



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:37 AM UTC

PDB ID : 5SXJ / pdb_00005sxj
Title : Crystal Structure of PI3Kalpha in complex with fragment 29
Authors : Gabelli, S.B.; Vogelstein, B.; Miller, M.S.; Amzel, L.M.
Deposited on : 2016-08-09
Resolution : 3.42 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

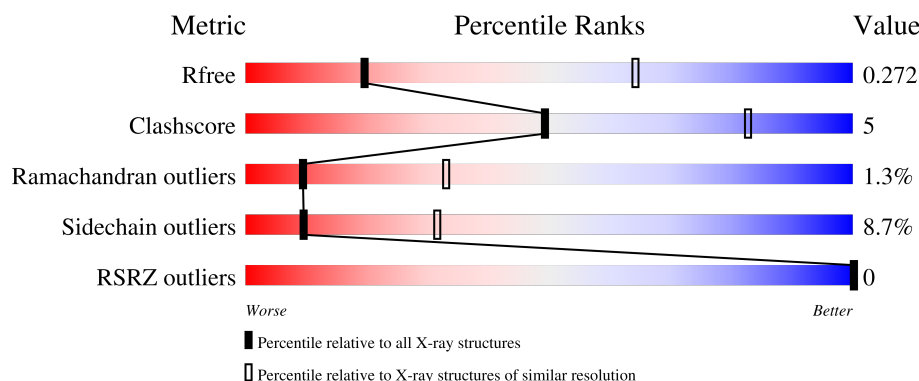
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.42 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	1210 (3.48-3.36)
Clashscore	190562	1234 (3.48-3.36)
Ramachandran outliers	187476	1222 (3.48-3.36)
Sidechain outliers	187428	1222 (3.48-3.36)
RSRZ outliers	180081	1210 (3.48-3.36)

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	 76% 17% • 5%
2	B	279	 61% 16% 23%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10420 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 Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic sub-unit alpha isoform.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1042	Total	C	N	O	P	S	0	0	0
			8538	5451	1460	1554	3	70			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-27	MET	-	initiating methionine	UNP P42336
A	-26	SER	-	expression tag	UNP P42336
A	-25	TYR	-	expression tag	UNP P42336
A	-24	TYR	-	expression tag	UNP P42336
A	-23	HIS	-	expression tag	UNP P42336
A	-22	HIS	-	expression tag	UNP P42336
A	-21	HIS	-	expression tag	UNP P42336
A	-20	HIS	-	expression tag	UNP P42336
A	-19	HIS	-	expression tag	UNP P42336
A	-18	HIS	-	expression tag	UNP P42336
A	-17	ASP	-	expression tag	UNP P42336
A	-16	TYR	-	expression tag	UNP P42336
A	-15	ASP	-	expression tag	UNP P42336
A	-14	ILE	-	expression tag	UNP P42336
A	-13	PRO	-	expression tag	UNP P42336
A	-12	THR	-	expression tag	UNP P42336
A	-11	THR	-	expression tag	UNP P42336
A	-10	GLU	-	expression tag	UNP P42336
A	-9	ASN	-	expression tag	UNP P42336
A	-8	LEU	-	expression tag	UNP P42336
A	-7	TYR	-	expression tag	UNP P42336
A	-6	PHE	-	expression tag	UNP P42336
A	-5	GLN	-	expression tag	UNP P42336
A	-4	GLY	-	expression tag	UNP P42336
A	-3	ALA	-	expression tag	UNP P42336
A	-2	MET	-	expression tag	UNP P42336

