



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 01:47 PM UTC

PDB ID : 6XTE / pdb_00006xte
Title : Human karyopherin RanBP5 (isoform-1)
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Deposited on : 2020-01-16
Resolution : 2.27 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

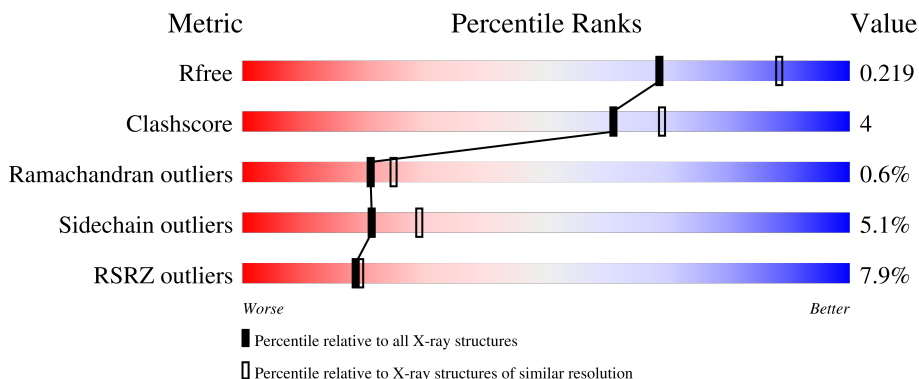
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.27 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	1096	8% 83% 14% ..
2	C	4	50% 50% 25% 25%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 8565 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 Importin-5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1075	Total	C	N	O	S	0	3	0
			8436	5362	1425	1582	67			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	ALA	-	expression tag	UNP O00410
A	21	MET	-	expression tag	UNP O00410

- Molecule 2 is a protein called Antipain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	0	0	0
			42	27	10	5			

- Molecule 3 is NICKEL (II) ION (CCD ID: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	2	Total	Ni	0	0
			2	2		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		

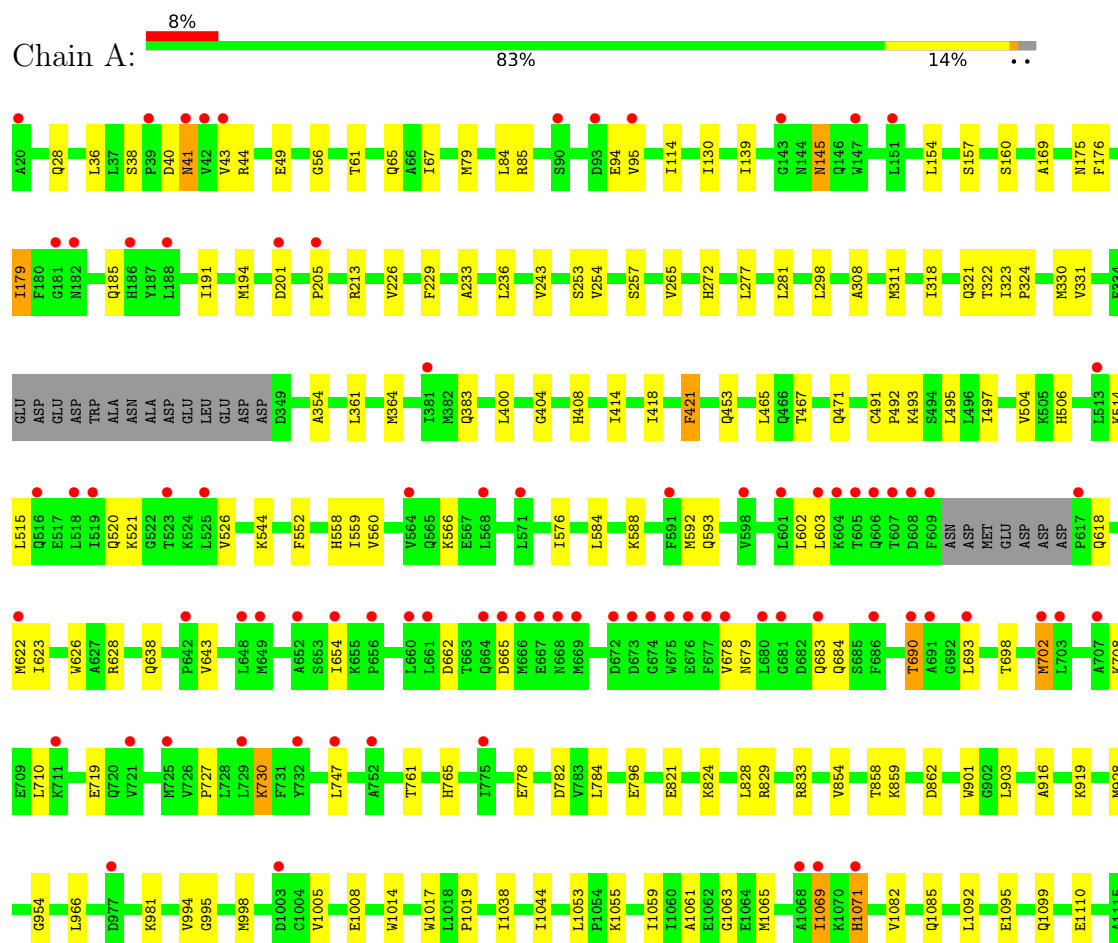
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	84	Total	O	0	0
			84	84		

