



Full wwPDB X-ray Structure Validation Report ⓘ

May 27, 2020 – 11:37 pm BST

PDB ID : 3PS6
Title : Quinazolines with intra-molecular hydrogen bonding scaffold (iMHBS) as PI3K/mTOR dual inhibitors.
Authors : Knighton, D.R.; Greasley, S.E.; Rogers, C.M.-L.
Deposited on : 2010-11-30
Resolution : 2.60 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

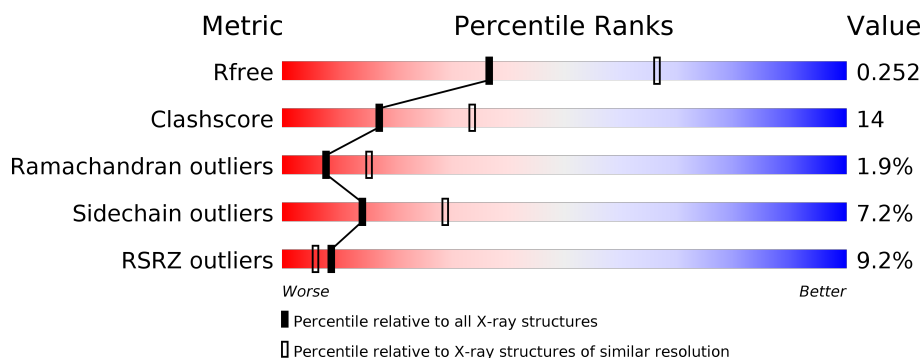
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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 on 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	966	<div> <div>8%</div> <div>58%</div> <div>26%</div> <div>•</div> <div>13%</div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 6802 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.

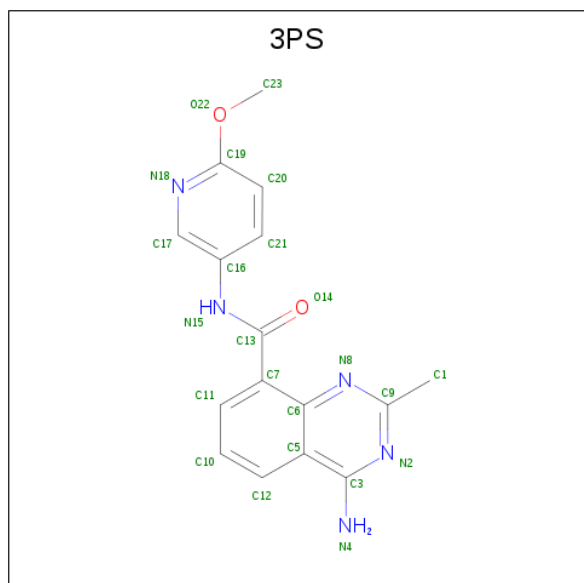
- Molecule 1 is a protein called Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma isoform.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	841	Total	C	N	O	S	0	0	0
			6779	4364	1147	1233	35			

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	143	MET	-	INITIATING METHIONINE	UNP P48736
A	1103	HIS	-	EXPRESSION TAG	UNP P48736
A	1104	HIS	-	EXPRESSION TAG	UNP P48736
A	1105	HIS	-	EXPRESSION TAG	UNP P48736
A	1106	HIS	-	EXPRESSION TAG	UNP P48736
A	1107	HIS	-	EXPRESSION TAG	UNP P48736
A	1108	HIS	-	EXPRESSION TAG	UNP P48736

- Molecule 2 is 4-amino-N-(6-methoxypyridin-3-yl)-2-methylquinazoline-8-carboxamide (three-letter code: 3PS) (formula: C₁₆H₁₅N₅O₂).

