



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 13, 2023 – 05:32 AM EDT

PDB ID : 4PXS
Title : Human GKRP bound to AMG-0265 (N-[(R)-(2-CHLOROPHENYL){7-[4-(2-HYDROXYPROPAN-2-YL) PYRIDIN-2-YL]-1-BENZOTHIOPHEN-2-YL} METHYL]CYCLOPROPANESULFONAMIDE) and Sorbitol-6-phosphate
Authors : Jordan, S.R.; Chmait, S.
Deposited on : 2014-03-24
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 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
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) : 2.35.1

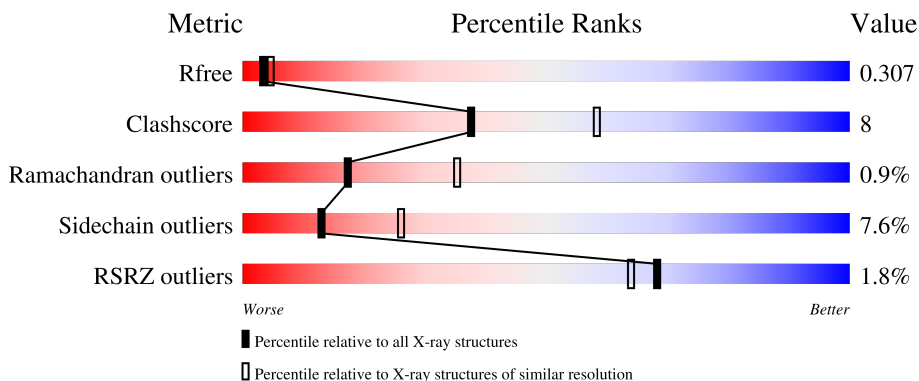
1 Overall quality at a glance

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 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	638	 2% 70% 20% • 8%
1	B	638	 % 73% 17% • 8%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	IOD	B	713	-	-	X	-
4	IOD	B	716	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 9315 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 Glucokinase regulatory protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	585	4521	2882	774	841	24	0	0	0
1	B	590	4554	2901	781	848	24	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

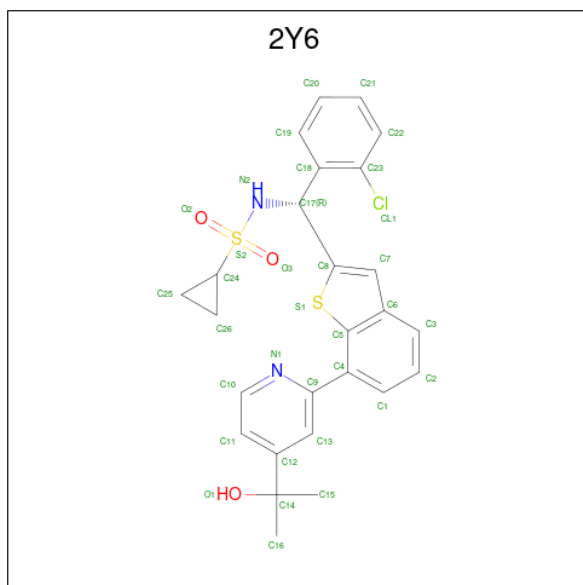
Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP Q14397
A	-10	ALA	-	expression tag	UNP Q14397
A	-9	HIS	-	expression tag	UNP Q14397
A	-8	HIS	-	expression tag	UNP Q14397
A	-7	HIS	-	expression tag	UNP Q14397
A	-6	HIS	-	expression tag	UNP Q14397
A	-5	HIS	-	expression tag	UNP Q14397
A	-4	HIS	-	expression tag	UNP Q14397
A	-3	ASP	-	expression tag	UNP Q14397
A	-2	GLU	-	expression tag	UNP Q14397
A	-1	VAL	-	expression tag	UNP Q14397
A	0	ASP	-	expression tag	UNP Q14397
A	626	GLY	-	expression tag	UNP Q14397
B	-11	MET	-	initiating methionine	UNP Q14397
B	-10	ALA	-	expression tag	UNP Q14397
B	-9	HIS	-	expression tag	UNP Q14397
B	-8	HIS	-	expression tag	UNP Q14397
B	-7	HIS	-	expression tag	UNP Q14397
B	-6	HIS	-	expression tag	UNP Q14397
B	-5	HIS	-	expression tag	UNP Q14397
B	-4	HIS	-	expression tag	UNP Q14397
B	-3	ASP	-	expression tag	UNP Q14397
B	-2	GLU	-	expression tag	UNP Q14397
B	-1	VAL	-	expression tag	UNP Q14397
B	0	ASP	-	expression tag	UNP Q14397