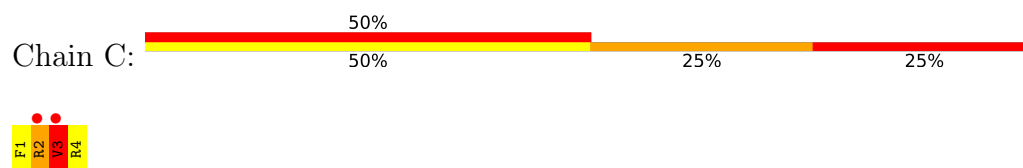
3 Residue-property plots [i](#)

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: Importin-5



• Molecule 2: Antipain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.09Å 96.31Å 156.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	78.49 – 2.27 78.49 – 2.27	Depositor EDS
% Data completeness (in resolution range)	67.1 (78.49-2.27) 67.1 (78.49-2.27)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.08 (at 2.27Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.199 , 0.260 0.213 , 0.219	Depositor DCC
R_{free} test set	2104 reflections (3.41%)	wwPDB-VP
Wilson B-factor (Å ²)	59.4	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8565	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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: CL, NI, CSO, FC0, RGL

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	0.78	0/8597	1.19	10/11647 (0.1%)
2	C	0.88	0/17	1.72	2/21 (9.5%)
All	All	0.78	0/8614	1.19	12/11668 (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
2	C	0	2

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	954	GLY	N-CA-C	8.83	123.33	112.73
1	A	862	ASP	CA-CB-CG	7.52	120.12	112.60
1	A	298	LEU	CA-C-N	6.08	128.71	120.38
1	A	298	LEU	C-N-CA	6.08	128.71	120.38
1	A	40	ASP	CA-CB-CG	5.64	118.24	112.60
1	A	683	GLN	CA-C-N	5.61	130.35	121.99
1	A	683	GLN	C-N-CA	5.61	130.35	121.99
1	A	421	PHE	CA-CB-CG	5.37	119.17	113.80
1	A	233	ALA	CA-C-N	5.24	127.82	120.28
1	A	233	ALA	C-N-CA	5.24	127.82	120.28
2	C	2	ARG	CA-C-N	5.11	130.90	121.70
2	C	2	ARG	C-N-CA	5.11	130.90	121.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	C	3	VAL	Peptide,Mainchain

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	8436	0	8383	71	0
2	C	42	0	43	1	0
3	A	2	0	0	0	0
4	A	1	0	0	0	0
5	A	84	0	0	0	0
All	All	8565	0	8426	71	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 4.

