.1
4	D	237	LYS	3.0
2	B	66	ASP	3.0
4	D	56	LYS	3.0
1	A	130	THR	2.9
2	B	27	LEU	2.8
1	A	157	THR	2.8
4	D	1	GLU	2.8
2	B	164	VAL	2.8
2	B	136	GLN	2.8
2	B	110	GLN	2.8
3	C	306	PRO	2.7
1	A	158	GLU	2.7
1	A	159	ASP	2.6
1	A	100	ARG	2.6
2	B	35	GLU	2.6
4	D	123	PHE	2.6
2	B	105	LYS	2.5
2	B	109	LEU	2.5
1	A	4	GLU	2.5
1	A	98	GLU	2.5
3	C	315	LYS	2.5
2	B	21	THR	2.4
1	A	160	VAL	2.4
1	A	47	GLU	2.4
4	D	125	ASN	2.3
2	B	126	SER	2.3
4	D	46	LYS	2.3
1	A	46	GLU	2.3
4	D	59	LYS	2.3
2	B	166	ARG	2.1
1	A	126	LYS	2.1
2	B	182	SER	2.1
2	B	87	GLU	2.1
1	A	180	PHE	2.1
2	B	20	GLY	2.1
3	C	314	LEU	2.1
1	A	128	VAL	2.1
1	A	55	GLU	2.0
2	B	112	HIS	2.0
1	A	154	LEU	2.0
2	B	165	PRO	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. The B-factors column lists the minimum, median, 95th 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	B-factors(Å ²)	Q<0.9
3	4DP	C	308	19/20	0.79	0.25	30,34,39,41	0

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.