



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 03:29 AM UTC

PDB ID : 4ANV / pdb_00004anv
Title : Complexes of PI3Kgamma with isoform selective inhibitors.
Authors : Foster, P.G.; Lougheed, J.C.
Deposited on : 2012-03-22
Resolution : 2.13 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

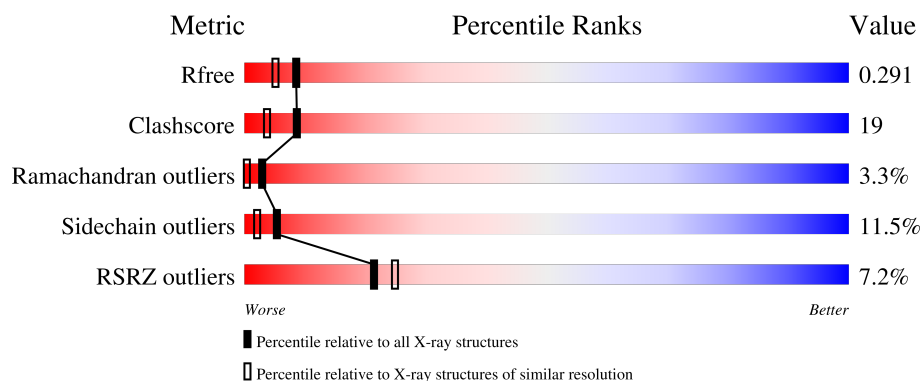
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.13 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	3689 (2.16-2.12)
Clashscore	190562	3812 (2.16-2.12)
Ramachandran outliers	187476	3773 (2.16-2.12)
Sidechain outliers	187428	3772 (2.16-2.12)
RSRZ outliers	180081	3691 (2.16-2.12)

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	980	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7111 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	848	Total	C	N	O	S	0	4	0
			6893	4426	1179	1252	36			

There are 21 discrepancies between the modelled and reference sequences:

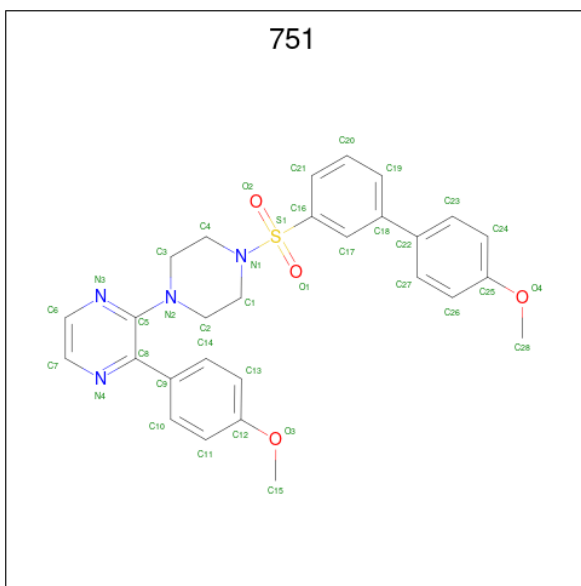
Chain	Residue	Modelled	Actual	Comment	Reference
A	139	MET	-	expression tag	UNP P48736
A	140	LEU	-	expression tag	UNP P48736
A	141	LEU	-	expression tag	UNP P48736
A	142	GLY	-	expression tag	UNP P48736
A	143	SER	-	expression tag	UNP P48736
A	1103	GLU	-	expression tag	UNP P48736
A	1104	PHE	-	expression tag	UNP P48736
A	1105	GLY	-	expression tag	UNP P48736
A	1106	LEU	-	expression tag	UNP P48736
A	1107	VAL	-	expression tag	UNP P48736
A	1108	PRO	-	expression tag	UNP P48736
A	1109	ARG	-	expression tag	UNP P48736
A	1110	GLY	-	expression tag	UNP P48736
A	1111	SER	-	expression tag	UNP P48736
A	1112	GLY	-	expression tag	UNP P48736
A	1113	HIS	-	expression tag	UNP P48736
A	1114	HIS	-	expression tag	UNP P48736
A	1115	HIS	-	expression tag	UNP P48736
A	1116	HIS	-	expression tag	UNP P48736
A	1117	HIS	-	expression tag	UNP P48736
A	1118	HIS	-	expression tag	UNP P48736

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

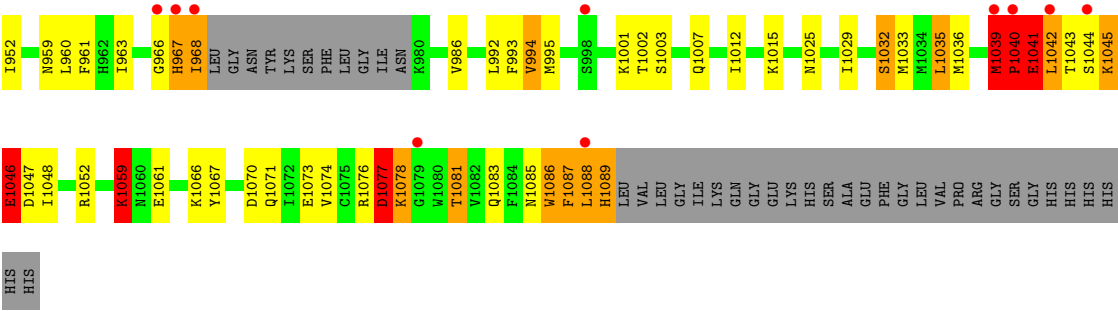
- Molecule 3 is 2-{4-[(4'-METHOXYBIPHENYL-3-YL)SULFONYL]PIPERAZIN-1-YL}-3-(4-METHOXYPHENYL)PYRAZINE (CCD ID: 751) (formula: $C_{28}H_{28}N_4O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	S	0	0
			37	28	4	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	176	Total 176	O 176	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	144.34Å 68.73Å 106.77Å 90.00° 94.91° 90.00°	Depositor
Resolution (Å)	106.60 – 2.13 106.38 – 2.13	Depositor EDS
% Data completeness (in resolution range)	94.9 (106.60-2.13) 94.9 (106.38-2.13)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.14Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.240 , 0.297 0.236 , 0.291	Depositor DCC
R_{free} test set	2804 reflections (4.89%)	wwPDB-VP
Wilson B-factor (Å ²)	48.0	Xtriage
Anisotropy	0.108	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7111	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% 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: 751, 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	1.16	16/7045 (0.2%)	1.24	37/9529 (0.4%)