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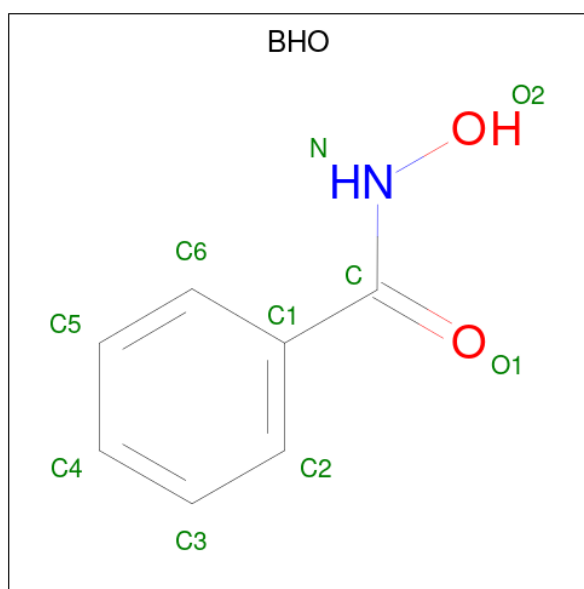
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Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P42336
A	0	SER	-	expression tag	UNP P42336

- Molecule 2 is a protein called Phosphatidylinositol 3-kinase regulatory subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	216	Total	C	N	O	S	0	0	0
			1862	1167	331	358	6			

- Molecule 3 is BENZHYDROXAMIC ACID (CCD ID: BHO) (formula: $C_7H_7NO_2$).

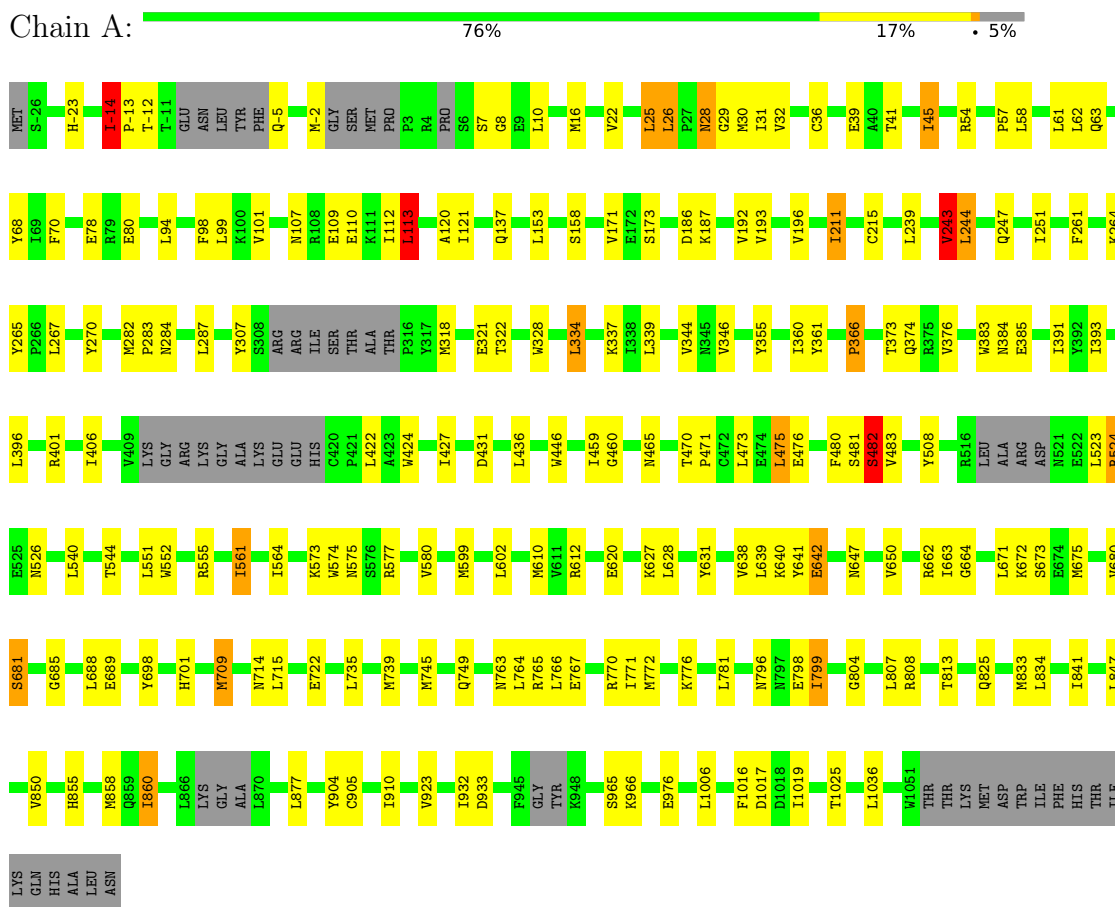


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	7	1	2		
3	A	1	Total	C	N	O	0	0
			10	7	1	2		