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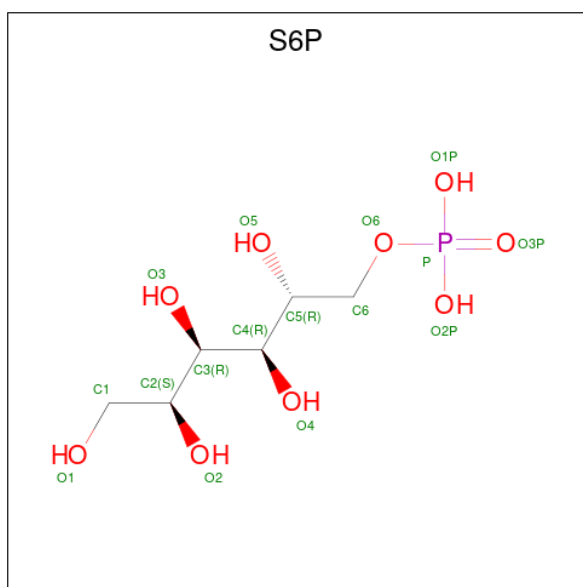
Chain	Residue	Modelled	Actual	Comment	Reference
B	626	GLY	-	expression tag	UNP Q14397

- Molecule 2 is N-[(R)-(2-chlorophenyl){7-[4-(2-hydroxypropan-2-yl)pyridin-2-yl]-1-benzothiophen-2-yl}methyl]cyclopropanesulfonamide (three-letter code: 2Y6) (formula: $C_{26}H_{25}ClN_2O_3S_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
			Total	C	Cl	N	O			S
2	A	1	34	26	1	2	3	2	0	0
2	B	1	34	26	1	2	3	2	0	0

- Molecule 3 is D-SORBITOL-6-PHOSPHATE (three-letter code: S6P) (formula: $C_6H_{15}O_9P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	P	0	0
			16	6	9	1		
3	B	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 4 is IODIDE ION (three-letter code: IOD) (formula: I).

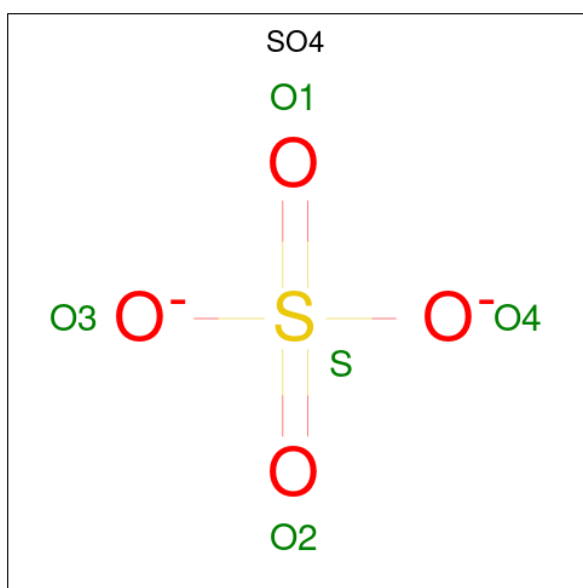
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	13	Total	I	0	0
			13	13		
4	B	16	Total	I	0	0
			16	16		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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

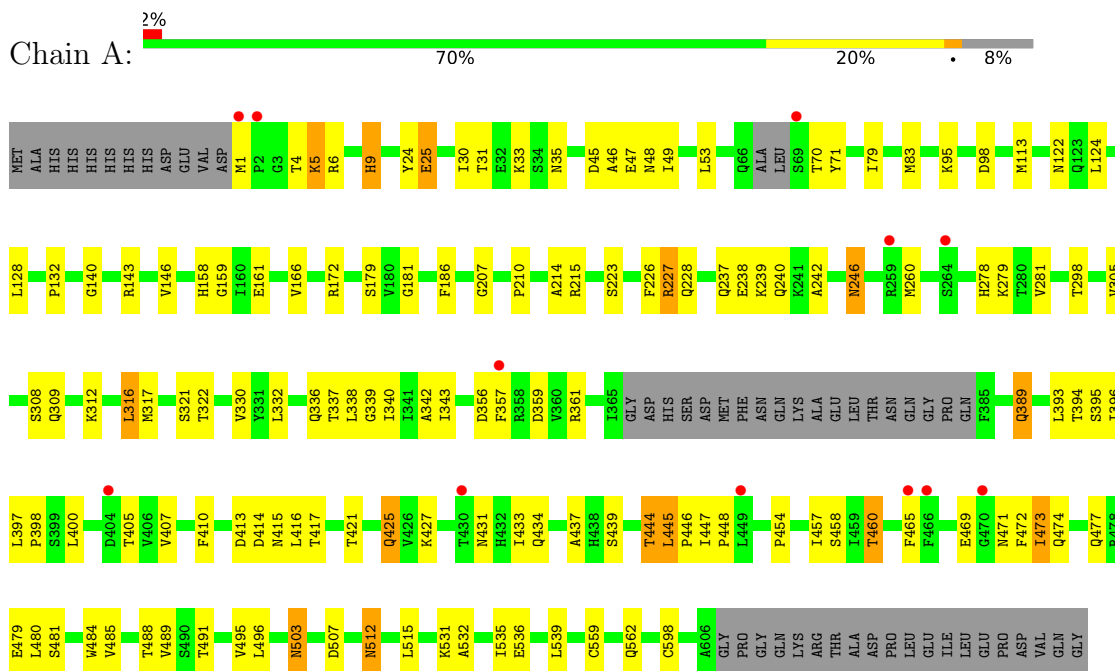
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	35	Total	O	0	0
			35	35		
7	B	49	Total	O	0	0
			49	49		