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	13

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1040	PRO	C-N	-11.89	1.17	1.33
1	A	1046	GLU	C-N	-9.92	1.20	1.33
1	A	900	GLY	C-N	-9.62	1.21	1.33
1	A	434	TYR	C-N	8.47	1.45	1.33
1	A	1047	ASP	C-N	7.08	1.42	1.33
1	A	846	GLN	CD-NE2	6.61	1.47	1.33
1	A	171	ASP	CA-C	6.33	1.61	1.52
1	A	902	PHE	N-CA	6.26	1.53	1.46
1	A	881	ILE	CA-CB	5.83	1.60	1.53
1	A	395	CYS	CB-SG	-5.76	1.62	1.81
1	A	480	TYR	CA-C	-5.57	1.45	1.52
1	A	675	SER	CA-C	-5.32	1.46	1.52
1	A	604	VAL	CA-CB	5.17	1.60	1.54
1	A	659	TYR	C-O	-5.16	1.16	1.23
1	A	1029	ILE	CA-CB	5.16	1.61	1.54
1	A	676	ALA	CA-CB	5.03	1.61	1.53

All (37) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	237	PRO	O-C-N	-13.94	104.24	122.22
1	A	210	TYR	N-CA-C	11.71	127.90	113.50
1	A	775	GLN	N-CA-C	9.26	123.61	111.75
1	A	210	TYR	CA-C-N	8.97	137.84	121.70
1	A	210	TYR	C-N-CA	8.97	137.84	121.70
1	A	434	TYR	O-C-N	8.19	133.67	123.10
1	A	1077	ASP	CA-C-N	7.51	135.22	121.70
1	A	1077	ASP	C-N-CA	7.51	135.22	121.70
1	A	777	SER	CA-C-N	7.38	134.99	121.70
1	A	777	SER	C-N-CA	7.38	134.99	121.70
1	A	1087	PHE	O-C-N	6.98	130.14	122.11
1	A	903	LYS	N-CA-C	6.87	120.71	109.24
1	A	904	ASP	N-CA-C	6.32	117.86	110.97
1	A	373	LEU	CA-C-N	6.20	127.59	119.84
1	A	373	LEU	C-N-CA	6.20	127.59	119.84
1	A	308	ASP	N-CA-C	6.20	116.26	108.45
1	A	547	MET	N-CA-C	6.14	117.63	109.83
1	A	961	PHE	N-CA-C	6.09	119.17	108.75
1	A	171	ASP	N-CA-C	5.96	120.39	113.18
1	A	1025	ASN	N-CA-C	5.73	117.98	111.11
1	A	561	THR	CB-CA-C	5.60	119.08	109.51
1	A	614	ARG	N-CA-C	5.59	119.21	111.55
1	A	852	GLU	N-CA-C	5.59	118.14	111.71
1	A	238	ASP	CA-C-N	-5.54	113.49	121.42
1	A	238	ASP	C-N-CA	-5.54	113.49	121.42
1	A	701	SER	N-CA-C	5.43	117.62	111.11
1	A	901	ALA	CA-C-O	-5.37	115.41	121.05
1	A	775	GLN	CA-C-N	5.21	131.08	121.70
1	A	775	GLN	C-N-CA	5.21	131.08	121.70
1	A	700	ARG	N-CA-C	5.17	116.91	111.28
1	A	901	ALA	CA-C-N	5.15	132.94	121.81
1	A	901	ALA	C-N-CA	5.15	132.94	121.81
1	A	1086	TRP	N-CA-C	-5.14	105.30	112.45
1	A	682	LEU	N-CA-C	5.12	117.27	111.02
1	A	171	ASP	N-CA-CB	-5.09	101.86	110.41
1	A	529	LEU	N-CA-C	5.08	121.03	109.81
1	A	902	PHE	N-CA-C	-5.02	100.88	108.46

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1039	MET	Peptide

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Mol	Chain	Res	Type	Group
1	A	1040	PRO	Peptide,Mainchain
1	A	1041	GLU	Peptide
1	A	1042	LEU	Peptide
1	A	1088	LEU	Peptide
1	A	209	GLU	Peptide
1	A	237	PRO	Mainchain
1	A	411	ASN	Peptide
1	A	528	ALA	Peptide
1	A	898	ASN	Peptide
1	A	901	ALA	Peptide
1	A	966	GLY	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	6893	0	6905	257	0
2	A	5	0	0	1	0
3	A	37	0	28	7	0
4	A	176	0	0	26	0
All	All	7111	0	6933	261	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 19.

