



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 09:42 AM UTC

PDB ID : 4L2Y / pdb_00004l2y
Title : Crystal Structure of p110alpha complexed with niSH2 of p85alpha and compound 9d
Authors : Zhang, J.; Zhao, Y.L.; Chen, Y.Y.; Huang, M.; Jiang, F.
Deposited on : 2013-06-05
Resolution : 2.80 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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

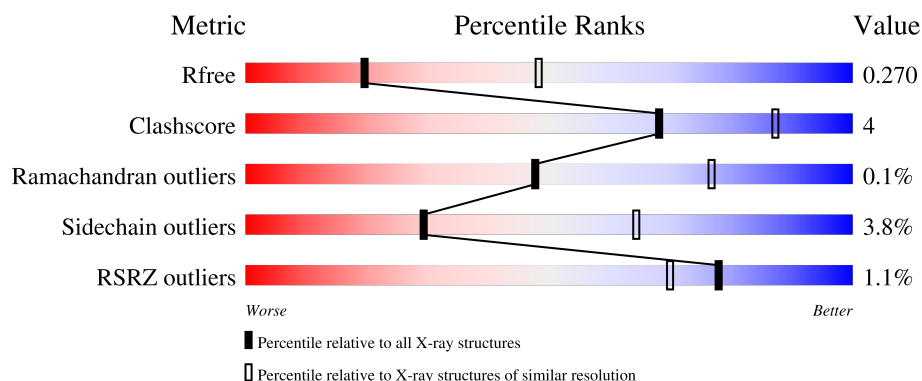
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	1068	
2	B	324	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10533 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 subunit alpha isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	991	Total	C	N	O	S	0	0	0
			8119	5198	1384	1470	67			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	277	Total	C	N	O	S	0	0	0
			2354	1474	420	452	8			

There are 26 discrepancies between the modelled and reference sequences:

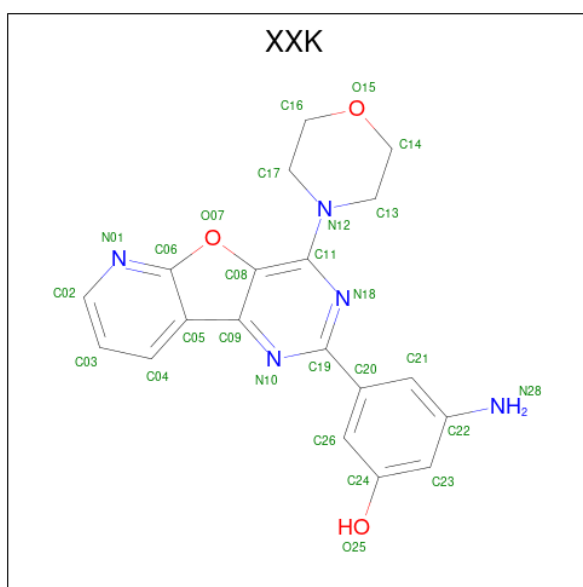
Chain	Residue	Modelled	Actual	Comment	Reference
B	292	MET	-	expression tag	UNP P27986
B	293	SER	-	expression tag	UNP P27986
B	294	TYR	-	expression tag	UNP P27986
B	295	TYR	-	expression tag	UNP P27986
B	296	HIS	-	expression tag	UNP P27986
B	297	HIS	-	expression tag	UNP P27986
B	298	HIS	-	expression tag	UNP P27986
B	299	HIS	-	expression tag	UNP P27986
B	300	HIS	-	expression tag	UNP P27986
B	301	HIS	-	expression tag	UNP P27986
B	302	ASP	-	expression tag	UNP P27986
B	303	TYR	-	expression tag	UNP P27986
B	304	ASP	-	expression tag	UNP P27986
B	305	ILE	-	expression tag	UNP P27986
B	306	PRO	-	expression tag	UNP P27986
B	307	THR	-	expression tag	UNP P27986
B	308	THR	-	expression tag	UNP P27986
B	309	GLU	-	expression tag	UNP P27986
B	310	ASN	-	expression tag	UNP P27986

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	311	LEU	-	expression tag	UNP P27986
B	312	TYR	-	expression tag	UNP P27986
B	313	PHE	-	expression tag	UNP P27986
B	314	GLN	-	expression tag	UNP P27986
B	315	SER	-	expression tag	UNP P27986
B	316	ILE	-	expression tag	UNP P27986
B	317	ALA	-	expression tag	UNP P27986