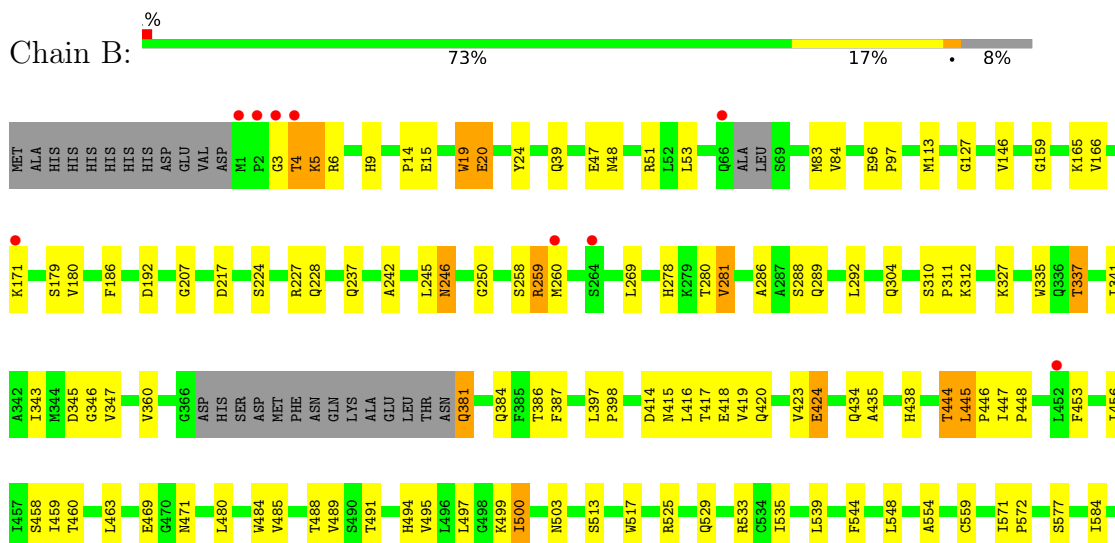
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Glucokinase regulatory protein



- Molecule 1: Glucokinase regulatory protein



Q588	GLY
A589	PRO
A606	GLY
	GLN
	LYS
	ARG
	THR
	ALA
	ASP
	PRO
	LEU
	GLU
	ILE
	LEU
	GLU
	PRO
	ASP
	VAL
	GLN
	GLY

4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	148.63Å 148.63Å 133.62Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	37.00 – 2.60 37.16 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.7 (37.00-2.60) 96.7 (37.16-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.234 , 0.307 0.237 , 0.307	Depositor DCC
R_{free} test set	2527 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	57.8	Xtrriage
Anisotropy	0.116	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 31.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtrriage
Estimated twinning fraction	0.023 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9315	wwPDB-VP
Average B, all atoms (Å ²)	63.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.96% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: IOD, 2Y6, S6P, SO4, GOL

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	0.60	0/4603	0.76	1/6228 (0.0%)
1	B	0.62	0/4637	0.79	2/6274 (0.0%)
All	All	0.61	0/9240	0.77	3/12502 (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	B	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	B	259	ARG	NE-CZ-NH1	8.58	124.59	120.30
1	B	259	ARG	NE-CZ-NH2	-7.16	116.72	120.30
1	A	507	ASP	CB-CG-OD1	5.22	122.99	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	19	TRP	Peptide

5.2 Too-close contacts [i](#)

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	4521	0	4618	74	0
1	B	4554	0	4647	67	0
2	A	34	0	25	2	0
2	B	34	0	25	4	0
3	A	16	0	13	1	0
3	B	16	0	13	1	0
4	A	13	0	0	3	0
4	B	16	0	0	7	0
5	B	12	0	16	0	0
6	B	15	0	0	1	0
7	A	35	0	0	0	0
7	B	49	0	0	0	1
All	All	9315	0	9357	143	1

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 8.