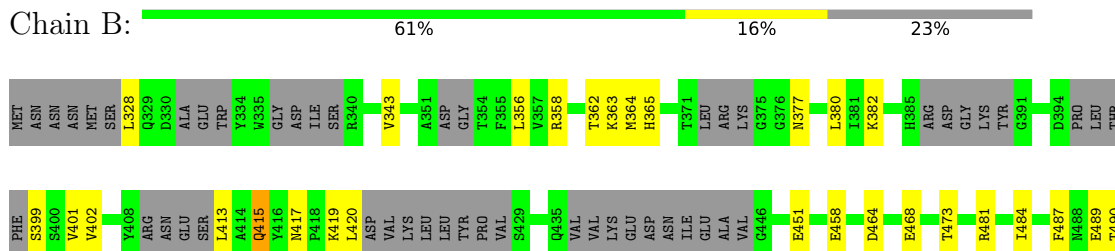
3 Residue-property plots

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: Phosphatidylinositol 4,5-bisphosphate 3-kinase catalytic subunit alpha isoform



- Molecule 2: Phosphatidylinositol 3-kinase regulatory subunit alpha



I491	F494	Q501	S505	I509	E510	K513	N527	R542	L545	Q552	K567	D578	Q579	Y580	L581	M582	W583	LEU	THR	GLN	LYS	GLY	VAL	ARG	GLN	LYS	LYS	LEU	ASN	E596	W597	L598	GLY	ASN
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	114.80Å 117.93Å 150.97Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	92.94 – 3.42 92.94 – 3.42	Depositor EDS
% Data completeness (in resolution range)	97.8 (92.94-3.42) 97.8 (92.94-3.42)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 3.39Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.213 , 0.279 0.213 , 0.272	Depositor DCC
R_{free} test set	1425 reflections (3.38%)	wwPDB-VP
Wilson B-factor (Å ²)	112.1	Xtriage
Anisotropy	0.260	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 98.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.010 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10420	wwPDB-VP
Average B, all atoms (Å ²)	138.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.32% 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: BHO, SEP

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	0.70	0/8699	0.96	3/11745 (0.0%)
2	B	0.67	0/1885	0.91	0/2506
All	All	0.69	0/10584	0.95	3/14251 (0.0%)

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
1	A	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	804	GLY	N-CA-C	7.60	121.69	112.49
1	A	94	LEU	N-CA-C	5.23	119.66	113.28
1	A	808	ARG	N-CA-C	5.15	119.05	112.87

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	LEU	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	8538	0	8497	97	0
2	B	1862	0	1819	19	0
3	A	20	0	14	0	0
All	All	10420	0	10330	111	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 5.