All (261) 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:814:GLU:OE1	1:A:827:THR:HG21	1.45	1.17
1:A:898:ASN:HB3	1:A:899:THR:HA	1.24	1.13
1:A:895:THR:HA	1:A:896:VAL:HB	1.23	1.12
1:A:497:PHE:HB3	1:A:1043:THR:O	1.49	1.11
1:A:693:HIS:O	4:A:2127:HOH:O	1.67	1.11
1:A:1040:PRO:HA	1:A:1041:GLU:C	1.69	1.10
1:A:899:THR:N	1:A:900:GLY:HA3	1.63	1.09
1:A:742:LEU:O	1:A:746:THR:HG23	1.55	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1036:MET:HE2	4:A:2172:HOH:O	1.52	1.07
1:A:967:HIS:C	1:A:968:ILE:N	2.24	0.96
1:A:696:PHE:HB3	4:A:2127:HOH:O	1.69	0.92
1:A:947:ARG:NH2	1:A:963:ILE:O	2.04	0.91
1:A:673:HIS:HD2	1:A:712:ARG:HE	1.19	0.89
1:A:219:CYS:SG	1:A:234:LYS:HG3	2.12	0.89
1:A:895:THR:CA	1:A:896:VAL:HB	2.03	0.89
1:A:651:LEU:HD22	1:A:655:ASP:HB3	1.55	0.89
1:A:846:GLN:NE2	4:A:2113:HOH:O	1.87	0.86
1:A:890:LYS:NZ	4:A:2151:HOH:O	2.05	0.84
1:A:433:ILE:HD12	1:A:484:MET:HE1	1.59	0.84
1:A:899:THR:H	1:A:900:GLY:HA3	1.42	0.83
1:A:898:ASN:CB	1:A:899:THR:HA	2.08	0.83
1:A:777:SER:HB3	1:A:778:GLN:HB3	1.62	0.80
1:A:895:THR:HA	1:A:896:VAL:CB	2.10	0.79
1:A:613:ARG:NH1	4:A:2086:HOH:O	2.17	0.78
1:A:240:THR:HG22	1:A:242:GLY:H	1.48	0.77
1:A:558:ILE:O	1:A:561:THR:HG22	1.85	0.76
1:A:428:LEU:HD22	1:A:465:ASN:HB3	1.65	0.75
1:A:746:THR:HG22	1:A:811:LEU:HD11	1.66	0.75
1:A:662:GLN:CG	4:A:2114:HOH:O	2.33	0.75
1:A:429:LEU:HB2	1:A:468:LEU:HD21	1.68	0.75
1:A:901:ALA:HB1	1:A:902:PHE:HD2	1.52	0.75
1:A:1040:PRO:HA	1:A:1041:GLU:O	1.87	0.75
1:A:240:THR:HG22	1:A:242:GLY:N	2.02	0.74
1:A:802[B]:LYS:NZ	4:A:2138:HOH:O	2.21	0.74
1:A:745:VAL:O	1:A:749:ILE:HD13	1.88	0.74
1:A:611:LEU:O	1:A:614:ARG:HG3	1.88	0.74
1:A:433:ILE:HD12	1:A:484:MET:CE	2.18	0.74
1:A:662:GLN:HG3	4:A:2114:HOH:O	1.86	0.74
1:A:433:ILE:HD12	1:A:484:MET:SD	2.28	0.73
1:A:901:ALA:HB1	1:A:902:PHE:CD2	2.24	0.73
1:A:233:ILE:HG22	1:A:235:VAL:HG23	1.69	0.73
1:A:316:ASP:O	4:A:2018:HOH:O	2.08	0.72
1:A:299:ASN:ND2	4:A:2038:HOH:O	2.22	0.71
1:A:435:CYS:HB3	1:A:459:GLN:HG3	1.72	0.71
1:A:148:GLN:O	1:A:152:ARG:HG3	1.91	0.71
1:A:775:GLN:HE22	1:A:798:ILE:HG13	1.56	0.71
1:A:777:SER:HB3	1:A:778:GLN:CB	2.21	0.70
1:A:435:CYS:HB3	1:A:459:GLN:CG	2.21	0.70
1:A:814:GLU:OE1	1:A:827:THR:CG2	2.32	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:748:ASP:O	1:A:752:LEU:HD13	1.93	0.69
1:A:860:LEU:HD21	1:A:1015:LYS:HD3	1.73	0.69
1:A:548:PRO:HG2	1:A:551:LEU:HD12	1.74	0.68
1:A:1044:SER:O	1:A:1045:LYS:C	2.35	0.68
1:A:207:LEU:HD21	1:A:211:LEU:HB3	1.76	0.68
1:A:379:LEU:HD12	1:A:380:THR:H	1.59	0.67
1:A:846:GLN:CD	4:A:2115:HOH:O	2.36	0.67
1:A:207:LEU:C	1:A:207:LEU:HD23	2.20	0.67
1:A:215:ILE:HG23	1:A:219:CYS:O	1.95	0.67
1:A:742:LEU:O	1:A:746:THR:CG2	2.39	0.66
1:A:949:ASN:HD22	1:A:949:ASN:C	2.04	0.65
1:A:806:SER:O	1:A:809:LYS:HD3	1.97	0.64
1:A:746:THR:HG22	1:A:811:LEU:CD1	2.27	0.63
3:A:1201:751:H31C	3:A:1201:751:C9	2.29	0.63
1:A:739:ILE:HG13	1:A:878:MET:HE1	1.81	0.62
1:A:207:LEU:CD2	1:A:211:LEU:HB3	2.30	0.62
1:A:410:TRP:HB3	1:A:412:VAL:HG22	1.82	0.62
1:A:779:LEU:HD22	1:A:780:PRO:HD2	1.82	0.62
1:A:1045:LYS:O	1:A:1046:GLU:CB	2.47	0.62
1:A:208:PRO:HG2	1:A:211:LEU:HD22	1.80	0.61
1:A:387:ILE:HD12	1:A:468:LEU:HD11	1.82	0.61
1:A:775:GLN:HB3	1:A:776:ASN:HB2	1.83	0.61
1:A:1032:SER:O	1:A:1036:MET:HG3	1.99	0.61
1:A:411:ASN:CG	1:A:411:ASN:O	2.43	0.61
1:A:827:THR:HG22	1:A:883:LYS:NZ	2.15	0.61
1:A:905:GLU:O	1:A:906:VAL:CB	2.47	0.60
1:A:893:GLN:C	1:A:895:THR:H	2.09	0.60
1:A:219:CYS:SG	1:A:234:LYS:CG	2.88	0.60
1:A:898:ASN:C	1:A:900:GLY:HA3	2.26	0.60
1:A:1074:VAL:O	1:A:1078:LYS:HG3	2.01	0.60
1:A:184:ARG:O	1:A:188:VAL:HG23	2.02	0.59
1:A:891:ILE:HG22	1:A:906:VAL:HG12	1.84	0.59
1:A:901:ALA:CB	1:A:902:PHE:CD2	2.85	0.59
1:A:673:HIS:CD2	1:A:712:ARG:HE	2.10	0.59
1:A:561:THR:CG2	1:A:591:LYS:HE2	2.32	0.59
1:A:905:GLU:O	1:A:906:VAL:HB	2.02	0.59
1:A:905:GLU:O	1:A:906:VAL:HG23	2.03	0.59
1:A:872:THR:HG21	1:A:878:MET:HE3	1.85	0.59