All (143) 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:B:3:GLY:O	4:B:710:IOD:I	2.72	0.77
1:A:228:GLN:HE22	1:B:228:GLN:HE22	1.35	0.75
1:A:340:ILE:HA	1:A:343:ILE:HD12	1.73	0.69
1:B:445:LEU:HG	4:B:713:IOD:I	2.65	0.67
1:A:485:VAL:O	1:A:489:VAL:HG23	1.95	0.67
1:A:53:LEU:HD12	1:A:488:THR:HG23	1.79	0.64
1:A:393:LEU:O	1:A:397:LEU:HB3	1.97	0.64
2:A:701:2Y6:S1	2:A:701:2Y6:N1	2.71	0.64
1:B:6:ARG:NH1	1:B:554:ALA:O	2.31	0.64
1:B:48:ASN:HD22	1:B:51:ARG:HE	1.44	0.63
2:B:701:2Y6:S1	2:B:701:2Y6:N1	2.71	0.63
1:B:415:ASN:OD1	1:B:418:GLU:HB2	1.99	0.62
1:A:124:LEU:HA	1:A:472:PHE:CZ	2.36	0.61
1:A:179:SER:OG	3:A:702:S6P:O2P	2.12	0.61
1:A:140:GLY:H	1:A:158:HIS:HE1	1.49	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:214:ALA:O	1:A:227:ARG:HD3	2.02	0.60
1:A:433:ILE:O	1:A:434:GLN:HG2	2.01	0.59
1:A:389:GLN:O	1:A:393:LEU:HD23	2.02	0.59
1:A:439:SER:O	1:A:460:THR:HA	2.03	0.59
1:B:447:ILE:N	1:B:448:PRO:HD2	2.17	0.59
1:B:259:ARG:NH2	1:B:345:ASP:OD1	2.36	0.59
1:A:298:THR:HG21	1:A:473:ILE:HD11	1.84	0.58
1:B:146:VAL:HG12	1:B:146:VAL:O	2.02	0.58
1:A:531:LYS:HE2	4:A:711:IOD:I	2.72	0.58
1:A:246:ASN:N	1:A:246:ASN:HD22	2.01	0.58
1:A:512:ASN:ND2	1:A:515:LEU:H	2.01	0.58
2:B:701:2Y6:C8	2:B:701:2Y6:H8	2.33	0.57
1:A:146:VAL:CG1	1:A:343:ILE:HG21	2.35	0.57
1:B:447:ILE:HD12	1:B:447:ILE:H	1.69	0.57
1:B:4:THR:HA	4:B:712:IOD:I	2.74	0.57
1:A:70:THR:OG1	1:A:71:TYR:N	2.38	0.57
1:A:278:HIS:O	1:A:281:VAL:HG22	2.05	0.56
1:B:529:GLN:NE2	1:B:533:ARG:HE	2.02	0.56
1:A:140:GLY:H	1:A:158:HIS:CE1	2.24	0.56
1:B:53:LEU:HD12	1:B:488:THR:HG23	1.88	0.56
1:B:84:VAL:HG13	1:B:292:LEU:CD1	2.37	0.55
1:B:96:GLU:N	1:B:97:PRO:HD3	2.21	0.55
1:B:469:GLU:HG2	4:B:716:IOD:I	2.78	0.54
1:B:286:ALA:HA	1:B:289:GLN:HE21	1.73	0.53
1:A:140:GLY:N	1:A:158:HIS:HE1	2.06	0.53
1:A:30:ILE:HD12	1:A:210:PRO:HD3	1.90	0.53
1:A:9:HIS:H	1:A:9:HIS:CD2	2.26	0.53
1:A:207:GLY:O	1:A:246:ASN:HA	2.08	0.53
1:A:481:SER:O	1:A:485:VAL:HG23	2.09	0.52
1:A:414:ASP:O	1:A:416:LEU:N	2.42	0.52
1:B:458:SER:OG	4:B:713:IOD:I	2.91	0.52
1:A:474:GLN:HA	1:A:477:GLN:HE21	1.75	0.52
1:B:9:HIS:H	1:B:9:HIS:CD2	2.28	0.51
1:B:146:VAL:O	1:B:146:VAL:CG1	2.58	0.51
1:A:246:ASN:HD22	1:A:246:ASN:H	1.58	0.51
1:A:503:ASN:HD22	1:A:503:ASN:C	2.14	0.51
1:B:435:ALA:HB2	1:B:453:PHE:CE1	2.46	0.50
1:A:512:ASN:HD22	1:A:515:LEU:H	1.59	0.50
1:B:444:THR:O	1:B:446:PRO:HD3	2.11	0.49
1:A:512:ASN:HD22	1:A:512:ASN:C	2.15	0.49
1:A:124:LEU:O	1:A:128:LEU:HG	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:LEU:HD12	1:A:400:LEU:N	2.28	0.48
1:B:517:TRP:CD2	2:B:701:2Y6:H11	2.49	0.48
1:A:223:SER:OG	1:B:192:ASP:OD1	2.31	0.48
1:B:84:VAL:HG13	1:B:292:LEU:HD12	1.95	0.48
1:B:480:LEU:HD21	1:B:484:TRP:CH2	2.48	0.48
1:A:46:ALA:HA	1:A:317:MET:HE1	1.96	0.47
1:A:95:LYS:HE3	1:A:281:VAL:HG12	1.95	0.47
1:A:237:GLN:HA	1:A:242:ALA:O	2.13	0.47
1:A:395:SER:HB3	1:A:396:ILE:HD12	1.96	0.47
1:A:305:VAL:O	1:A:308:SER:OG	2.15	0.47
1:A:309:GLN:NE2	1:A:458:SER:O	2.47	0.47
1:A:316:LEU:HD11	1:A:407:VAL:HG21	1.97	0.47
1:B:127:GLY:O	4:B:716:IOD:I	3.02	0.47
1:A:113:MET:HA	1:A:113:MET:HE2	1.97	0.47
1:B:415:ASN:HD21	1:B:417:THR:HB	1.79	0.47
1:B:179:SER:OG	3:B:702:S6P:O3P	2.19	0.47