All (111) 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:328:LEU:HD13	2:B:402:VAL:HG23	1.51	0.93
1:A:8:GLY:HA2	1:A:714:ASN:HD21	1.35	0.91
1:A:639:LEU:HD22	1:A:650:VAL:HG22	1.64	0.79
2:B:343:VAL:HG13	2:B:356:LEU:HD11	1.77	0.67
1:A:739:MET:HE2	1:A:764:LEU:HD21	1.78	0.65
1:A:715:LEU:HD21	1:A:735:LEU:HD12	1.80	0.64
1:A:612:ARG:NH1	1:A:642:GLU:OE1	2.32	0.62
1:A:735:LEU:HD22	1:A:771:ILE:HG13	1.80	0.62
1:A:10:LEU:HD13	1:A:16:MET:HE2	1.82	0.61
1:A:749:GLN:HE21	1:A:763:ASN:HA	1.66	0.60
1:A:552:TRP:CZ3	1:A:555:ARG:HD3	2.39	0.58
1:A:540:LEU:HD21	1:A:1016:PHE:CD1	2.39	0.57
1:A:192:VAL:HG12	1:A:193:VAL:N	2.20	0.57
2:B:501:GLN:O	2:B:505:SER:N	2.36	0.56
1:A:799:ILE:CD1	1:A:847:LEU:HD22	2.35	0.56
1:A:602:LEU:HB3	1:A:638:VAL:HG11	1.87	0.55
1:A:26:LEU:HD12	1:A:30:MET:O	2.07	0.55
1:A:770:ARG:HE	1:A:772:MET:HE1	1.72	0.55
1:A:599:MET:HE1	1:A:631:TYR:CB	2.37	0.54
1:A:640:LYS:HE2	1:A:680:VAL:HG11	1.89	0.54
1:A:642:GLU:HG2	1:A:647:ASN:CG	2.33	0.54
1:A:45:ILE:HD11	1:A:70:PHE:CZ	2.43	0.53
1:A:10:LEU:HD13	1:A:16:MET:CE	2.38	0.53
1:A:120:ALA:O	1:A:672:LYS:CE	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:THR:O	1:A:45:ILE:HG23	2.09	0.53
1:A:28:ASN:HD22	1:A:62:LEU:HD21	1.74	0.53
1:A:98:PHE:CE2	2:B:490:THR:HG23	2.44	0.52
1:A:282:MET:O	1:A:284:ASN:ND2	2.42	0.52
1:A:599:MET:HE1	1:A:631:TYR:HB2	1.90	0.52
1:A:120:ALA:O	1:A:672:LYS:HE2	2.10	0.51
1:A:551:LEU:HD21	1:A:564:ILE:HD11	1.92	0.51
1:A:739:MET:O	1:A:745:MET:HE3	2.10	0.51
1:A:339:LEU:HD12	1:A:475:LEU:HA	1.93	0.51
1:A:265:TYR:HB2	1:A:270:TYR:CE1	2.46	0.51
2:B:328:LEU:HD13	2:B:402:VAL:CG2	2.32	0.51
1:A:524:ARG:NH1	1:A:526:ASN:HD22	2.10	0.50
1:A:243:VAL:HG12	1:A:247:GLN:HE21	1.76	0.50
1:A:339:LEU:CD1	1:A:475:LEU:HA	2.41	0.50
1:A:675:MET:HE1	1:A:685:GLY:N	2.26	0.50
1:A:113:LEU:HD13	1:A:113:LEU:N	2.27	0.49
1:A:628:LEU:HD23	1:A:663:ILE:HD13	1.94	0.49
2:B:487:PHE:HE2	2:B:545:LEU:HD22	1.77	0.49
1:A:121:ILE:HD11	1:A:689:GLU:HA	1.94	0.49
1:A:57:PRO:HB2	1:A:58:LEU:HD12	1.94	0.49
1:A:540:LEU:HD21	1:A:1016:PHE:HD1	1.78	0.49
1:A:910:ILE:O	1:A:1025:THR:HG21	2.13	0.49
1:A:739:MET:CE	1:A:764:LEU:HD21	2.43	0.48
1:A:446:TRP:CZ2	1:A:465:ASN:HA	2.49	0.48
2:B:484:ILE:HG13	2:B:545:LEU:HD23	1.96	0.48
1:A:675:MET:HE3	1:A:681:SER:HA	1.96	0.47
1:A:1019:ILE:HG22	1:A:1019:ILE:O	2.14	0.47
1:A:344:VAL:HG11	1:A:422:LEU:HD13	1.96	0.47
1:A:739:MET:HE1	1:A:781:LEU:HD22	1.95	0.47
1:A:833:MET:HE1	1:A:904:TYR:HA	1.96	0.47
1:A:355:TYR:HA	1:A:383:TRP:HZ2	1.79	0.46
1:A:391:ILE:HD13	1:A:396:LEU:HD23	1.97	0.46
1:A:764:LEU:HD23	1:A:766:LEU:CD2	2.45	0.46