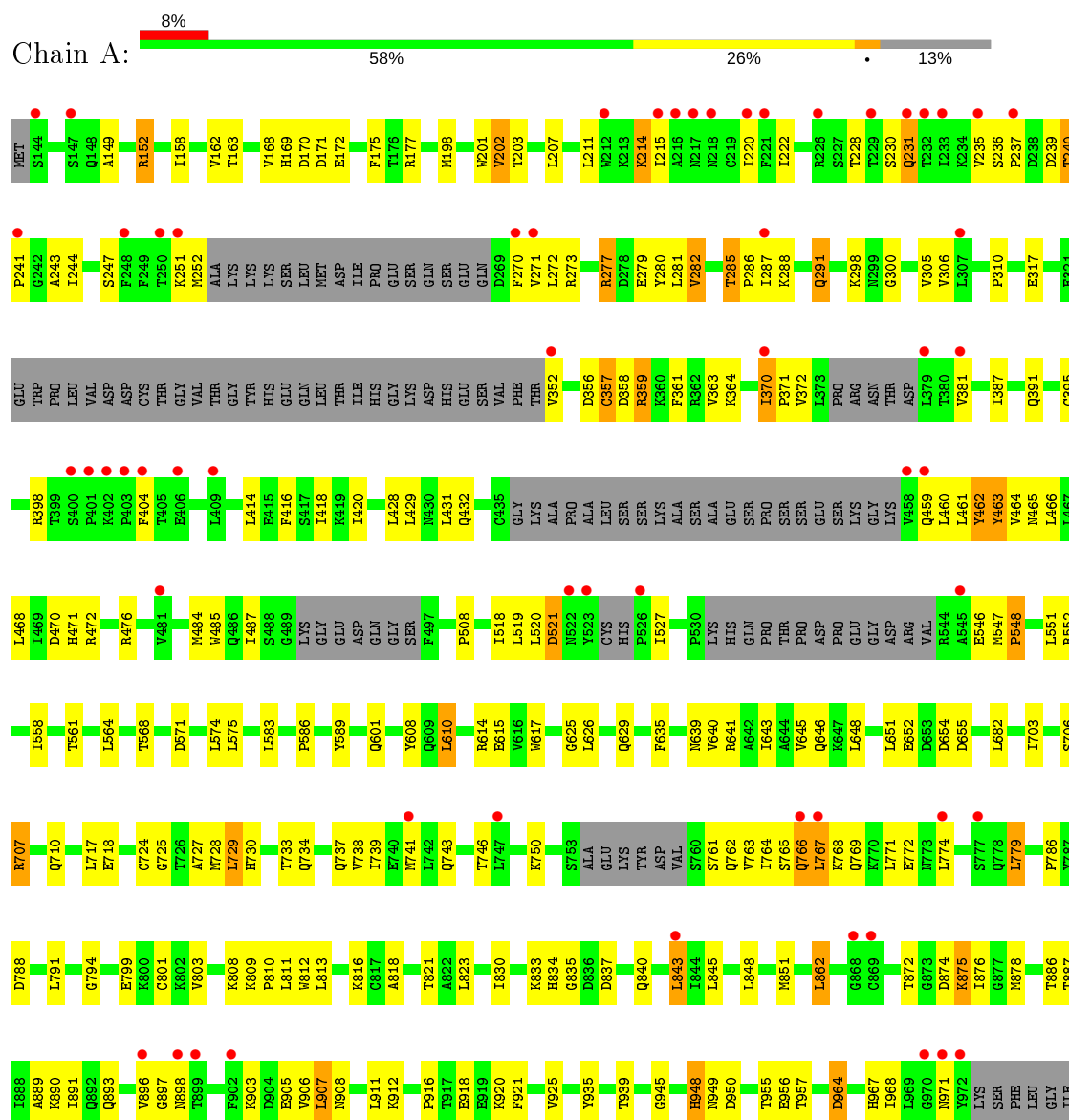


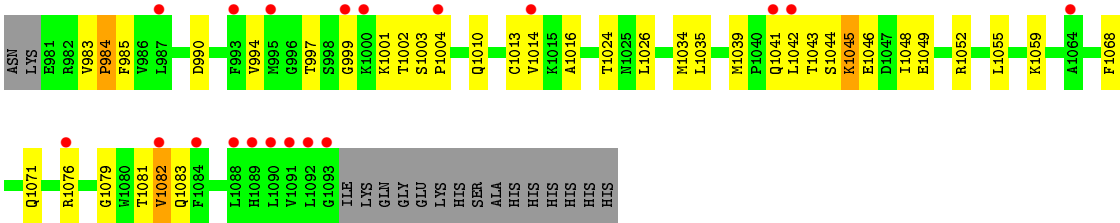
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			23	16	5	2		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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 gamma isoform





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.04Å 67.49Å 106.64Å 90.00° 95.50° 90.00°	Depositor
Resolution (Å)	44.76 – 2.60 44.76 – 2.60	Depositor EDS
% Data completeness (in resolution range)	97.6 (44.76-2.60) 97.9 (44.76-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.61Å)	Xtriage
Refinement program	CNS, BUSTER 2.9.6	Depositor
R, R_{free}	0.256 , 0.251 0.256 , 0.252	Depositor DCC
R_{free} test set	1557 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	62.8	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6802	wwPDB-VP
Average B, all atoms (Å ²)	76.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.26% 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: 3PS

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	0.47	2/6924 (0.0%)	0.70	2/9371 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	462	TYR	CA-C	-5.80	1.37	1.52
1	A	463	TYR	CZ-OH	5.40	1.47	1.37

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	357	CYS	N-CA-CB	8.22	125.40	110.60
1	A	356	ASP	C-N-CA	-5.71	107.41	121.70