1:B:535:ILE:O	1:B:539:LEU:HG	2.14	0.47
1:B:397:LEU:N	1:B:398:PRO:HD2	2.30	0.47
1:B:180:VAL:HG11	1:B:258:SER:HB2	1.96	0.47
1:B:438:HIS:HA	1:B:459:ILE:O	2.14	0.46
1:A:122:ASN:OD1	1:A:132:PRO:HB2	2.15	0.46
1:B:245:LEU:HG	1:B:269:LEU:HD21	1.97	0.46
1:B:420:GLN:O	1:B:424:GLU:HB2	2.16	0.46
1:B:517:TRP:CG	2:B:701:2Y6:H11	2.51	0.46
1:A:33:LYS:HG2	4:A:710:IOD:I	2.85	0.46
1:A:317:MET:HE2	1:A:496:LEU:HD11	1.98	0.46
1:B:237:GLN:HA	1:B:242:ALA:O	2.15	0.46
1:B:3:GLY:O	1:B:5:LYS:N	2.48	0.46
1:B:310:SER:N	1:B:311:PRO:CD	2.79	0.46
1:B:337:THR:N	6:B:722:SO4:O3	2.49	0.46
1:B:246:ASN:HD22	1:B:246:ASN:N	2.14	0.45
1:B:335:TRP:CH2	1:B:419:VAL:HG22	2.51	0.45
1:A:397:LEU:N	1:A:398:PRO:CD	2.79	0.45
1:B:113:MET:HE2	1:B:113:MET:HA	1.97	0.45
1:A:421:THR:O	1:A:425:GLN:NE2	2.50	0.45
1:A:79:ILE:O	1:A:83:MET:HG3	2.16	0.45
1:A:410:PHE:O	1:A:437:ALA:HA	2.17	0.45
1:B:312:LYS:HE3	1:B:456:ILE:O	2.16	0.45
1:A:48:ASN:O	1:A:49:ILE:C	2.55	0.45
1:B:146:VAL:O	1:B:347:VAL:HG21	2.17	0.45
1:B:159:GLY:HA2	1:B:186:PHE:CE1	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:338:LEU:CD1	1:A:338:LEU:N	2.79	0.45
1:A:532:ALA:O	1:A:536:GLU:HG3	2.16	0.44
1:B:146:VAL:HG13	1:B:343:ILE:CG2	2.47	0.44
1:B:381:GLN:HA	1:B:381:GLN:HE21	1.82	0.44
1:B:544:PHE:CG	1:B:584:ILE:HG21	2.51	0.44
1:A:146:VAL:CG1	1:A:343:ILE:CG2	2.95	0.44
1:B:420:GLN:HA	1:B:423:VAL:HG12	2.00	0.44
1:B:14:PRO:HG2	1:B:19:TRP:CD2	2.52	0.44
1:B:207:GLY:O	1:B:246:ASN:HA	2.18	0.44
1:B:447:ILE:N	1:B:448:PRO:CD	2.80	0.44
1:A:312:LYS:HB3	1:A:457:ILE:HG12	2.00	0.43
1:A:535:ILE:O	1:A:539:LEU:HG	2.18	0.43
1:B:571:ILE:HB	1:B:572:PRO:HD3	2.01	0.43
2:A:701:2Y6:H8	2:A:701:2Y6:C8	2.49	0.43
1:B:96:GLU:N	1:B:97:PRO:CD	2.82	0.43
1:A:444:THR:O	1:A:446:PRO:HD3	2.18	0.43
1:B:280:THR:HG21	1:B:288:SER:HA	2.00	0.43
1:A:445:LEU:O	1:A:446:PRO:C	2.57	0.43
1:A:337:THR:CG2	1:A:479:GLU:HG2	2.49	0.43
1:A:447:ILE:N	1:A:448:PRO:HD2	2.34	0.43
1:A:480:LEU:HD21	1:A:484:TRP:CH2	2.54	0.43
1:A:9:HIS:CD2	1:A:9:HIS:N	2.87	0.42
1:A:5:LYS:HB3	4:A:709:IOD:I	2.89	0.42
1:A:159:GLY:HA2	1:A:186:PHE:CE1	2.53	0.42
1:A:330:VAL:HG22	1:A:405:THR:HB	2.00	0.42
1:B:588:GLN:O	1:B:589:ALA:C	2.57	0.42
1:A:5:LYS:O	1:A:6:ARG:C	2.56	0.42
1:B:414:ASP:O	1:B:416:LEU:HD13	2.19	0.42
1:B:491:THR:O	1:B:495:VAL:HG23	2.19	0.42
1:A:356:ASP:N	1:A:359:ASP:OD1	2.53	0.42
1:B:278:HIS:O	1:B:281:VAL:HG23	2.20	0.42
1:B:495:VAL:HG22	1:B:500:ILE:HG12	2.02	0.42
1:A:316:LEU:HD22	1:A:316:LEU:O	2.20	0.42
1:B:384:GLN:NE2	1:B:387:PHE:CE1	2.88	0.42
1:A:336:GLN:O	1:A:339:GLY:N	2.54	0.41
1:B:346:GLY:HA3	1:B:360:VAL:O	2.20	0.41
1:A:332:LEU:HB3	1:A:342:ALA:HB1	2.01	0.41
1:A:491:THR:O	1:A:495:VAL:HG23	2.20	0.41
1:A:317:MET:CE	1:A:496:LEU:HD11	2.51	0.41
1:B:485:VAL:O	1:B:489:VAL:HG23	2.21	0.41
1:A:339:GLY:O	1:A:342:ALA:HB3	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:TYR:C	1:B:24:TYR:CD1	2.94	0.41
1:B:250:GLY:HA2	4:B:705:IOD:I	2.91	0.41
1:B:494:HIS:HA	1:B:497:LEU:HD12	2.03	0.40
1:A:31:THR:HG21	1:A:181:GLY:HA2	2.04	0.40
1:A:24:TYR:O	1:A:25:GLU:C	2.59	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:840:HOH:O	7:B:843:HOH:O[5_555]	2.06	0.14