All (71) 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:A:1069:ILE:HG23	1:A:1071:HIS:CE1	2.11	0.85
1:A:998:MET:HE1	1:A:1014:TRP:CG	2.22	0.74
1:A:994:VAL:HG12	1:A:998:MET:HE2	1.71	0.73
1:A:588:LYS:HE2	1:A:592:MET:HE1	1.73	0.71
1:A:243:VAL:HA	1:A:254:VAL:HG13	1.82	0.61
1:A:903:LEU:HD22	1:A:928:MET:HG2	1.83	0.60
1:A:281:LEU:HD21	1:A:321:GLN:HB2	1.83	0.59
1:A:36:LEU:HB3	1:A:79:MET:HE3	1.85	0.58
1:A:995:GLY:HA2	1:A:998:MET:HE3	1.85	0.57
1:A:467:THR:HA	1:A:471:GLN:HG3	1.87	0.56
1:A:708:LYS:HB3	1:A:747:LEU:HD22	1.87	0.56
1:A:176:PHE:O	1:A:179:ILE:HG12	2.06	0.55
1:A:492:PRO:HD2	1:A:495:LEU:HD12	1.89	0.55
1:A:829:ARG:O	1:A:833:ARG:HG3	2.07	0.55
1:A:966:LEU:HD22	1:A:1005:VAL:HG23	1.89	0.55
1:A:821:GLU:HA	1:A:824:LYS:HD2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:ARG:HD3	1:A:253:SER:HB3	1.89	0.54
1:A:638:GLN:HG3	1:A:710:LEU:HD22	1.90	0.54
1:A:330:MET:HA	1:A:354:ALA:HA	1.90	0.53
1:A:493:LYS:O	1:A:497:ILE:HG12	2.08	0.53
1:A:330:MET:HE1	1:A:361:LEU:HD22	1.91	0.53
1:A:1069:ILE:HG23	1:A:1071:HIS:NE2	2.24	0.52
1:A:277:LEU:HB3	1:A:318:ILE:HG21	1.92	0.52
1:A:465:LEU:HD13	1:A:506:HIS:CD2	2.44	0.51
1:A:157:SER:HB2	1:A:169:ALA:HB2	1.92	0.51
1:A:191:ILE:HA	1:A:194:MET:HE2	1.92	0.50
1:A:1038:ILE:HD13	1:A:1082:VAL:HG11	1.93	0.50
1:A:404:GLY:O	1:A:408:HIS:HB3	2.12	0.49
1:A:243:VAL:HA	1:A:254:VAL:CG1	2.43	0.49
1:A:504:VAL:HG13	1:A:552:PHE:HE2	1.77	0.48
1:A:1008:GLU:HG2	1:A:1044:ILE:CD1	2.43	0.48
1:A:1008:GLU:HG2	1:A:1044:ILE:HD13	1.95	0.48
1:A:584:LEU:HD13	1:A:628:ARG:HG2	1.96	0.47
1:A:453:GLN:HG2	1:A:491:CYS:HB2	1.96	0.47
1:A:414:ILE:HD12	1:A:418:ILE:HD11	1.96	0.47
1:A:520:GLN:HG3	1:A:521:LYS:HG2	1.96	0.47
1:A:84:LEU:HD23	1:A:130:ILE:HD13	1.97	0.47
1:A:1061:ALA:C	1:A:1063:GLY:H	2.23	0.46
1:A:602:LEU:HD11	1:A:622:MET:HG2	1.97	0.46
1:A:61:THR:O	1:A:65:GLN:HG2	2.14	0.46
1:A:859:LYS:NZ	2:C:1:FC0:CZ	2.79	0.46
1:A:1069:ILE:CG2	1:A:1071:HIS:NE2	2.79	0.46
1:A:1014:TRP:HA	1:A:1017:TRP:CE3	2.51	0.46
1:A:322:THR:HG21	1:A:364:MET:HE1	1.97	0.46
1:A:514:LYS:HE2	1:A:526:VAL:HB	1.98	0.46
1:A:1019:PRO:HB3	1:A:1059:ILE:HG23	1.97	0.45
1:A:698:THR:O	1:A:702:MET:HG2	2.16	0.45
1:A:1038:ILE:HG21	1:A:1082:VAL:HG13	1.99	0.45
1:A:602:LEU:HD23	1:A:626:TRP:NE1	2.31	0.45
1:A:504:VAL:HG13	1:A:552:PHE:CE2	2.52	0.44
1:A:67:ILE:HG22	1:A:114:ILE:HD13	2.00	0.44
1:A:308:ALA:HB1	1:A:311:MET:HE3	1.99	0.44
1:A:858:THR:HG22	1:A:901:TRP:CE2	2.53	0.43
1:A:139:ILE:HD13	1:A:145:ASN:HA	1.99	0.43
1:A:690:THR:HA	1:A:693:LEU:HD12	2.01	0.43
1:A:229:PHE:CZ	1:A:265:VAL:CG2	3.01	0.43
1:A:1053:LEU:HD12	1:A:1092:LEU:HD21	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:GLY:HA3	1:A:95:VAL:HG22	2.00	0.43
1:A:662:ASP:HA	1:A:684:GLN:HA	2.00	0.42
1:A:727:PRO:HA	1:A:730:LYS:HE2	2.02	0.42
1:A:515:LEU:HD13	1:A:559:ILE:HG12	2.00	0.42
1:A:236:LEU:HD23	1:A:272:HIS:HB2	2.02	0.42
1:A:41:ASN:HA	1:A:44:ARG:HB3	2.02	0.42
1:A:778:GLU:HB3	1:A:784:LEU:HD13	2.01	0.42
1:A:323:ILE:HB	1:A:324:PRO:HD3	2.02	0.42
1:A:1055:LYS:HE3	1:A:1059:ILE:HD11	2.01	0.41
1:A:761:THR:HG22	1:A:765:HIS:CE1	2.55	0.41
1:A:854:VAL:O	1:A:858:THR:HG23	2.21	0.41
1:A:916:ALA:HA	1:A:919:LYS:HE2	2.03	0.41
1:A:1069:ILE:HG23	1:A:1071:HIS:CD2	2.56	0.40
1:A:1069:ILE:CG2	1:A:1071:HIS:CD2	3.04	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	1071/1096 (98%)	1028 (96%)	38 (4%)	5 (0%)	24	29
2	C	1/4 (25%)	0	0	1 (100%)	0	0
All	All	1072/1100 (98%)	1028 (96%)	38 (4%)	6 (1%)	21	25