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	6779	0	6801	188	0
2	A	23	0	15	3	0
All	All	6802	0	6816	189	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 (189) 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:202:VAL:HG11	1:A:285:THR:HG21	1.37	1.04
1:A:887:THR:HB	1:A:890:LYS:HD2	1.46	0.98
1:A:558:ILE:HG21	1:A:575:LEU:HD21	1.53	0.89
1:A:997:THR:HG21	1:A:1076:ARG:HH12	1.44	0.82
1:A:558:ILE:O	1:A:561:THR:HG22	1.85	0.77
1:A:202:VAL:CG1	1:A:285:THR:HG21	2.17	0.74
1:A:903:LYS:HE2	1:A:905:GLU:HB3	1.70	0.74
1:A:614:ARG:HG2	1:A:617:TRP:HB3	1.68	0.74
1:A:1035:LEU:HD23	1:A:1039:MET:HG3	1.69	0.72
1:A:997:THR:CG2	1:A:1076:ARG:HH12	2.04	0.70
1:A:903:LYS:HB3	1:A:906:VAL:HG23	1.74	0.70
1:A:746:THR:HA	1:A:811:LEU:HD11	1.71	0.70
1:A:162:VAL:HG21	1:A:718:GLU:OE1	1.92	0.69
1:A:764:ILE:O	1:A:768:LYS:HG2	1.92	0.69
1:A:547:MET:HB3	1:A:552:ARG:HH12	1.55	0.69
1:A:215:ILE:HD11	1:A:220:ILE:HD11	1.75	0.68
1:A:235:VAL:HG13	1:A:239:ASP:HB2	1.77	0.66
1:A:908:ASN:HD22	1:A:994:VAL:HA	1.59	0.66
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.78	0.65
1:A:149:ALA:HA	1:A:152:ARG:NH1	2.11	0.65
1:A:835:GLY:H	1:A:875:LYS:HB3	1.61	0.65
1:A:568:THR:HG23	1:A:571:ASP:H	1.62	0.65
1:A:964:ASP:HA	2:A:1:3PS:H23A	1.80	0.64
1:A:240:THR:HG23	1:A:243:ALA:HB3	1.79	0.64
1:A:291:GLN:HA	1:A:291:GLN:HE21	1.61	0.64
1:A:1035:LEU:HD12	1:A:1048:ILE:HD13	1.81	0.62
1:A:470:ASP:HB3	1:A:476:ARG:NH2	2.14	0.62
1:A:470:ASP:HB3	1:A:476:ARG:HH21	1.64	0.62
1:A:1001:LYS:HG2	1:A:1002:THR:H	1.65	0.62
1:A:983:VAL:HG12	1:A:1082:VAL:HG11	1.82	0.62
1:A:564:LEU:HB2	1:A:1052:ARG:HD2	1.82	0.62
1:A:724:CYS:HB2	1:A:728:MET:HE3	1.81	0.61
1:A:241:PRO:HD3	1:A:285:THR:O	2.00	0.61
1:A:1013:CYS:HB3	1:A:1068:PHE:CE2	2.36	0.61
1:A:583:LEU:HD22	1:A:610:LEU:HD22	1.83	0.61
1:A:984:PRO:HB2	1:A:985:PHE:CD2	2.36	0.60
1:A:1013:CYS:HB3	1:A:1068:PHE:HE2	1.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:ARG:HH11	1:A:152:ARG:HB2	1.66	0.59
1:A:461:LEU:HB3	1:A:462:TYR:CE2	2.37	0.59
1:A:359:ARG:HB2	1:A:359:ARG:HH11	1.68	0.59
1:A:202:VAL:HG12	1:A:203:THR:H	1.68	0.58
1:A:508:PRO:HG3	1:A:707:ARG:HD3	1.85	0.58
1:A:948:HIS:N	1:A:948:HIS:CD2	2.71	0.58
1:A:546:GLU:HG3	1:A:547:MET:H	1.68	0.58
1:A:935:TYR:O	1:A:939:THR:HG22	2.04	0.58
1:A:359:ARG:O	1:A:420:ILE:HG12	2.04	0.58
1:A:921:PHE:O	1:A:925:VAL:HG23	2.03	0.58
1:A:271:VAL:HG23	1:A:282:VAL:HG13	1.87	0.57
1:A:734:GLN:O	1:A:738:VAL:HG23	2.04	0.57
1:A:949:ASN:HB2	1:A:1083:GLN:NE2	2.19	0.56
2:A:1:3PS:N8	2:A:1:3PS:N15	2.45	0.55
1:A:651:LEU:HD22	1:A:655:ASP:HB3	1.87	0.55
1:A:725:GLY:O	1:A:729:LEU:HB2	2.07	0.55
1:A:767:LEU:HD12	1:A:803:VAL:HG23	1.88	0.55
1:A:916:PRO:HD2	1:A:920:LYS:HD2	1.88	0.55
1:A:706:SER:O	1:A:710:GLN:HB3	2.06	0.55
1:A:767:LEU:O	1:A:771:LEU:HG	2.06	0.55
1:A:428:LEU:HD22	1:A:465:ASN:HB3	1.88	0.55
1:A:222:ILE:HD12	1:A:235:VAL:HG21	1.88	0.55
1:A:761:SER:HA	1:A:764:ILE:HD12	1.89	0.54