1:A:651:LEU:HD22	1:A:655:ASP:CB	2.31	0.59
1:A:701:SER:HB3	4:A:2129:HOH:O	2.02	0.58
1:A:893:GLN:C	1:A:895:THR:N	2.60	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:561:THR:HG22	1:A:591:LYS:HE2	1.84	0.58
1:A:316:ASP:OD1	1:A:689:LYS:NZ	2.26	0.58
1:A:799:GLU:CD	1:A:799:GLU:H	2.12	0.58
1:A:949:ASN:H	1:A:1083:GLN:HE22	1.51	0.57
1:A:925:VAL:O	1:A:929:VAL:HG23	2.04	0.57
1:A:697:TRP:CD1	4:A:2127:HOH:O	2.57	0.57
1:A:741:MET:HB3	1:A:774:LEU:HD21	1.86	0.57
1:A:898:ASN:HB3	1:A:899:THR:CA	2.16	0.57
3:A:1201:751:H31C	3:A:1201:751:C14	2.35	0.57
1:A:429:LEU:HB2	1:A:468:LEU:CD2	2.35	0.57
1:A:145:GLU:HA	1:A:146:GLU:O	2.05	0.56
1:A:948:HIS:CD2	1:A:1083:GLN:NE2	2.72	0.56
1:A:1077:ASP:N	1:A:1078:LYS:HB2	2.20	0.56
1:A:899:THR:N	1:A:900:GLY:CA	2.48	0.56
1:A:561:THR:HG21	1:A:565:ASN:HD22	1.70	0.56
1:A:207:LEU:HD23	1:A:208:PRO:N	2.21	0.55
1:A:837:ASP:OD1	1:A:839:ARG:HD3	2.06	0.55
1:A:240:THR:CG2	1:A:242:GLY:H	2.19	0.55
1:A:288:LYS:NZ	2:A:1200:SO4:O4	2.36	0.55
1:A:583:LEU:HD22	1:A:589:TYR:OH	2.07	0.55
1:A:944:ILE:O	4:A:2159:HOH:O	2.18	0.54
1:A:435:CYS:HB3	1:A:459:GLN:HG2	1.90	0.54
1:A:354:LEU:HB2	1:A:529:LEU:H	1.72	0.54
1:A:986:VAL:HA	4:A:2166:HOH:O	2.08	0.54
1:A:1044:SER:O	1:A:1046:GLU:N	2.41	0.54
1:A:888:ILE:HD11	1:A:960:LEU:HD11	1.89	0.53
1:A:304:HIS:CD2	1:A:823:LEU:HD23	2.44	0.53
1:A:497:PHE:CB	1:A:1043:THR:O	2.41	0.53
1:A:222:ILE:HD12	1:A:235:VAL:HG21	1.89	0.53
1:A:993:PHE:O	1:A:994:VAL:HB	2.09	0.53
1:A:742:LEU:HD22	1:A:813:LEU:HD11	1.90	0.53
1:A:1059:LYS:H	1:A:1059:LYS:HD2	1.73	0.53
1:A:1087:PHE:O	1:A:1089:HIS:HA	2.09	0.53
1:A:506:THR:OG1	4:A:2006:HOH:O	2.19	0.52
1:A:624:VAL:CG1	1:A:628:MET:HE2	2.40	0.52
1:A:1067:TYR:O	1:A:1070:ASP:HB2	2.09	0.52
1:A:673:HIS:HD2	1:A:712:ARG:NE	1.99	0.52
1:A:379:LEU:CD1	1:A:380:THR:H	2.21	0.52
1:A:735:GLN:O	1:A:739:ILE:HD13	2.10	0.52
1:A:193:PRO:HD2	4:A:2019:HOH:O	2.09	0.52
1:A:547:MET:HE2	1:A:551:LEU:C	2.34	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:772:GLU:O	1:A:776:ASN:HB3	2.10	0.52
1:A:796:LEU:HD13	1:A:815:PHE:CE2	2.45	0.51
1:A:236:SER:OG	1:A:237:PRO:HD2	2.10	0.51
1:A:993:PHE:O	1:A:994:VAL:CB	2.59	0.51
1:A:564:LEU:HD12	1:A:1052:ARG:HD2	1.93	0.51
1:A:777:SER:CB	1:A:778:GLN:CB	2.88	0.51
1:A:1087:PHE:O	1:A:1089:HIS:CA	2.59	0.51
1:A:233:ILE:HD11	1:A:248:PHE:HA	1.93	0.51
1:A:523:TYR:O	1:A:525:HIS:N	2.44	0.51
1:A:1035:LEU:HA	1:A:1039:MET:HB2	1.93	0.50
1:A:520:LEU:O	1:A:522:ASN:N	2.44	0.50
1:A:853:SER:O	1:A:857:THR:HG23	2.12	0.50
1:A:891:ILE:HG13	4:A:2149:HOH:O	2.11	0.50
1:A:899:THR:O	1:A:899:THR:OG1	2.28	0.50
3:A:1201:751:C9	3:A:1201:751:C3	2.89	0.50
1:A:633:CYS:SG	1:A:1036:MET:HE1	2.52	0.50
1:A:1081:THR:O	1:A:1085:ASN:N	2.38	0.50
1:A:151:GLN:HA	1:A:154:LEU:HD12	1.94	0.49
1:A:608:TYR:OH	1:A:637:ASP:OD1	2.29	0.49
1:A:905:GLU:O	1:A:906:VAL:CG2	2.60	0.49
1:A:952:ILE:HD11	1:A:986:VAL:HG21	1.94	0.49
1:A:614:ARG:HA	4:A:2088:HOH:O	2.12	0.49
1:A:795:ALA:HB3	1:A:816:LYS:HD2	1.94	0.49
1:A:749:ILE:O	1:A:753:SER:OG	2.30	0.49
1:A:597:LYS:HD3	1:A:600:GLN:NE2	2.28	0.49
1:A:862:LEU:HD12	1:A:934:GLY:HA2	1.95	0.48
1:A:207:LEU:C	1:A:207:LEU:CD2	2.85	0.48
1:A:373:LEU:N	1:A:374:PRO:HD2	2.28	0.48
1:A:198:MET:SD	1:A:271:VAL:HG11	2.53	0.48
1:A:233:ILE:CG2	1:A:234:LYS:N	2.76	0.48
1:A:523:TYR:C	1:A:525:HIS:H	2.22	0.48
1:A:583:LEU:HD22	1:A:589:TYR:CZ	2.49	0.48
1:A:893:GLN:HA	1:A:895:THR:HG23	1.95	0.48
1:A:862:LEU:HD12	1:A:934:GLY:CA	2.44	0.47
1:A:967:HIS:CA	1:A:968:ILE:N	2.76	0.47
1:A:1073:GLU:OE1	1:A:1076:ARG:HD3	2.14	0.47
1:A:549:ASN:HD21	1:A:553:LYS:NZ	2.13	0.47
1:A:1077:ASP:CA	1:A:1078:LYS:HB2	2.44	0.47
1:A:165:VAL:HG12	1:A:165:VAL:O	2.15	0.47
1:A:1036:MET:CE	4:A:2172:HOH:O	2.30	0.47
1:A:163:THR:O	1:A:165:VAL:HG23	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:829:GLY:CA	1:A:881:ILE:HD12	2.44	0.47
1:A:847:ILE:HG21	1:A:942:LEU:HD21	1.97	0.47
1:A:706:SER:O	1:A:710:GLN:HB3	2.15	0.47