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	579/638 (91%)	534 (92%)	39 (7%)	6 (1%)	15	32
1	B	584/638 (92%)	542 (93%)	38 (6%)	4 (1%)	22	43
All	All	1163/1276 (91%)	1076 (92%)	77 (7%)	10 (1%)	17	35

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	415	ASN
1	B	4	THR
1	B	20	GLU
1	A	260	MET
1	A	279	LYS
1	A	469	GLU
1	B	260	MET
1	A	389	GLN

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Mol	Chain	Res	Type
1	A	454	PRO
1	B	165	LYS

5.3.2 Protein sidechains [i](#)

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	498/542 (92%)	456 (92%)	42 (8%)	11	21
1	B	501/542 (92%)	467 (93%)	34 (7%)	16	32
All	All	999/1084 (92%)	923 (92%)	76 (8%)	13	26

All (76) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	4	THR
1	A	5	LYS
1	A	9	HIS
1	A	25	GLU
1	A	35	ASN
1	A	45	ASP
1	A	47	GLU
1	A	98	ASP
1	A	143	ARG
1	A	161	GLU
1	A	166	VAL
1	A	172	ARG
1	A	215	ARG
1	A	226	PHE
1	A	227	ARG
1	A	238	GLU
1	A	239	LYS
1	A	240	GLN
1	A	246	ASN
1	A	316	LEU

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Mol	Chain	Res	Type
1	A	321	SER
1	A	322	THR
1	A	357	PHE
1	A	361	ARG
1	A	394	THR
1	A	413	ASP
1	A	417	THR
1	A	425	GLN
1	A	427	LYS
1	A	431	ASN
1	A	444	THR
1	A	445	LEU
1	A	460	THR
1	A	465	PHE
1	A	471	ASN
1	A	473	ILE
1	A	503	ASN
1	A	512	ASN
1	A	559	CYS
1	A	562	GLN
1	A	598	CYS
1	B	5	LYS
1	B	15	GLU
1	B	20	GLU
1	B	39	GLN
1	B	47	GLU
1	B	83	MET
1	B	166	VAL
1	B	171	LYS
1	B	217	ASP
1	B	224	SER
1	B	227	ARG
1	B	246	ASN
1	B	281	VAL
1	B	304	GLN
1	B	327	LYS
1	B	337	THR
1	B	341	ILE
1	B	381	GLN
1	B	386	THR
1	B	424	GLU
1	B	434	GLN

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Mol	Chain	Res	Type
1	B	444	THR
1	B	445	LEU
1	B	460	THR
1	B	463	LEU
1	B	471	ASN
1	B	499	LYS
1	B	500	ILE
1	B	503	ASN
1	B	513	SER
1	B	525	ARG
1	B	548	LEU
1	B	559	CYS
1	B	577	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (36) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	HIS
1	A	35	ASN
1	A	55	GLN
1	A	91	GLN
1	A	123	GLN
1	A	130	GLN
1	A	158	HIS
1	A	190	GLN
1	A	196	ASN
1	A	246	ASN
1	A	336	GLN
1	A	389	GLN
1	A	425	GLN
1	A	431	ASN
1	A	471	ASN
1	A	477	GLN
1	A	503	ASN
1	A	512	ASN
1	A	529	GLN
1	B	9	HIS
1	B	39	GLN
1	B	48	ASN
1	B	196	ASN
1	B	197	ASN
1	B	228	GLN

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Mol	Chain	Res	Type
1	B	246	ASN
1	B	289	GLN
1	B	304	GLN
1	B	381	GLN
1	B	384	GLN
1	B	389	GLN
1	B	425	GLN
1	B	434	GLN
1	B	471	ASN
1	B	503	ASN
1	B	529	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 38 ligands modelled in this entry, 29 are monoatomic - leaving 9 for Mogul analysis.