1:A:352:VAL:O	1:A:527:ILE:HA	2.08	0.54
1:A:387:ILE:HD12	1:A:418:ILE:HD12	1.89	0.54
1:A:431:LEU:O	1:A:463:TYR:HA	2.08	0.54
1:A:625:GLY:O	1:A:629:GLN:HG3	2.07	0.54
1:A:464:VAL:HB	1:A:484:MET:HG2	1.90	0.53
1:A:843:LEU:HG	1:A:1034:MET:HG3	1.90	0.53
1:A:803:VAL:CG1	1:A:809:LYS:HB3	2.40	0.52
1:A:908:ASN:ND2	1:A:994:VAL:HA	2.24	0.52
1:A:763:VAL:HA	1:A:766:GLN:HE22	1.74	0.52
1:A:645:VAL:HA	1:A:648:LEU:HD12	1.92	0.52
1:A:948:HIS:CD2	1:A:948:HIS:H	2.26	0.52
1:A:767:LEU:HD22	1:A:771:LEU:HD11	1.91	0.51
1:A:848:LEU:HD12	1:A:851:MET:CE	2.40	0.51
1:A:239:ASP:O	1:A:287:ILE:HG13	2.10	0.51
1:A:461:LEU:HB3	1:A:462:TYR:CD2	2.45	0.51
1:A:432:GLN:HB3	1:A:460:LEU:CD1	2.41	0.51
1:A:520:LEU:O	1:A:521:ASP:C	2.49	0.51
1:A:172:GLU:HG3	1:A:471:HIS:ND1	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:ARG:O	1:A:414:LEU:HD21	2.11	0.50
1:A:750:LYS:HE3	1:A:834:HIS:O	2.11	0.50
1:A:801:CYS:HA	1:A:812:TRP:O	2.11	0.50
1:A:198:MET:HB3	1:A:282:VAL:HG21	1.94	0.50
1:A:466:LEU:CD1	1:A:476:ARG:HH11	2.25	0.49
1:A:848:LEU:HD12	1:A:851:MET:HE3	1.93	0.49
1:A:837:ASP:HB3	1:A:840:GLN:HE21	1.77	0.49
1:A:955:THR:C	1:A:957:THR:H	2.16	0.49
1:A:766:GLN:H	1:A:766:GLN:NE2	2.10	0.49
1:A:903:LYS:HB3	1:A:906:VAL:CG2	2.43	0.49
1:A:273:ARG:O	1:A:305:VAL:HG13	2.13	0.48
1:A:739:ILE:O	1:A:743:GLN:HG3	2.14	0.48
1:A:285:THR:HG22	1:A:286:PRO:HD2	1.96	0.48
1:A:774:LEU:O	1:A:779:LEU:HB3	2.14	0.48
1:A:743:GLN:NE2	1:A:872:THR:OG1	2.47	0.48
1:A:236:SER:HB3	1:A:239:ASP:OD1	2.14	0.47
1:A:466:LEU:HD11	1:A:476:ARG:HH11	1.79	0.47
1:A:270:PHE:HA	1:A:310:PRO:HD3	1.96	0.47
1:A:361:PHE:CD2	1:A:387:ILE:HD11	2.49	0.47
1:A:1083:GLN:HA	1:A:1083:GLN:NE2	2.29	0.47
1:A:198:MET:CB	1:A:282:VAL:HG21	2.44	0.47
1:A:1003:SER:HB2	1:A:1004:PRO:HD2	1.97	0.47
1:A:762:GLN:O	1:A:766:GLN:NE2	2.49	0.46
1:A:908:ASN:HA	1:A:911:LEU:HD12	1.97	0.46
1:A:983:VAL:HG23	1:A:984:PRO:HD2	1.97	0.46
1:A:1010:GLN:O	1:A:1014:VAL:HG23	2.16	0.46
1:A:240:THR:HG23	1:A:243:ALA:CB	2.45	0.46
1:A:746:THR:HA	1:A:811:LEU:CD1	2.41	0.46
1:A:983:VAL:CG1	1:A:1082:VAL:HG11	2.45	0.46
1:A:168:VAL:HG13	1:A:170:ASP:H	1.81	0.46
1:A:635:PHE:O	1:A:641:ARG:HD2	2.16	0.46
1:A:171:ASP:O	1:A:175:PHE:HB2	2.16	0.46
1:A:364:LYS:HB3	1:A:519:LEU:HB3	1.98	0.46
1:A:277:ARG:NH2	1:A:788:ASP:OD2	2.46	0.46
1:A:277:ARG:NH2	1:A:791:LEU:HG	2.30	0.46
1:A:1024:THR:HA	1:A:1055:LEU:HD13	1.98	0.46
1:A:207:LEU:HB2	1:A:288:LYS:HD2	1.97	0.46
1:A:272:LEU:HB3	1:A:305:VAL:HG11	1.98	0.46
1:A:552:ARG:HB2	1:A:552:ARG:HH11	1.81	0.46
1:A:564:LEU:HD11	1:A:1048:ILE:HG22	1.96	0.46
1:A:803:VAL:HG13	1:A:809:LYS:HB3	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:370:ILE:HD12	1:A:372:VAL:O	2.16	0.45
1:A:1068:PHE:O	1:A:1071:GLN:HB2	2.17	0.45
1:A:280:TYR:HB3	1:A:282:VAL:HG22	1.97	0.45
1:A:862:LEU:HD11	1:A:1016:ALA:HB2	1.98	0.45
1:A:149:ALA:HA	1:A:152:ARG:HH11	1.78	0.45
1:A:214:LYS:NZ	1:A:300:GLY:HA2	2.32	0.45