1:A:544:THR:HG22	2:B:380:LEU:HB3	1.97	0.46
2:B:417:ASN:HB3	2:B:420:LEU:HD12	1.97	0.46
1:A:709:MET:HG3	1:A:841:ILE:HD13	1.98	0.45
1:A:765:ARG:HD3	1:A:796:ASN:HD21	1.80	0.45
1:A:561:ILE:O	1:A:564:ILE:HG22	2.16	0.45
1:A:374:GLN:N	1:A:374:GLN:OE1	2.50	0.45
1:A:-14:ILE:N	1:A:-13:PRO:CD	2.80	0.45
1:A:334:LEU:HA	1:A:393:ILE:HD11	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:LEU:HD21	2:B:494:PHE:CE1	2.52	0.44
1:A:68:TYR:CD1	1:A:101:VAL:HG12	2.52	0.44
1:A:283:PRO:C	1:A:284:ASN:HD22	2.25	0.44
1:A:480:PHE:O	1:A:482:SER:N	2.50	0.44
1:A:239:LEU:C	1:A:239:LEU:HD13	2.43	0.44
1:A:261:PHE:HA	1:A:270:TYR:CE2	2.53	0.44
2:B:413:LEU:HB3	2:B:420:LEU:HD13	1.98	0.44
1:A:610:MET:HA	1:A:610:MET:HE2	1.99	0.43
2:B:343:VAL:HG21	2:B:358:ARG:HD3	1.99	0.43
2:B:473:THR:HG23	2:B:552:GLN:NE2	2.33	0.43
1:A:698:TYR:CD1	1:A:701:HIS:HB2	2.53	0.43
1:A:120:ALA:O	1:A:672:LYS:HE3	2.18	0.43
1:A:965:SER:HA	1:A:976:GLU:HG3	2.01	0.43
1:A:932:ILE:HD12	1:A:933:ASP:CB	2.49	0.43
1:A:764:LEU:HD23	1:A:766:LEU:HD21	2.00	0.42
2:B:343:VAL:HG21	2:B:358:ARG:CD	2.49	0.42
1:A:243:VAL:HG12	1:A:244:LEU:N	2.35	0.42
1:A:321:GLU:HG3	1:A:322:THR:HG23	2.01	0.42
1:A:675:MET:HE1	1:A:681:SER:O	2.19	0.42
1:A:328:TRP:CD1	1:A:577:ARG:HD2	2.54	0.42
1:A:29:GLY:HA3	2:B:501:GLN:HB3	2.01	0.42
1:A:406:ILE:HG22	1:A:422:LEU:HD12	2.01	0.42
2:B:578:ASP:HA	2:B:581:LEU:HB2	2.02	0.42
1:A:641:TYR:OH	1:A:1006:LEU:HB2	2.19	0.42
1:A:709:MET:CE	1:A:847:LEU:HD21	2.49	0.42
1:A:860:ILE:HG21	1:A:877:LEU:HD12	2.00	0.42
1:A:360:ILE:O	1:A:366:PRO:HD2	2.19	0.42
2:B:413:LEU:HA	2:B:415:GLN:HE21	1.84	0.42
1:A:192:VAL:HG21	1:A:211:ILE:HD11	2.02	0.42
1:A:799:ILE:HD12	1:A:847:LEU:HD22	2.00	0.42
1:A:243:VAL:O	1:A:244:LEU:C	2.63	0.42
1:A:28:ASN:ND2	1:A:62:LEU:HD21	2.35	0.41
1:A:192:VAL:HG12	1:A:193:VAL:H	1.85	0.41
1:A:431:ASP:C	1:A:431:ASP:OD1	2.63	0.41
1:A:671:LEU:HB2	1:A:688:LEU:HD21	2.01	0.41
1:A:361:TYR:HA	1:A:366:PRO:HD3	2.01	0.41
1:A:284:ASN:HD22	1:A:284:ASN:N	2.19	0.41
2:B:491:ILE:CD1	2:B:542:ARG:HE	2.32	0.41
1:A:574:TRP:HA	1:A:580:VAL:CG2	2.51	0.41
1:A:663:ILE:O	1:A:664:GLY:C	2.63	0.41
1:A:709:MET:CE	1:A:847:LEU:HD11	2.51	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:770:ARG:NE	1:A:772:MET:HE1	2.34	0.41
1:A:337:LYS:HB3	1:A:476:GLU:HB3	2.02	0.40
1:A:424:TRP:CH2	1:A:460:GLY:HA3	2.56	0.40
1:A:30:MET:SD	2:B:527:ASN:ND2	2.95	0.40
1:A:446:TRP:CH2	1:A:465:ASN:HA	2.57	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	1021/1096 (93%)	916 (90%)	92 (9%)	13 (1%)	9	33
2	B	194/279 (70%)	175 (90%)	16 (8%)	3 (2%)	8	30
All	All	1215/1375 (88%)	1091 (90%)	108 (9%)	16 (1%)	9	33