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	$\# Z > 2$
6	SO4	B	722	-	4,4,4	0.47	0	6,6,6	0.46	0
6	SO4	B	723	-	4,4,4	0.41	0	6,6,6	0.43	0
5	GOL	B	720	-	5,5,5	0.66	0	5,5,5	1.05	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	2Y6	B	701	-	32,38,38	2.01	4 (12%)	43,58,58	2.42	11 (25%)
6	SO4	B	721	-	4,4,4	0.56	0	6,6,6	0.34	0
3	S6P	A	702	-	15,15,15	1.37	1 (6%)	21,21,21	1.38	2 (9%)
5	GOL	B	719	-	5,5,5	0.35	0	5,5,5	0.34	0
3	S6P	B	702	-	15,15,15	1.65	3 (20%)	21,21,21	1.31	4 (19%)
2	2Y6	A	701	-	32,38,38	1.97	5 (15%)	43,58,58	2.32	16 (37%)

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
5	GOL	B	720	-	-	4/4/4/4	-
2	2Y6	B	701	-	-	5/23/31/31	0/5/5/5
3	S6P	A	702	-	-	2/20/20/20	-
5	GOL	B	719	-	-	3/4/4/4	-
3	S6P	B	702	-	-	0/20/20/20	-
2	2Y6	A	701	-	-	6/23/31/31	0/5/5/5

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	701	2Y6	C4-C9	-6.50	1.40	1.49
2	B	701	2Y6	O2-S2	6.03	1.50	1.43
2	A	701	2Y6	O3-S2	5.78	1.50	1.43
2	A	701	2Y6	C4-C9	-5.19	1.42	1.49
2	A	701	2Y6	O1-C14	-5.03	1.37	1.44
3	B	702	S6P	P-O3P	3.72	1.62	1.50
2	A	701	2Y6	O2-S2	3.48	1.47	1.43
2	B	701	2Y6	O3-S2	3.39	1.47	1.43
3	A	702	S6P	P-O3P	3.34	1.61	1.50
3	B	702	S6P	C6-C5	3.26	1.56	1.51
2	B	701	2Y6	C18-C17	-2.85	1.49	1.52
3	B	702	S6P	P-O2P	2.70	1.65	1.54
2	A	701	2Y6	C16-C14	-2.02	1.50	1.52

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	2Y6	O3-S2-O2	-9.17	112.36	119.24
2	B	701	2Y6	C19-C18-C23	6.44	123.22	116.81
2	B	701	2Y6	O2-S2-N2	-6.34	100.13	107.76
2	B	701	2Y6	C22-C23-C18	-6.12	116.44	121.99
2	A	701	2Y6	C17-N2-S2	-5.27	110.42	121.88
2	B	701	2Y6	O3-S2-O2	-5.16	115.37	119.24
2	B	701	2Y6	C4-C5-S1	4.18	132.32	124.59
2	A	701	2Y6	O3-S2-N2	3.91	112.48	107.76
2	A	701	2Y6	C13-C9-N1	-3.41	117.72	122.16
2	B	701	2Y6	C17-N2-S2	-3.23	114.85	121.88
2	A	701	2Y6	C22-C23-C18	-3.19	119.10	121.99
2	A	701	2Y6	O2-S2-N2	-2.97	104.18	107.76
2	B	701	2Y6	C9-C4-C5	-2.90	118.48	123.29
2	A	701	2Y6	C4-C5-S1	2.86	129.87	124.59
3	A	702	S6P	O2P-P-O6	2.77	114.10	106.73
3	B	702	S6P	C5-C4-C3	-2.65	108.32	112.47
2	B	701	2Y6	C16-C14-C15	-2.53	107.40	110.49
3	A	702	S6P	O1-C1-C2	-2.50	105.63	111.07
2	A	701	2Y6	C19-C18-C23	2.39	119.18	116.81
3	B	702	S6P	C6-C5-C4	2.35	116.75	112.20
3	B	702	S6P	O3-C3-C4	-2.35	104.00	109.47
2	A	701	2Y6	C10-N1-C9	2.35	120.52	117.23
2	B	701	2Y6	O3-S2-N2	2.28	110.51	107.76
2	A	701	2Y6	C9-C13-C12	2.28	122.17	120.13
2	A	701	2Y6	C13-C12-C14	2.23	123.22	120.43
2	B	701	2Y6	C18-C23-CL1	2.22	122.71	120.41
2	B	701	2Y6	C20-C19-C18	-2.18	118.23	121.01
2	A	701	2Y6	O1-C14-C15	2.18	111.47	107.08
2	A	701	2Y6	C1-C4-C9	2.13	122.02	118.04
2	A	701	2Y6	C9-C4-C5	-2.08	119.84	123.29
2	A	701	2Y6	C15-C14-C12	-2.06	107.21	110.91
2	A	701	2Y6	C18-C23-CL1	2.06	122.55	120.41
3	B	702	S6P	O2P-P-O1P	2.02	115.34	107.64

There are no chirality outliers.