1:A:775:GLN:HE22	1:A:798:ILE:CG1	2.23	0.47
1:A:1071:GLN:HA	1:A:1071:GLN:NE2	2.30	0.47
1:A:368:ILE:HG21	1:A:433:ILE:HD11	1.97	0.47
1:A:893:GLN:HA	1:A:895:THR:CG2	2.45	0.47
1:A:968:ILE:HG21	1:A:1039:MET:HE3	1.96	0.47
1:A:182:THR:HB	1:A:183:PRO:CD	2.45	0.46
1:A:895:THR:HG21	1:A:898:ASN:ND2	2.31	0.46
1:A:933:ALA:O	1:A:937:VAL:HG23	2.15	0.46
1:A:359:ARG:HG3	1:A:359:ARG:HH11	1.80	0.46
1:A:628:MET:O	1:A:1033:MET:HE1	2.16	0.46
1:A:564:LEU:HD11	1:A:1048:ILE:HG22	1.96	0.46
1:A:483:HIS:CD2	1:A:510:LYS:HD3	2.51	0.46
1:A:930:TYR:CE1	1:A:1012:ILE:HD13	2.50	0.46
1:A:302:GLU:HB2	1:A:304:HIS:CE1	2.50	0.46
1:A:433:ILE:CD1	1:A:484:MET:SD	3.00	0.46
1:A:949:ASN:C	1:A:949:ASN:ND2	2.72	0.46
1:A:886:THR:CB	4:A:2149:HOH:O	2.64	0.45
1:A:287:ILE:HG13	1:A:293:VAL:HG21	1.96	0.45
1:A:827:THR:HG22	1:A:883:LYS:HZ3	1.81	0.45
1:A:622:LEU:HD21	1:A:651:LEU:HG	1.98	0.45
1:A:968:ILE:CD1	1:A:968:ILE:C	2.90	0.45
1:A:1087:PHE:O	1:A:1088:LEU:C	2.59	0.45
1:A:591:LYS:NZ	4:A:2089:HOH:O	2.46	0.45
1:A:662:GLN:HE21	1:A:662:GLN:HB3	1.56	0.45
1:A:405:THR:HG22	1:A:406:GLU:H	1.81	0.45
1:A:738:VAL:HG21	1:A:783:PHE:CD1	2.51	0.45
1:A:661:LEU:O	1:A:665:GLN:HG2	2.16	0.45
1:A:745:VAL:O	1:A:745:VAL:HG12	2.16	0.45
1:A:771:LEU:HB2	1:A:798:ILE:HD13	1.99	0.45
1:A:897:GLY:O	1:A:898:ASN:C	2.60	0.44
1:A:735:GLN:O	1:A:739:ILE:CD1	2.66	0.44
1:A:881:ILE:HG23	3:A:1201:751:H282	2.00	0.44
1:A:523:TYR:C	1:A:525:HIS:N	2.76	0.44
1:A:561:THR:CG2	1:A:565:ASN:HD22	2.30	0.44
1:A:862:LEU:N	1:A:862:LEU:CD2	2.81	0.44
1:A:949:ASN:H	1:A:1083:GLN:NE2	2.14	0.44
1:A:463:TYR:CE2	1:A:501[B]:LYS:HA	2.53	0.43
1:A:236:SER:OG	1:A:237:PRO:CD	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:LYS:NZ	1:A:654:ASP:OD2	2.40	0.43
1:A:1044:SER:O	1:A:1046:GLU:CB	2.66	0.43
1:A:158:ILE:HG23	1:A:703:ILE:HD13	2.00	0.43
1:A:1086:TRP:O	1:A:1089:HIS:C	2.62	0.43
1:A:701:SER:CB	4:A:2129:HOH:O	2.64	0.43
1:A:827:THR:HG22	1:A:883:LYS:HZ1	1.82	0.43
1:A:208:PRO:C	1:A:210:TYR:H	2.26	0.43
1:A:608:TYR:N	1:A:608:TYR:CD1	2.86	0.43
1:A:702:GLU:O	1:A:706:SER:HB3	2.19	0.43
1:A:830:ILE:CG2	1:A:878:MET:HB2	2.49	0.43
1:A:701:SER:OG	1:A:871:SER:HB3	2.18	0.43
1:A:898:ASN:CB	1:A:899:THR:CA	2.88	0.43
1:A:829:GLY:HA3	1:A:881:ILE:HD12	2.02	0.42
1:A:302:GLU:HB2	1:A:304:HIS:HE1	1.84	0.42
1:A:901:ALA:HA	1:A:902:PHE:CD2	2.54	0.42
1:A:834:HIS:CG	1:A:835:GLY:N	2.88	0.42
1:A:904:ASP:N	1:A:904:ASP:OD1	2.53	0.42
1:A:767:LEU:HD22	1:A:803:VAL:CG2	2.49	0.42
1:A:891:ILE:HD11	4:A:2149:HOH:O	2.20	0.42
1:A:354:LEU:HD11	1:A:475:LEU:HD23	2.02	0.41
1:A:435:CYS:N	1:A:459:GLN:O	2.52	0.41
1:A:191:ARG:HD2	1:A:686:LEU:O	2.20	0.41
1:A:908:ASN:HD22	1:A:994:VAL:HG22	1.85	0.41
1:A:968:ILE:C	1:A:968:ILE:HD13	2.46	0.41
1:A:1071:GLN:HA	1:A:1071:GLN:HE21	1.84	0.41
1:A:762:GLN:HA	1:A:765:SER:HB3	2.03	0.41
1:A:810:PRO:HG2	3:A:1201:751:H42C	2.02	0.41
1:A:881:ILE:HG23	3:A:1201:751:C28	2.49	0.41
1:A:225:HIS:CE1	1:A:304:HIS:HD2	2.38	0.41
1:A:395:CYS:SG	1:A:418:ILE:HG22	2.60	0.41
1:A:462:TYR:CE2	1:A:486:GLN:HG3	2.56	0.41
1:A:471:HIS:CD2	1:A:471:HIS:H	2.39	0.41
1:A:992:LEU:O	1:A:995:MET:HB2	2.20	0.41
1:A:1003:SER:O	1:A:1007:GLN:HG3	2.20	0.41
1:A:1087:PHE:O	1:A:1089:HIS:N	2.53	0.41
1:A:224:ILE:HD12	1:A:248:PHE:CD1	2.55	0.41
1:A:273:ARG:HG3	1:A:280:TYR:CE1	2.55	0.41
1:A:405:THR:HG22	1:A:406:GLU:N	2.36	0.41
1:A:930:TYR:CD1	1:A:1012:ILE:HD13	2.56	0.41
1:A:245:LEU:HD13	1:A:245:LEU:HA	1.94	0.40
1:A:655:ASP:O	1:A:659:TYR:HD2	2.05	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:862:LEU:HD12	1:A:934:GLY:N	2.37	0.40
1:A:883:LYS:HD3	4:A:2142:HOH:O	2.21	0.40
1:A:1032:SER:HB2	1:A:1048:ILE:HG23	2.02	0.40
3:A:1201:751:H283	3:A:1201:751:H24	1.82	0.40
1:A:661:LEU:HD21	1:A:842:MET:HB3	2.03	0.40
1:A:145:GLU:CA	1:A:146:GLU:O	2.69	0.40
1:A:208:PRO:C	1:A:210:TYR:N	2.80	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	833/980 (85%)	751 (90%)	55 (7%)	27 (3%)	3 0