1:A:171:ASP:CG	1:A:472:ARG:HH12	2.19	0.45
1:A:830:ILE:HG21	1:A:878:MET:HE3	1.99	0.45
1:A:651:LEU:HD22	1:A:655:ASP:CB	2.47	0.45
1:A:786:PRO:HD2	1:A:878:MET:CE	2.47	0.45
1:A:945:GLY:C	1:A:985:PHE:HA	2.38	0.44
1:A:903:LYS:HG2	1:A:905:GLU:H	1.83	0.44
1:A:887:THR:HG22	1:A:889:ALA:H	1.83	0.44
1:A:462:TYR:HA	1:A:485:TRP:O	2.17	0.44
1:A:733:THR:HG22	1:A:737:GLN:NE2	2.33	0.44
1:A:810:PRO:HB3	1:A:833:LYS:HB2	1.99	0.44
1:A:463:TYR:CD2	1:A:487:ILE:HD11	2.52	0.44
1:A:520:LEU:O	1:A:521:ASP:O	2.35	0.44
1:A:741:MET:HB3	1:A:774:LEU:HD13	1.99	0.44
1:A:887:THR:CG2	1:A:950:ASP:HA	2.47	0.44
1:A:948:HIS:HE1	1:A:967:HIS:HD2	1.65	0.44
1:A:395:CYS:CB	1:A:418:ILE:HD11	2.48	0.44
1:A:990:ASP:O	1:A:994:VAL:HG23	2.18	0.44
1:A:306:VAL:HG21	1:A:821:THR:CG2	2.48	0.44
1:A:985:PHE:CD2	1:A:985:PHE:N	2.86	0.44
1:A:395:CYS:HB2	1:A:418:ILE:HD11	2.00	0.43
1:A:230:SER:O	1:A:231:GLN:HB2	2.18	0.43
1:A:727:ALA:O	1:A:730:HIS:HB3	2.19	0.43
1:A:763:VAL:HA	1:A:766:GLN:NE2	2.33	0.43
1:A:997:THR:HG21	1:A:1076:ARG:NH1	2.23	0.43
1:A:558:ILE:HG21	1:A:575:LEU:CD2	2.35	0.43
1:A:834:HIS:HB2	1:A:876:ILE:HD12	1.99	0.43
1:A:608:TYR:CE1	1:A:639:ASN:ND2	2.87	0.43
1:A:640:VAL:O	1:A:643:ILE:HG12	2.19	0.43
1:A:874:ASP:C	1:A:876:ILE:H	2.22	0.43
1:A:794:GLY:CA	1:A:818:ALA:HB2	2.49	0.42
1:A:240:THR:O	1:A:244:ILE:HG13	2.19	0.42
1:A:652:GLU:HG3	1:A:654:ASP:HB3	2.02	0.42
1:A:984:PRO:HG2	1:A:1071:GLN:O	2.20	0.42
1:A:158:ILE:HG23	1:A:703:ILE:HD13	2.01	0.42
1:A:761:SER:HA	1:A:764:ILE:CD1	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:912:LYS:NZ	1:A:918:GLU:HG2	2.35	0.42
1:A:558:ILE:CG2	1:A:575:LEU:HD21	2.36	0.42
1:A:765:SER:O	1:A:769:GLN:HG3	2.20	0.42
1:A:907:LEU:HD23	1:A:911:LEU:HD11	2.00	0.42
1:A:363:VAL:HG12	1:A:416:PHE:HE1	1.85	0.42
1:A:364:LYS:O	1:A:518:ILE:HA	2.19	0.42
1:A:548:PRO:HD2	1:A:551:LEU:HD12	2.02	0.42
1:A:586:PRO:HA	1:A:589:TYR:CD1	2.55	0.42
1:A:918:GLU:O	1:A:921:PHE:HB3	2.20	0.41
1:A:768:LYS:O	1:A:772:GLU:HG3	2.21	0.41
1:A:786:PRO:HD2	1:A:878:MET:HE2	2.02	0.41
1:A:201:TRP:CE2	1:A:291:GLN:HG3	2.56	0.41
1:A:1045:LYS:HE3	1:A:1049:GLU:OE1	2.21	0.41
1:A:152:ARG:NH1	1:A:152:ARG:HB2	2.32	0.41
1:A:547:MET:O	1:A:548:PRO:O	2.38	0.41
1:A:811:LEU:HD23	1:A:813:LEU:HD21	2.03	0.41
1:A:830:ILE:CG2	1:A:878:MET:HB2	2.51	0.41
1:A:162:VAL:HG23	1:A:163:THR:N	2.36	0.41
1:A:964:ASP:OD1	2:A:1:3PS:H23B	2.20	0.41
1:A:1001:LYS:O	1:A:1076:ARG:NH2	2.46	0.40
1:A:1043:THR:O	1:A:1045:LYS:N	2.55	0.40
1:A:1035:LEU:CD2	1:A:1039:MET:HG3	2.45	0.40
1:A:172:GLU:HG3	1:A:471:HIS:CG	2.57	0.40
1:A:163:THR:HG22	1:A:177:ARG:HH12	1.85	0.40
1:A:247:SER:C	1:A:251:LYS:HB2	2.42	0.40
1:A:241:PRO:HB3	1:A:281:LEU:O	2.22	0.40
1:A:211:LEU:HD21	1:A:298:LYS:HA	2.03	0.40
1:A:891:ILE:O	1:A:906:VAL:HG11	2.22	0.40
1:A:750:LYS:NZ	1:A:834:HIS:HD2	2.18	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	821/966 (85%)	727 (89%)	78 (10%)	16 (2%)	8	15