- Molecule 3 is 3-amino-5-[4-(morpholin-4-yl)pyrido[3',2':4,5]furo[3,2-d]pyrimidin-2-yl]phenol (CCD ID: XXK) (formula: C₁₉H₁₇N₅O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			27	19	5	3		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		
4	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		

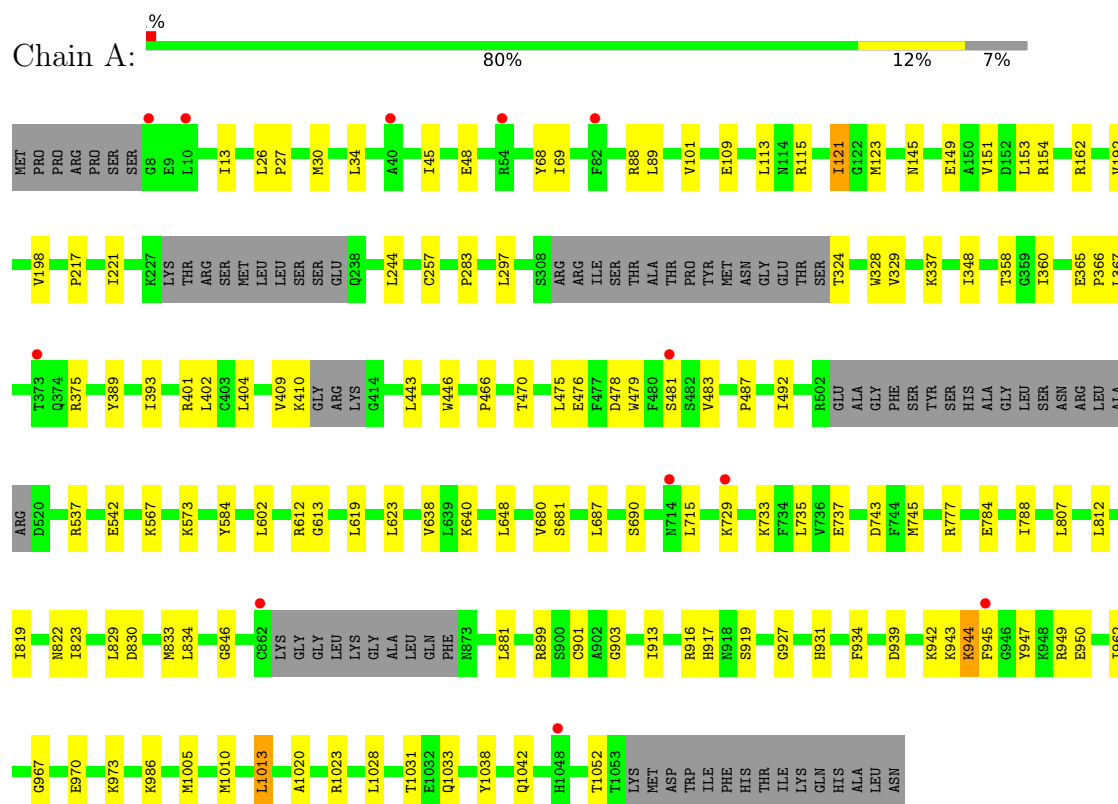
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	17	Total	O	0	0
			17	17		

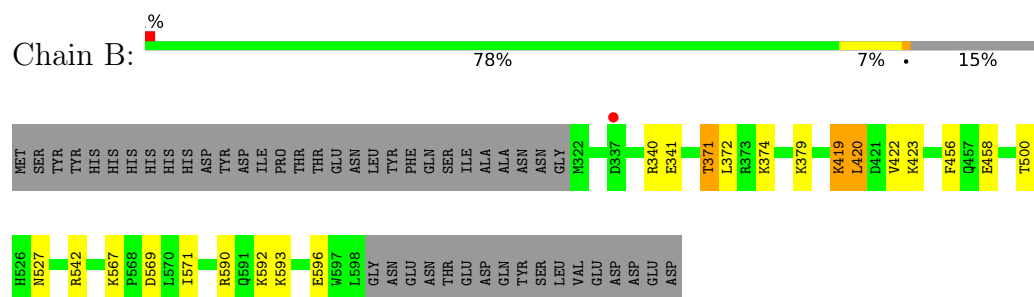
3 Residue-property plots

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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	70.94Å 136.97Å 150.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.30 – 2.80 48.30 – 2.80	Depositor EDS
% Data completeness (in resolution range)	96.2 (48.30-2.80) 96.3 (48.30-2.80)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.41 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.215 , 0.271 0.214 , 0.270	Depositor DCC
R_{free} test set	1781 reflections (4.82%)	wwPDB-VP
Wilson B-factor (Å ²)	67.8	Xtriage
Anisotropy	0.352	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10533	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.17% 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: XXK, GOL, SO4

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	0.58	0/8301	0.77	0/11219
2	B	0.51	0/2394	0.78	0/3207
All	All	0.57	0/10695	0.77	0/14426

There are no bond length outliers.