All (27) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	374	PRO
1	A	521	ASP
1	A	761	SER
1	A	776	ASN
1	A	778	GLN
1	A	896	VAL
1	A	898	ASN
1	A	906	VAL
1	A	994	VAL
1	A	1042	LEU
1	A	1059	LYS
1	A	1078	LYS
1	A	146	GLU
1	A	213	LYS

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Mol	Chain	Res	Type
1	A	268	GLN
1	A	1045	LYS
1	A	1046	GLU
1	A	1040	PRO
1	A	209	GLU
1	A	532	HIS
1	A	916	PRO
1	A	211	LEU
1	A	894	SER
1	A	1077	ASP
1	A	524	CYS
1	A	310	PRO
1	A	529	LEU

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	761/874 (87%)	674 (89%)	87 (11%)	5 2

All (87) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	153	GLN
1	A	168	VAL
1	A	195	LEU
1	A	207	LEU
1	A	233	ILE
1	A	238	ASP
1	A	240	THR
1	A	245	LEU
1	A	268	GLN
1	A	269	ASP
1	A	272	LEU
1	A	273	ARG
1	A	281	LEU

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Mol	Chain	Res	Type
1	A	298	LYS
1	A	306	VAL
1	A	310	PRO
1	A	319	ARG
1	A	320	LYS
1	A	351	THR
1	A	359	ARG
1	A	372	VAL
1	A	379	LEU
1	A	391	GLN
1	A	395	CYS
1	A	406	GLU
1	A	409	LEU
1	A	410	TRP
1	A	433	ILE
1	A	467	LEU
1	A	475	LEU
1	A	477	ARG
1	A	522	ASN
1	A	525	HIS
1	A	529	LEU
1	A	544	ARG
1	A	546	GLU
1	A	549	ASN
1	A	561	THR
1	A	575	LEU
1	A	583	LEU
1	A	603	ILE
1	A	628	MET
1	A	643	ILE
1	A	662	GLN
1	A	705	GLN
1	A	707	ARG
1	A	721	LEU
1	A	729	LEU
1	A	746	THR
1	A	747	LEU
1	A	753	SER
1	A	766	GLN
1	A	779	LEU
1	A	796	LEU
1	A	798	ILE

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Mol	Chain	Res	Type
1	A	807	LYS
1	A	823	LEU
1	A	826	GLU
1	A	827	THR
1	A	841	ASP
1	A	842	MET
1	A	845	LEU
1	A	862	LEU
1	A	870	ILE
1	A	886	THR
1	A	890	LYS
1	A	894	SER
1	A	896	VAL
1	A	905	GLU
1	A	911	LEU
1	A	922	GLN
1	A	949	ASN
1	A	959	ASN
1	A	967	HIS
1	A	968	ILE
1	A	1001	LYS
1	A	1002	THR
1	A	1032	SER
1	A	1035	LEU
1	A	1039	MET
1	A	1040	PRO
1	A	1041	GLU
1	A	1059	LYS
1	A	1061	GLU
1	A	1066	LYS
1	A	1081	THR
1	A	1089	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (34) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	148	GLN
1	A	167	ASN
1	A	218	ASN
1	A	225	HIS
1	A	299	ASN
1	A	304	HIS

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Mol	Chain	Res	Type
1	A	386	ASN
1	A	388	GLN
1	A	389	HIS
1	A	532	HIS
1	A	549	ASN
1	A	565	ASN
1	A	600	GLN
1	A	609	GLN
1	A	619	GLN
1	A	639	ASN
1	A	662	GLN
1	A	673	HIS
1	A	705	GLN
1	A	734	GLN
1	A	766	GLN
1	A	775	GLN
1	A	776	ASN
1	A	893	GLN
1	A	898	ASN
1	A	908	ASN
1	A	922	GLN
1	A	948	HIS
1	A	949	ASN
1	A	951	ASN
1	A	1007	GLN
1	A	1071	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 oligosaccharides in this entry.