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	231	GLN
1	A	548	PRO
1	A	971	ASN
1	A	1044	SER
1	A	1045	LYS
1	A	896	VAL
1	A	897	GLY
1	A	999	GLY
1	A	1079	GLY
1	A	521	ASP
1	A	956	GLU
1	A	228	THR
1	A	237	PRO
1	A	875	LYS
1	A	371	PRO
1	A	984	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	748/864 (87%)	694 (93%)	54 (7%)	14	29

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	152	ARG
1	A	169	HIS
1	A	202	VAL
1	A	214	LYS
1	A	240	THR

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Mol	Chain	Res	Type
1	A	252	MET
1	A	277	ARG
1	A	279	GLU
1	A	282	VAL
1	A	285	THR
1	A	291	GLN
1	A	317	GLU
1	A	357	CYS
1	A	358	ASP
1	A	359	ARG
1	A	370	ILE
1	A	381	VAL
1	A	391	GLN
1	A	404	PHE
1	A	459	GLN
1	A	574	LEU
1	A	601	GLN
1	A	610	LEU
1	A	615	GLU
1	A	626	LEU
1	A	646	GLN
1	A	682	LEU
1	A	707	ARG
1	A	717	LEU
1	A	729	LEU
1	A	766	GLN
1	A	767	LEU
1	A	779	LEU
1	A	799	GLU
1	A	808	LYS
1	A	816	LYS
1	A	823	LEU
1	A	843	LEU
1	A	845	LEU
1	A	862	LEU
1	A	886	THR
1	A	893	GLN
1	A	898	ASN
1	A	907	LEU
1	A	948	HIS
1	A	964	ASP
1	A	968	ILE

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Mol	Chain	Res	Type
1	A	1026	LEU
1	A	1041	GLN
1	A	1042	LEU
1	A	1046	GLU
1	A	1059	LYS
1	A	1081	THR
1	A	1082	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (25) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	153	GLN
1	A	217	ASN
1	A	291	GLN
1	A	304	HIS
1	A	391	GLN
1	A	554	GLN
1	A	565	ASN
1	A	600	GLN
1	A	734	GLN
1	A	737	GLN
1	A	743	GLN
1	A	762	GLN
1	A	766	GLN
1	A	773	ASN
1	A	776	ASN
1	A	834	HIS
1	A	840	GLN
1	A	893	GLN
1	A	908	ASN
1	A	951	ASN
1	A	959	ASN
1	A	967	HIS
1	A	1007	GLN
1	A	1083	GLN
1	A	1085	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand 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$
2	3PS	A	1	-	25,25,25	2.28	8 (32%)	33,35,35	2.00	9 (27%)

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	3PS	A	1	-	-	2/10/10/10	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	3PS	C3-C5	-6.77	1.38	1.45
2	A	1	3PS	C17-C16	4.86	1.48	1.39
2	A	1	3PS	C7-C6	-3.19	1.38	1.43
2	A	1	3PS	C21-C16	-2.90	1.34	1.39
2	A	1	3PS	C21-C20	2.55	1.43	1.38
2	A	1	3PS	C20-C19	-2.51	1.34	1.39
2	A	1	3PS	C17-N18	2.36	1.39	1.34
2	A	1	3PS	C6-N8	-2.02	1.33	1.37

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	3PS	C16-C17-N18	-5.28	119.39	124.13
2	A	1	3PS	C17-N18-C19	4.78	120.83	116.63
2	A	1	3PS	C20-C21-C16	4.37	125.35	120.30
2	A	1	3PS	C21-C16-C17	-3.73	114.09	117.80
2	A	1	3PS	O22-C19-C20	-2.77	111.90	116.71
2	A	1	3PS	O14-C13-C7	-2.68	118.02	121.72
2	A	1	3PS	C9-N2-C3	-2.20	114.66	118.08
2	A	1	3PS	N8-C9-N2	2.01	129.39	125.73
2	A	1	3PS	C1-C9-N8	-2.00	114.04	117.16

There are no chirality outliers.