There are no bond angle outliers.

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	8119	0	8122	65	0
2	B	2354	0	2330	16	0
3	A	27	0	16	1	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
5	A	6	0	8	0	0
6	A	17	0	0	1	0
All	All	10533	0	10476	76	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 (76) 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:358:THR:HG21	1:A:389:TYR:OH	1.82	0.80
1:A:1005:MET:HE3	1:A:1010:MET:HE1	1.69	0.75
1:A:829:LEU:HD11	1:A:986:LYS:HB3	1.73	0.71
1:A:358:THR:HG23	1:A:402:LEU:HD11	1.76	0.67
1:A:807:LEU:HD12	1:A:846:GLY:HA3	1.81	0.63
1:A:479:TRP:CZ3	1:A:481:SER:HA	2.35	0.62
2:B:590:ARG:HG3	2:B:592:LYS:H	1.67	0.59
1:A:192:VAL:HG23	1:A:283:PRO:HB2	1.85	0.57
1:A:812:LEU:HD13	1:A:1005:MET:HE2	1.86	0.57
1:A:1038:TYR:O	1:A:1042:GLN:HG2	2.04	0.57
1:A:1020:ALA:CB	2:B:341:GLU:HG2	2.34	0.57
2:B:374:LYS:HZ2	2:B:420:LEU:HA	1.70	0.57
1:A:917:HIS:CE1	1:A:919:SER:HB2	2.41	0.55
1:A:410:LYS:NZ	2:B:569:ASP:OD1	2.39	0.55
1:A:348:ILE:HD12	1:A:348:ILE:H	1.72	0.55
2:B:422:VAL:HG22	2:B:423:LYS:H	1.72	0.54
1:A:404:LEU:HD11	1:A:443:LEU:HD23	1.90	0.54
1:A:916:ARG:HD2	1:A:931:HIS:ND1	2.23	0.53
1:A:542:GLU:OE1	2:B:340:ARG:HD3	2.08	0.53
1:A:944:LYS:HA	2:B:456:PHE:HE2	1.73	0.53
1:A:1020:ALA:HB1	2:B:341:GLU:HG2	1.92	0.52
1:A:492:ILE:HG21	1:A:584:TYR:HD2	1.74	0.52
1:A:337:LYS:HB3	1:A:476:GLU:HB3	1.92	0.52
2:B:374:LYS:NZ	2:B:420:LEU:HA	2.24	0.51
1:A:881:LEU:HD11	1:A:927:GLY:HA2	1.92	0.50
2:B:590:ARG:HE	2:B:592:LYS:HG2	1.75	0.50
1:A:68:TYR:HB3	1:A:101:VAL:CG2	2.42	0.50
1:A:947:TYR:HD2	1:A:949:ARG:HB3	1.76	0.50
1:A:27:PRO:HD3	1:A:101:VAL:HG13	1.93	0.50
1:A:401:ARG:HD3	6:A:1212:HOH:O	2.11	0.50
1:A:446:TRP:CH2	1:A:466:PRO:HD2	2.48	0.49
1:A:733:LYS:O	1:A:737:GLU:HG2	2.12	0.49
1:A:943:LYS:O	1:A:944:LYS:HB2	2.13	0.49
1:A:962:ILE:HG23	1:A:967:GLY:HA2	1.94	0.49
1:A:34:LEU:HD11	1:A:48:GLU:HB3	1.93	0.49
1:A:30:MET:HA	2:B:527:ASN:HD21	1.78	0.48
1:A:819:ILE:O	1:A:823:ILE:HG12	2.13	0.48
2:B:422:VAL:HG22	2:B:423:LYS:N	2.28	0.48
1:A:833:MET:HA	1:A:833:MET:HE2	1.96	0.48
1:A:745:MET:HA	1:A:745:MET:HE2	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:THR:CG2	1:A:402:LEU:HD11	2.43	0.47
1:A:970:GLU:HB3	1:A:973:LYS:HB3	1.97	0.47
1:A:949:ARG:HG2	1:A:950:GLU:N	2.29	0.46
1:A:537:ARG:O	1:A:567:LYS:NZ	2.43	0.46
1:A:913:ILE:HD13	1:A:934:PHE:HD1	1.79	0.46
2:B:593:LYS:O	2:B:596:GLU:HG2	2.16	0.46
1:A:360:ILE:HG22	1:A:367:LEU:HD12	1.98	0.45
1:A:1023:ARG:HG2	1:A:1028:LEU:HD12	1.98	0.45
1:A:145:ASN:O	1:A:149:GLU:HB2	2.16	0.45
1:A:151:VAL:HA	1:A:154:ARG:HG3	1.99	0.45
1:A:619:LEU:HD22	1:A:623:LEU:HD22	1.99	0.45
1:A:943:LYS:C	1:A:945:PHE:H	2.26	0.44
1:A:939:ASP:CG	1:A:942:LYS:HB3	2.43	0.43
1:A:68:TYR:HB3	1:A:101:VAL:HG22	2.00	0.43
1:A:640:LYS:HE2	1:A:680:VAL:HG11	2.01	0.43
1:A:365:GLU:HA	1:A:366:PRO:HD3	1.87	0.43
1:A:121:ILE:HG22	1:A:123:MET:HG2	1.99	0.43
1:A:917:HIS:HE1	1:A:919:SER:HB2	1.83	0.43
1:A:613:GLY:HA2	1:A:648:LEU:HD12	2.02	0.42
1:A:833:MET:CE	1:A:903:GLY:HA3	2.49	0.42
2:B:567:LYS:O	2:B:571:ILE:HG12	2.18	0.42
1:A:324:THR:HA	1:A:483:VAL:O	2.18	0.42
1:A:479:TRP:CH2	1:A:481:SER:HA	2.53	0.42
1:A:26:LEU:HD12	1:A:30:MET:HB2	2.00	0.42
1:A:830:ASP:O	1:A:899:ARG:HD3	2.19	0.42
1:A:328:TRP:CE2	1:A:487:PRO:HG2	2.55	0.42
1:A:715:LEU:HD22	1:A:735:LEU:HD12	2.02	0.41
1:A:602:LEU:O	1:A:612:ARG:NH2	2.53	0.41
1:A:88:ARG:HD2	1:A:743:ASP:HB3	2.02	0.41
2:B:371:THR:HA	2:B:379:LYS:O	2.21	0.41
1:A:375:ARG:H	1:A:375:ARG:HG2	1.66	0.40
2:B:419:LYS:HE2	2:B:420:LEU:HD23	2.01	0.40
1:A:162:ARG:HB3	1:A:297:LEU:HD13	2.04	0.40
1:A:45:ILE:HD11	1:A:89:LEU:HD12	2.04	0.40
1:A:1010:MET:HE3	1:A:1013:LEU:HD11	2.04	0.40
3:A:1101:XXK:H9	3:A:1101:XXK:O07	2.21	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	979/1068 (92%)	942 (96%)	36 (4%)	1 (0%)	48	77
2	B	275/324 (85%)	272 (99%)	3 (1%)	0	100	100
All	All	1254/1392 (90%)	1214 (97%)	39 (3%)	1 (0%)	48	77