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	28	ASN
1	A	264	LYS
1	A	481	SER
1	A	681	SER
1	A	-23	HIS
1	A	186	ASP
2	B	415	GLN
1	A	482	SER
1	A	966	LYS
2	B	377	ASN
1	A	471	PRO
1	A	307	TYR
2	B	567	LYS

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Mol	Chain	Res	Type
1	A	366	PRO
1	A	243	VAL
1	A	-14	ILE

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	952/996 (96%)	871 (92%)	81 (8%)	10	32
2	B	203/259 (78%)	184 (91%)	19 (9%)	8	28
All	All	1155/1255 (92%)	1055 (91%)	100 (9%)	9	31

All (100) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-14	ILE
1	A	-12	THR
1	A	-5	GLN
1	A	-2	MET
1	A	22	VAL
1	A	25	LEU
1	A	26	LEU
1	A	31	ILE
1	A	32	VAL
1	A	36	CYS
1	A	39	GLU
1	A	45	ILE
1	A	54	ARG
1	A	61	LEU
1	A	63	GLN
1	A	78	GLU
1	A	80	GLU
1	A	99	LEU
1	A	107	ASN
1	A	109	GLU

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Mol	Chain	Res	Type
1	A	110	GLU
1	A	112	ILE
1	A	113	LEU
1	A	137	GLN
1	A	153	LEU
1	A	171	VAL
1	A	173	SER
1	A	187	LYS
1	A	196	VAL
1	A	211	ILE
1	A	215	CYS
1	A	243	VAL
1	A	244	LEU
1	A	251	ILE
1	A	267	LEU
1	A	287	LEU
1	A	318	MET
1	A	334	LEU
1	A	346	VAL
1	A	373	THR
1	A	376	VAL
1	A	384	ASN
1	A	385	GLU
1	A	401	ARG
1	A	427	ILE
1	A	436	LEU
1	A	459	ILE
1	A	470	THR
1	A	473	LEU
1	A	475	LEU
1	A	482	SER
1	A	483	VAL
1	A	508	TYR
1	A	523	LEU
1	A	524	ARG
1	A	561	ILE
1	A	573	LYS
1	A	575	ASN
1	A	620	GLU
1	A	627	LYS
1	A	642	GLU
1	A	662	ARG