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1071	HIS
2	C	3	VAL
1	A	201	ASP
1	A	160	SER

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Mol	Chain	Res	Type
1	A	205	PRO
1	A	185	GLN

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	916/951 (96%)	871 (95%)	45 (5%)	22	31
2	C	2/2 (100%)	0	2 (100%)	0	0
All	All	918/953 (96%)	871 (95%)	47 (5%)	21	29

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	GLN
1	A	38	SER
1	A	41	ASN
1	A	43	VAL
1	A	49	GLU
1	A	85	ARG
1	A	94	GLU
1	A	145	ASN
1	A	154	LEU
1	A	175	ASN
1	A	179	ILE
1	A	226	VAL
1	A	257	SER
1	A	331	VAL
1	A	383	GLN
1	A	400	LEU
1	A	421	PHE
1	A	544	LYS
1	A	558	HIS
1	A	560	VAL
1	A	566	LYS

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Mol	Chain	Res	Type
1	A	576	ILE
1	A	593	GLN
1	A	603	LEU
1	A	618	GLN
1	A	623	ILE
1	A	643	VAL
1	A	654	ILE
1	A	665	ASP
1	A	678	VAL
1	A	679	ASN
1	A	690	THR
1	A	702	MET
1	A	719	GLU
1	A	730	LYS
1	A	782	ASP
1	A	796	GLU
1	A	828	LEU
1	A	981	LYS
1	A	1065	MET
1	A	1069	ILE
1	A	1085	GLN
1	A	1095	GLU
1	A	1099	GLN
1	A	1110	GLU
2	C	2	ARG
2	C	3	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	A	144	ASN
1	A	146	GLN
1	A	272	HIS
1	A	439	ASN
1	A	502	ASN
1	A	506	HIS
1	A	529	GLN
1	A	618	GLN
1	A	900	GLN
1	A	912	HIS
1	A	983	ASN

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Mol	Chain	Res	Type
1	A	1052	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	RGL	C	4	2	9,10,10	2.70	3 (33%)	5,11,11	2.11	2 (40%)
2	FC0	C	1	2	12,13,15	0.35	0	15,15,19	0.53	0
1	CSO	A	891	1	3,6,7	0.80	0	1,6,8	1.71	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	RGL	C	4	2	-	6/8/9/9	-
2	FC0	C	1	2	-	3/7/9/12	0/1/1/1
1	CSO	A	891	1	-	0/1/5/7	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	4	RGL	O-C	5.66	1.41	1.20
2	C	4	RGL	CZ-NE	5.19	1.43	1.33
2	C	4	RGL	CZ-NH2	2.19	1.40	1.32

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	RGL	NE-CZ-NH2	-3.94	113.91	120.67
2	C	4	RGL	NH1-CZ-NH2	2.41	126.92	120.07