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	217	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	910/974 (93%)	876 (96%)	34 (4%)	30	65
2	B	258/301 (86%)	248 (96%)	10 (4%)	28	64
All	All	1168/1275 (92%)	1124 (96%)	44 (4%)	29	64

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ILE
1	A	69	ILE
1	A	109	GLU
1	A	113	LEU
1	A	115	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	121	ILE
1	A	153	LEU
1	A	198	VAL
1	A	221	ILE
1	A	244	LEU
1	A	257	CYS
1	A	329	VAL
1	A	393	ILE
1	A	409	VAL
1	A	470	THR
1	A	475	LEU
1	A	478	ASP
1	A	573	LYS
1	A	638	VAL
1	A	681	SER
1	A	687	LEU
1	A	690	SER
1	A	729	LYS
1	A	777	ARG
1	A	784	GLU
1	A	788	ILE
1	A	822	ASN
1	A	834	LEU
1	A	901	CYS
1	A	944	LYS
1	A	1013	LEU
1	A	1031	THR
1	A	1033	GLN
1	A	1052	THR
2	B	371	THR
2	B	372	LEU
2	B	419	LYS
2	B	420	LEU
2	B	458	GLU
2	B	500	THR
2	B	501	GLN
2	B	510	GLU
2	B	525	MET
2	B	542	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	HIS
1	A	59	HIS
1	A	180	HIS
1	A	183	ASN
1	A	189	GLN
1	A	467	ASN
1	A	530	GLN
1	A	597	GLN
1	A	661	GLN
1	A	670	HIS
1	A	728	GLN
1	A	738	GLN
1	A	825	GLN
1	A	875	HIS
1	A	918	ASN
1	A	1014	GLN
2	B	323	ASN
2	B	441	ASN
2	B	453	ASN
2	B	457	GLN
2	B	501	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 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
5	GOL	A	1103	-	5,5,5	0.26	0	5,5,5	0.33	0