5.6 Ligand geometry

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	751	A	1201	-	41,41,41	2.35	7 (17%)	55,58,58	2.30	17 (30%)
2	SO4	A	1200	-	4,4,4	0.26	0	6,6,6	0.91	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	751	A	1201	-	-	14/28/38/38	0/5/5/5

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1201	751	C16-S1	9.49	1.89	1.76
3	A	1201	751	C9-C8	-6.37	1.42	1.49
3	A	1201	751	O2-S1	5.99	1.49	1.43
3	A	1201	751	C18-C22	-3.48	1.40	1.49
3	A	1201	751	S1-N1	2.98	1.67	1.63
3	A	1201	751	O1-S1	2.66	1.46	1.43
3	A	1201	751	C4-N1	-2.26	1.45	1.47

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1201	751	C16-S1-N1	-7.19	98.59	107.28
3	A	1201	751	O1-S1-N1	6.45	112.76	106.69
3	A	1201	751	C2-N2-C3	6.16	125.43	111.57
3	A	1201	751	C1-N1-S1	-4.69	108.33	117.06
3	A	1201	751	C21-C16-S1	4.55	124.25	119.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1201	751	C1-N1-C4	3.82	116.50	112.12
3	A	1201	751	C21-C16-C17	-3.11	116.83	120.68
3	A	1201	751	C20-C21-C16	3.04	122.05	118.95
3	A	1201	751	O2-S1-C16	2.94	111.76	108.10
3	A	1201	751	C6-N3-C5	2.92	121.67	115.05
3	A	1201	751	C28-O4-C25	-2.92	111.23	117.50
3	A	1201	751	C7-N4-C8	2.80	122.30	116.84
3	A	1201	751	C18-C17-C16	2.62	121.93	119.95
3	A	1201	751	C15-O3-C12	2.57	123.02	117.50
3	A	1201	751	C4-C3-N2	2.30	115.62	110.78
3	A	1201	751	C6-C7-N4	-2.02	119.35	122.19
3	A	1201	751	C7-C6-N3	-2.01	119.36	122.19

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1201	751	C8-C5-N2-C2
3	A	1201	751	C4-N1-S1-O2
3	A	1201	751	C4-N1-S1-C16
3	A	1201	751	N3-C5-N2-C2
3	A	1201	751	C4-N1-S1-O1
3	A	1201	751	C1-N1-S1-O2
3	A	1201	751	C26-C25-O4-C28
3	A	1201	751	C1-N1-S1-O1
3	A	1201	751	C24-C25-O4-C28
3	A	1201	751	C1-N1-S1-C16
3	A	1201	751	C11-C12-O3-C15
3	A	1201	751	C13-C12-O3-C15
3	A	1201	751	C17-C16-S1-O1
3	A	1201	751	C21-C16-S1-O1

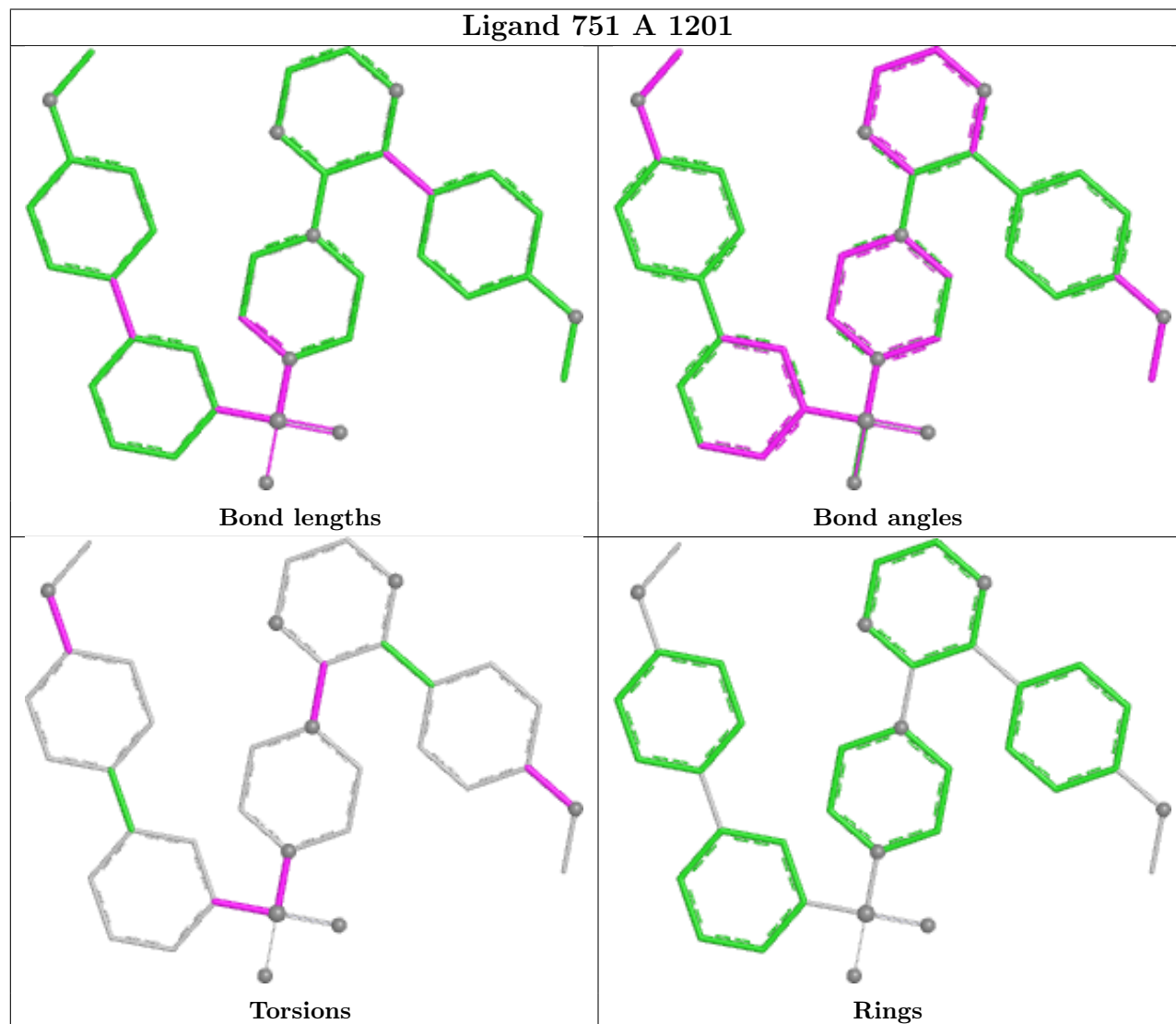
There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1201	751	7	0
2	A	1200	SO4	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