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1	FC0	N-CA-CB-CG
2	C	1	FC0	O1-C1-N-CA
2	C	4	RGL	O-C-CA-CB
2	C	4	RGL	NH1-CZ-NE-CD
2	C	4	RGL	NH2-CZ-NE-CD
2	C	4	RGL	CA-CB-CG-CD
2	C	1	FC0	CB-CA-N-C1
2	C	4	RGL	NE-CD-CG-CB
2	C	4	RGL	CG-CD-NE-CZ

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	FC0	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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	1074/1096 (97%)	0.62	83 (7%)	19 20	24, 67, 112, 172	3 (0%)
2	C	2/4 (50%)	3.35	2 (100%)	0 0	88, 88, 88, 105	0
All	All	1076/1100 (97%)	0.62	85 (7%)	18 19	24, 67, 112, 172	3 (0%)

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	729	LEU	4.7
1	A	181	GLY	4.6
1	A	732	TYR	4.5
1	A	678	VAL	4.5
1	A	205	PRO	4.4
1	A	591	PHE	4.4
1	A	668	ASN	4.3
2	C	3	VAL	4.2
1	A	606	GLN	3.7
1	A	666	MET	3.6
1	A	201	ASP	3.6
1	A	605	THR	3.6
1	A	673	ASP	3.6
1	A	664	GLN	3.5
1	A	609	PHE	3.5
1	A	677	PHE	3.5
1	A	516	GLN	3.5
1	A	598	VAL	3.4
1	A	674	GLY	3.4
1	A	725	MET	3.3
1	A	617	PRO	3.3
1	A	1003	ASP	3.2
1	A	1068	ALA	3.2
1	A	665	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	571	LEU	3.1
1	A	603	LEU	3.1
1	A	525	LEU	3.1
1	A	675	TRP	3.1
1	A	564	VAL	3.1
1	A	43	VAL	3.0
1	A	601	LEU	3.0
1	A	669	MET	3.0
1	A	186	HIS	2.9
1	A	680	LEU	2.9
1	A	752	ALA	2.9
1	A	607	THR	2.8
1	A	691	ALA	2.8
1	A	977	ASP	2.8
1	A	143	GLY	2.8
1	A	686	PHE	2.8
1	A	667	GLU	2.7
1	A	1069	ILE	2.7
1	A	90	SER	2.7
1	A	20	ALA	2.7
1	A	39	PRO	2.7
1	A	147	TRP	2.7
1	A	523	THR	2.6
1	A	654	ILE	2.6
1	A	604	LYS	2.6
1	A	681	GLY	2.5
1	A	703	LEU	2.5
1	A	672	ASP	2.5
1	A	656	PRO	2.5
1	A	683	GLN	2.5
2	C	2	ARG	2.5
1	A	660	LEU	2.5
1	A	747	LEU	2.5
1	A	721	VAL	2.4
1	A	622	MET	2.4
1	A	1071	HIS	2.4
1	A	642	PRO	2.3
1	A	42	VAL	2.3
1	A	518	LEU	2.3
1	A	608	ASP	2.3
1	A	711	LYS	2.3
1	A	513	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	652	ALA	2.3
1	A	707	ALA	2.2
1	A	95	VAL	2.2
1	A	676	GLU	2.2
1	A	775	ILE	2.2
1	A	693	LEU	2.2
1	A	702	MET	2.2
1	A	690	THR	2.2
1	A	93	ASP	2.2
1	A	649	MET	2.1
1	A	568	LEU	2.1
1	A	661	LEU	2.1
1	A	182	ASN	2.1
1	A	648	LEU	2.1
1	A	519	ILE	2.1
1	A	41	ASN	2.0
1	A	381	ILE	2.0
1	A	151	LEU	2.0
1	A	188	LEU	2.0

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

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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
2	FC0	C	1	13/15	0.46	0.21	100,104,106,106	0
2	RGL	C	4	11/11	0.86	0.19	69,72,78,81	0
1	CSO	A	891	7/8	0.88	0.11	52,54,59,60	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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($\text{\AA}^2$)	Q<0.9
4	CL	A	1203	1/1	0.88	0.16	90,90,90,90	0
3	NI	A	1201	1/1	0.95	0.12	108,108,108,108	0
3	NI	A	1202	1/1	0.98	0.08	79,79,79,79	0

6.5 Other polymers [i](#)

There are no such residues in this entry.