3	XXK	A	1101	-	30,31,31	1.47	4 (13%)	35,45,45	1.92	8 (22%)
4	SO4	A	1102	-	4,4,4	0.44	0	6,6,6	0.08	0
4	SO4	B	701	-	4,4,4	0.41	0	6,6,6	0.18	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
3	XXK	A	1101	-	-	0/8/16/16	0/5/5/5
5	GOL	A	1103	-	-	0/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1101	XXK	C08-C11	4.94	1.49	1.40
3	A	1101	XXK	C22-N28	3.19	1.49	1.38
3	A	1101	XXK	O07-C08	-2.42	1.35	1.38
3	A	1101	XXK	O07-C06	-2.36	1.35	1.38

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1101	XXK	C13-N12-C17	5.81	124.64	111.57
3	A	1101	XXK	O07-C08-C11	5.00	131.47	126.48
3	A	1101	XXK	C08-C11-N18	-3.94	115.35	123.81
3	A	1101	XXK	C11-N18-C19	3.57	124.30	115.92
3	A	1101	XXK	C03-C04-C05	-3.17	114.98	120.23
3	A	1101	XXK	C08-O07-C06	2.13	108.35	105.66
3	A	1101	XXK	C05-C09-N10	2.13	132.85	127.61
3	A	1101	XXK	O07-C06-N01	2.05	129.23	123.39

There are no chirality outliers.

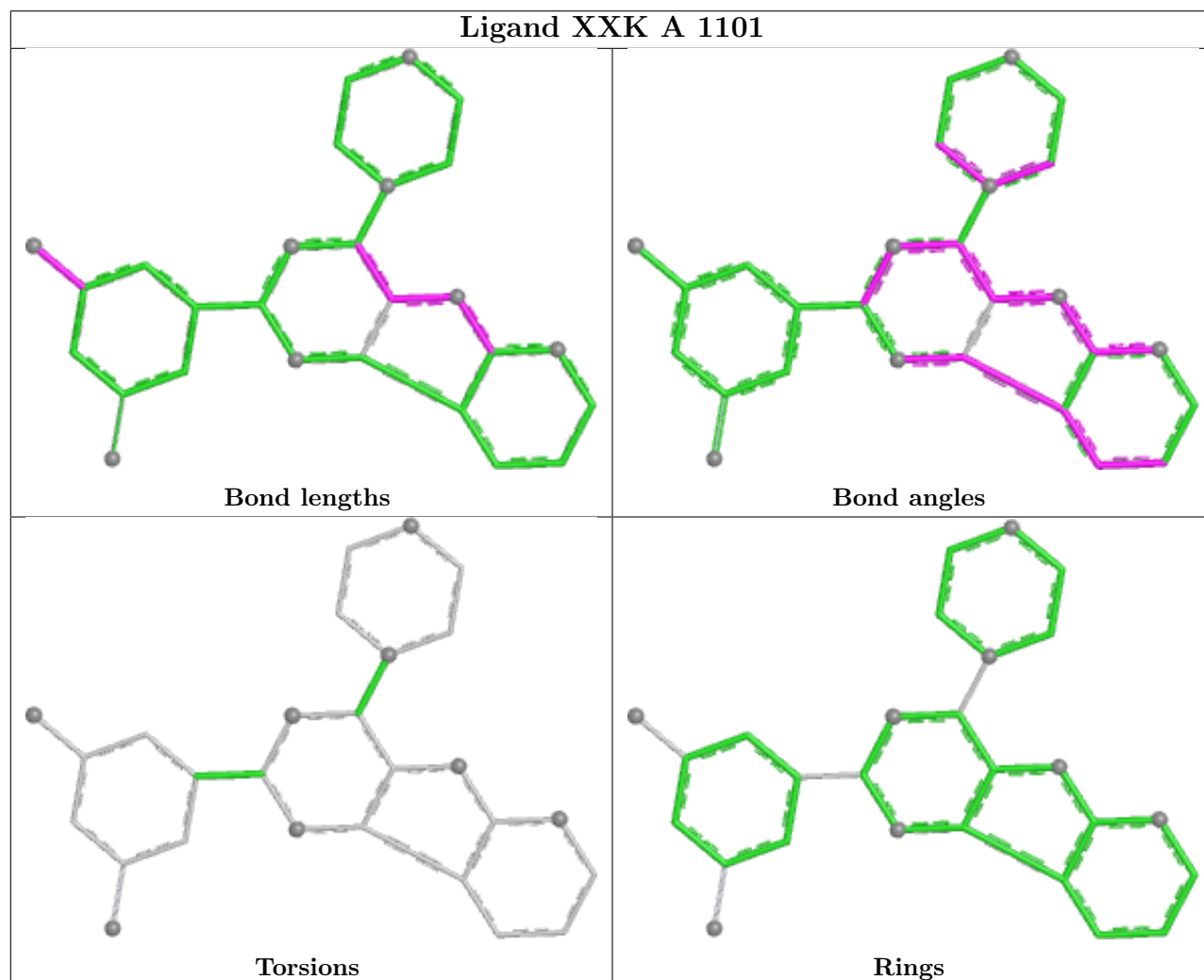
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1101	XXK	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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 [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	991/1068 (92%)	-0.03	12 (1%) 76 68	43, 77, 134, 206	2 (0%)
2	B	277/324 (85%)	-0.05	2 (0%) 84 77	54, 81, 139, 171	0
All	All	1268/1392 (91%)	-0.03	14 (1%) 78 70	43, 79, 135, 206	2 (0%)