All (2) torsion outliers are listed below:

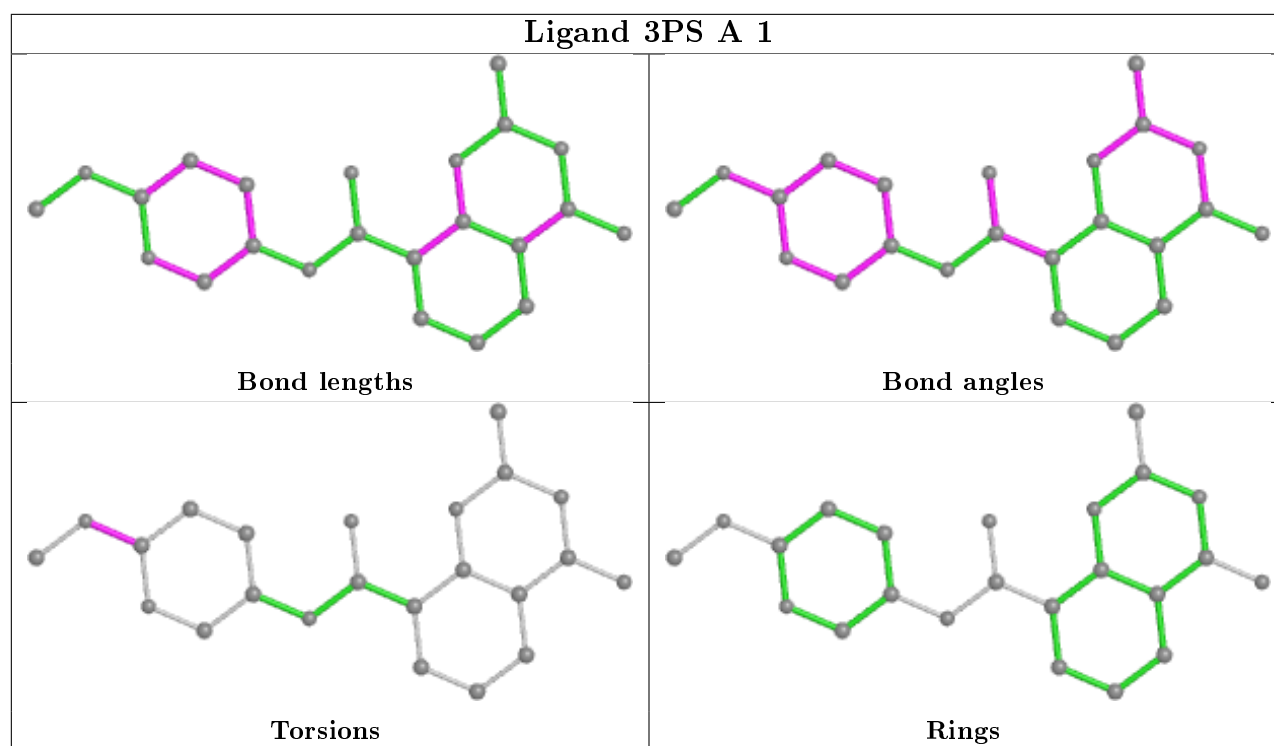
Mol	Chain	Res	Type	Atoms
2	A	1	3PS	N18-C19-O22-C23
2	A	1	3PS	C20-C19-O22-C23

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	3PS	3	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

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	841/966 (87%)	0.63	77 (9%) 9 6	33, 74, 112, 140	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	235	VAL	6.7
1	A	1090	LEU	6.5
1	A	370	ILE	5.2
1	A	774	LEU	5.2
1	A	404	PHE	4.5
1	A	970	GLY	4.5
1	A	220	ILE	4.2
1	A	522	ASN	4.0
1	A	307	LEU	3.9
1	A	147	SER	3.9
1	A	1041	GLN	3.9
1	A	1089	HIS	3.8
1	A	995	MET	3.8
1	A	216	ALA	3.8
1	A	971	ASN	3.8
1	A	898	ASN	3.8
1	A	1092	LEU	3.7
1	A	526	PRO	3.6
1	A	270	PHE	3.5
1	A	379	LEU	3.4
1	A	1082	VAL	3.4
1	A	899	THR	3.4
1	A	352	VAL	3.4
1	A	777	SER	3.3
1	A	767	LEU	3.2
1	A	459	GLN	3.1
1	A	1091	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	217	ASN	3.0
1	A	458	VAL	3.0
1	A	381	VAL	2.9
1	A	402	LYS	2.9
1	A	545	ALA	2.9
1	A	987	LEU	2.8
1	A	766	GLN	2.7
1	A	1042	LEU	2.7
1	A	747	LEU	2.7
1	A	231	GLN	2.7
1	A	233	ILE	2.7
1	A	403	PRO	2.7
1	A	972	TYR	2.7
1	A	232	THR	2.6
1	A	401	PRO	2.6
1	A	1088	LEU	2.6
1	A	523	TYR	2.6
1	A	1064	ALA	2.6
1	A	271	VAL	2.5
1	A	1084	PHE	2.5
1	A	229	THR	2.5
1	A	993	PHE	2.5
1	A	248	PHE	2.5
1	A	218	ASN	2.5
1	A	144	SER	2.5
1	A	212	TRP	2.5
1	A	406	GLU	2.5
1	A	902	PHE	2.4
1	A	869	CYS	2.3
1	A	1093	GLY	2.3
1	A	221	PHE	2.3
1	A	409	LEU	2.3
1	A	1014	VAL	2.3
1	A	400	SER	2.3
1	A	1004	PRO	2.3
1	A	287	ILE	2.3
1	A	896	VAL	2.2
1	A	241	PRO	2.2
1	A	1000	LYS	2.2
1	A	843	LEU	2.2
1	A	226	ARG	2.2
1	A	741	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	999	GLY	2.1
1	A	215	ILE	2.1
1	A	481	VAL	2.1
1	A	237	PRO	2.1
1	A	250	THR	2.1
1	A	251	LYS	2.0
1	A	1076	ARG	2.0
1	A	868	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