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	A	3

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	967:HIS	C	968:ILE	N	2.24
1	A	1046:GLU	C	1047:ASP	N	1.20
1	A	1040:PRO	C	1041:GLU	N	1.17

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	848/980 (86%)	0.68	61 (7%) 21 25	20, 50, 80, 91	4 (0%)

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	968	ILE	5.0
1	A	896	VAL	4.7
1	A	376	ASN	3.7
1	A	229	THR	3.7
1	A	1040	PRO	3.7
1	A	823	LEU	3.7
1	A	764	ILE	3.6
1	A	1042	LEU	3.4
1	A	759	VAL	3.4
1	A	223	VAL	3.3
1	A	779	LEU	3.3
1	A	210	TYR	3.1
1	A	249	PHE	3.0
1	A	763	VAL	3.0
1	A	1088	LEU	2.9
1	A	147	SER	2.9
1	A	898	ASN	2.9
1	A	895	THR	2.9
1	A	489	GLY	2.8
1	A	859	SER	2.8
1	A	544	ARG	2.7
1	A	1044	SER	2.7
1	A	761	SER	2.7
1	A	233	ILE	2.7
1	A	149	ALA	2.6
1	A	967	HIS	2.6
1	A	998	SER	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	523	TYR	2.6
1	A	244	ILE	2.6
1	A	548	PRO	2.6
1	A	741	MET	2.5
1	A	966	GLY	2.5
1	A	374	PRO	2.5
1	A	372	VAL	2.4
1	A	248	PHE	2.4
1	A	497	PHE	2.4
1	A	774	LEU	2.4
1	A	252	MET	2.4
1	A	219	CYS	2.4
1	A	1079	GLY	2.3
1	A	435	CYS	2.3
1	A	150	PHE	2.3
1	A	909	HIS	2.3
1	A	767	LEU	2.3
1	A	570	GLU	2.2
1	A	775	GLN	2.2
1	A	754	ALA	2.2
1	A	830	ILE	2.2
1	A	297	LEU	2.2
1	A	144	SER	2.2
1	A	228	THR	2.2
1	A	546	GLU	2.1
1	A	923	ALA	2.1
1	A	522	ASN	2.1
1	A	241	PRO	2.1
1	A	152	ARG	2.1
1	A	190	SER	2.1
1	A	550	GLN	2.1
1	A	1039	MET	2.0
1	A	306	VAL	2.0
1	A	552	ARG	2.0

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

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 [i](#)

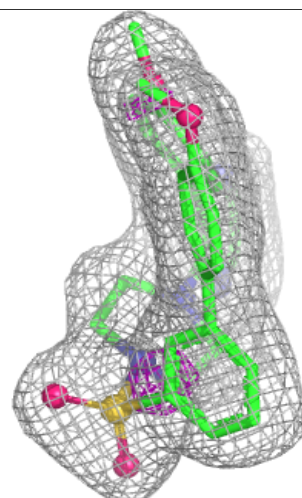
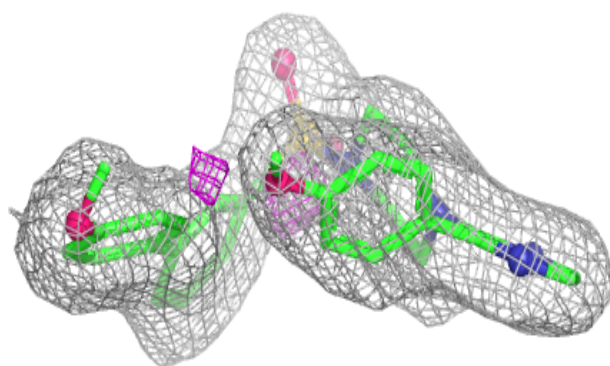
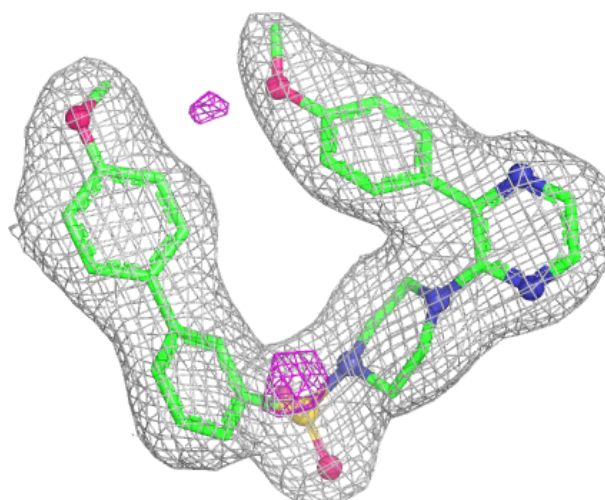
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
2	SO4	A	1200	5/5	0.94	0.09	56,56,57,60	0
3	751	A	1201	37/37	0.96	0.06	35,42,47,48	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 751 A 1201:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.