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	54	ARG	3.6
1	A	729	LYS	3.6
1	A	40	ALA	3.1
2	B	525	MET	2.9
1	A	481	SER	2.8
1	A	8	GLY	2.8
2	B	337	ASP	2.8
1	A	862	CYS	2.5
1	A	714	ASN	2.5
1	A	945	PHE	2.3
1	A	10	LEU	2.2
1	A	1048	HIS	2.2
1	A	373	THR	2.2
1	A	82	PHE	2.2

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

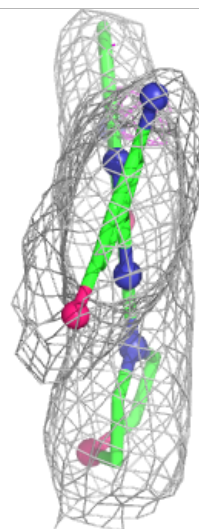
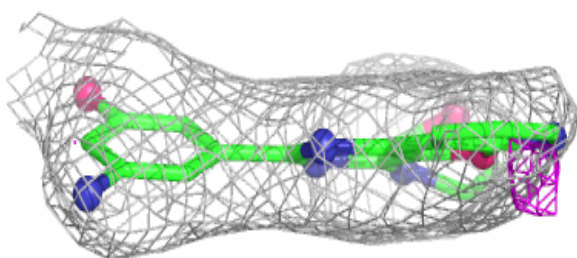
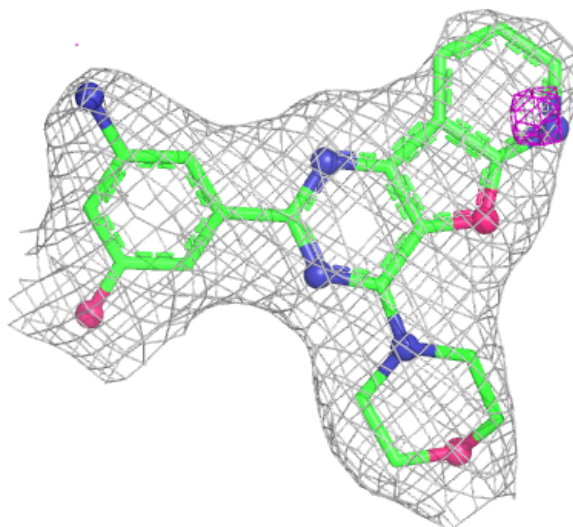
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	SO4	A	1102	5/5	0.73	0.09	125,127,130,131	0
3	XXK	A	1101	27/27	0.95	0.07	54,57,62,65	0
4	SO4	B	701	5/5	0.95	0.08	79,79,79,82	0
5	GOL	A	1103	6/6	0.95	0.10	69,72,72,75	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around XXK A 1101:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.