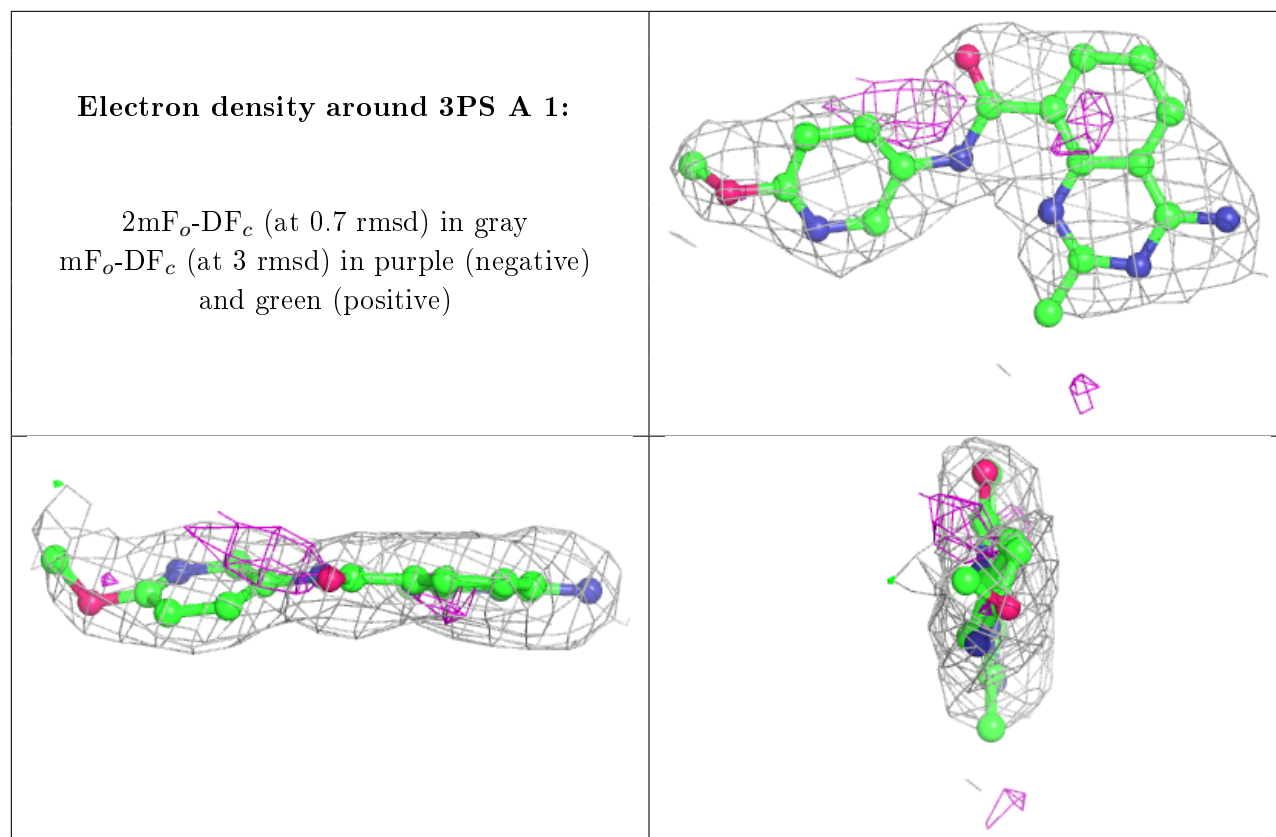
There are no carbohydrates in this entry.

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(Å ²)	Q<0.9
2	3PS	A	1	23/23	0.89	0.20	58,61,65,66	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.