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Mol	Chain	Res	Type
1	A	673	SER
1	A	709	MET
1	A	722	GLU
1	A	767	GLU
1	A	776	LYS
1	A	798	GLU
1	A	799	ILE
1	A	807	LEU
1	A	813	THR
1	A	825	GLN
1	A	834	LEU
1	A	850	VAL
1	A	855	HIS
1	A	858	MET
1	A	860	ILE
1	A	905	CYS
1	A	923	VAL
1	A	1017	ASP
1	A	1036	LEU
2	B	362	THR
2	B	363	LYS
2	B	364	MET
2	B	365	HIS
2	B	382	LYS
2	B	399	SER
2	B	401	VAL
2	B	419	LYS
2	B	451	GLU
2	B	458	GLU
2	B	464	ASP
2	B	468	GLU
2	B	481	ARG
2	B	489	GLU
2	B	509	ILE
2	B	510	GLU
2	B	513	LYS
2	B	579	GLN
2	B	597	TRP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	180	HIS
1	A	219	GLN
1	A	247	GLN
1	A	345	ASN
1	A	370	ASN
1	A	450	HIS
1	A	526	ASN
1	A	582	GLN
1	A	605	ASN
1	A	643	GLN
1	A	676	HIS
1	A	714	ASN
1	A	785	ASN
1	A	796	ASN
1	A	803	ASN
1	A	822	ASN
1	A	855	HIS
1	A	875	HIS
1	A	885	ASN
1	A	931	HIS
1	A	1014	GLN
1	A	1044	ASN
1	A	1047	HIS
2	B	378	ASN
2	B	385	HIS
2	B	415	GLN
2	B	432	GLN
2	B	457	GLN
2	B	501	GLN
2	B	522	GLN
2	B	527	ASN
2	B	564	ASN
2	B	579	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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
1	SEP	A	7	1	8,9,10	0.81	0	7,12,14	1.53	1 (14%)
1	SEP	A	158	1	8,9,10	0.59	0	7,12,14	1.43	1 (14%)
1	SEP	A	790	1	8,9,10	0.61	0	7,12,14	1.13	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
1	SEP	A	7	1	-	6/6/8/10	-
1	SEP	A	158	1	-	2/6/8/10	-
1	SEP	A	790	1	-	5/6/8/10	-

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	SEP	OG-CB-CA	3.08	111.14	108.14
1	A	158	SEP	OG-CB-CA	2.43	110.51	108.14

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	7	SEP	N-CA-CB-OG
1	A	7	SEP	C-CA-CB-OG
1	A	7	SEP	CB-OG-P-O2P
1	A	158	SEP	N-CA-CB-OG
1	A	158	SEP	C-CA-CB-OG
1	A	790	SEP	N-CA-CB-OG
1	A	790	SEP	C-CA-CB-OG
1	A	790	SEP	CB-OG-P-O2P

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Mol	Chain	Res	Type	Atoms
1	A	790	SEP	CB-OG-P-O3P
1	A	790	SEP	CB-OG-P-O1P
1	A	7	SEP	CB-OG-P-O3P
1	A	7	SEP	CA-CB-OG-P
1	A	7	SEP	CB-OG-P-O1P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands 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	$\# Z > 2$
3	BHO	A	1101	-	10,10,10	0.96	0	12,12,12	1.16	1 (8%)
3	BHO	A	1102	-	10,10,10	0.75	0	12,12,12	1.41	1 (8%)

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	BHO	A	1101	-	-	6/6/6/6	0/1/1/1
3	BHO	A	1102	-	-	5/6/6/6	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1102	BHO	C1-C-N	3.99	122.42	116.26
3	A	1101	BHO	C1-C-N	3.29	121.34	116.26

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1101	BHO	N-C-C1-C2
3	A	1101	BHO	N-C-C1-C6
3	A	1101	BHO	C1-C-N-O2
3	A	1101	BHO	O1-C-N-O2
3	A	1102	BHO	C1-C-N-O2
3	A	1102	BHO	O1-C-N-O2
3	A	1101	BHO	O1-C-C1-C6
3	A	1101	BHO	O1-C-C1-C2
3	A	1102	BHO	N-C-C1-C2
3	A	1102	BHO	N-C-C1-C6
3	A	1102	BHO	O1-C-C1-C2

There are no ring outliers.

No monomer is involved in short contacts.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	1039/1096 (94%)	-0.56	0 100 100	67, 120, 191, 244	0
2	B	216/279 (77%)	-0.28	0 100 100	108, 194, 250, 295	0
All	All	1255/1375 (91%)	-0.51	0 100 100	67, 129, 216, 295	0

There are no RSRZ outliers to report.

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
1	SEP	A	7	10/11	0.79	0.09	155,180,211,218	0
1	SEP	A	158	10/11	0.81	0.06	144,178,229,232	0
1	SEP	A	790	10/11	0.86	0.08	108,120,186,200	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
3	BHO	A	1102	10/10	0.78	0.09	213,221,233,233	0
3	BHO	A	1101	10/10	0.86	0.19	170,194,203,205	0

6.5 Other polymers [i](#)

There are no such residues in this entry.