All (20) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	701	2Y6	C5-C4-C9-C13
2	A	701	2Y6	C5-C4-C9-N1
2	A	701	2Y6	C1-C4-C9-C13
2	A	701	2Y6	C1-C4-C9-N1
2	B	701	2Y6	C5-C4-C9-C13

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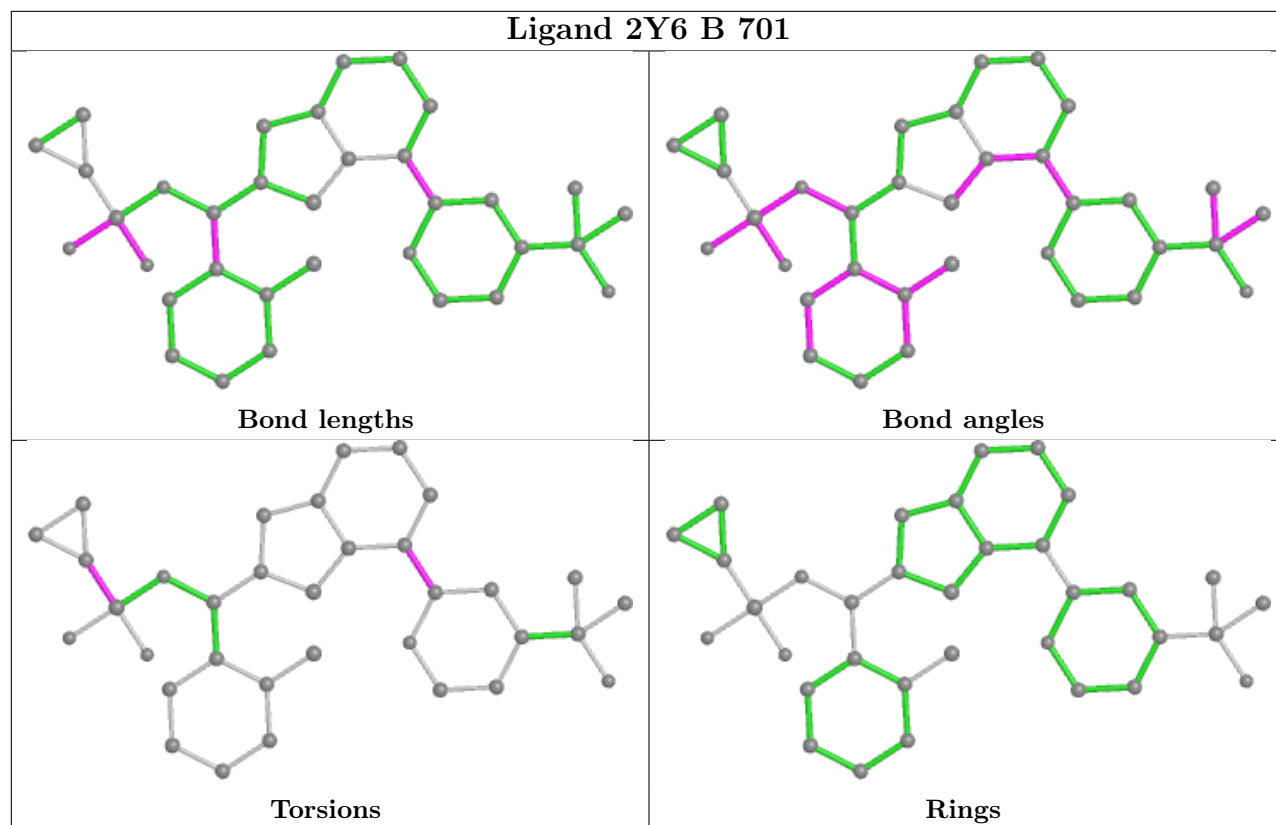
Mol	Chain	Res	Type	Atoms
2	B	701	2Y6	C5-C4-C9-N1
2	B	701	2Y6	C1-C4-C9-C13
2	B	701	2Y6	C1-C4-C9-N1
5	B	719	GOL	O1-C1-C2-O2
5	B	720	GOL	O1-C1-C2-C3
5	B	720	GOL	C1-C2-C3-O3
3	A	702	S6P	O1-C1-C2-O2
5	B	719	GOL	O1-C1-C2-C3
3	A	702	S6P	O1-C1-C2-C3
5	B	720	GOL	O2-C2-C3-O3
5	B	720	GOL	O1-C1-C2-O2
5	B	719	GOL	O2-C2-C3-O3
2	A	701	2Y6	C25-C24-S2-O3
2	A	701	2Y6	C26-C24-S2-O3
2	B	701	2Y6	C26-C24-S2-O2

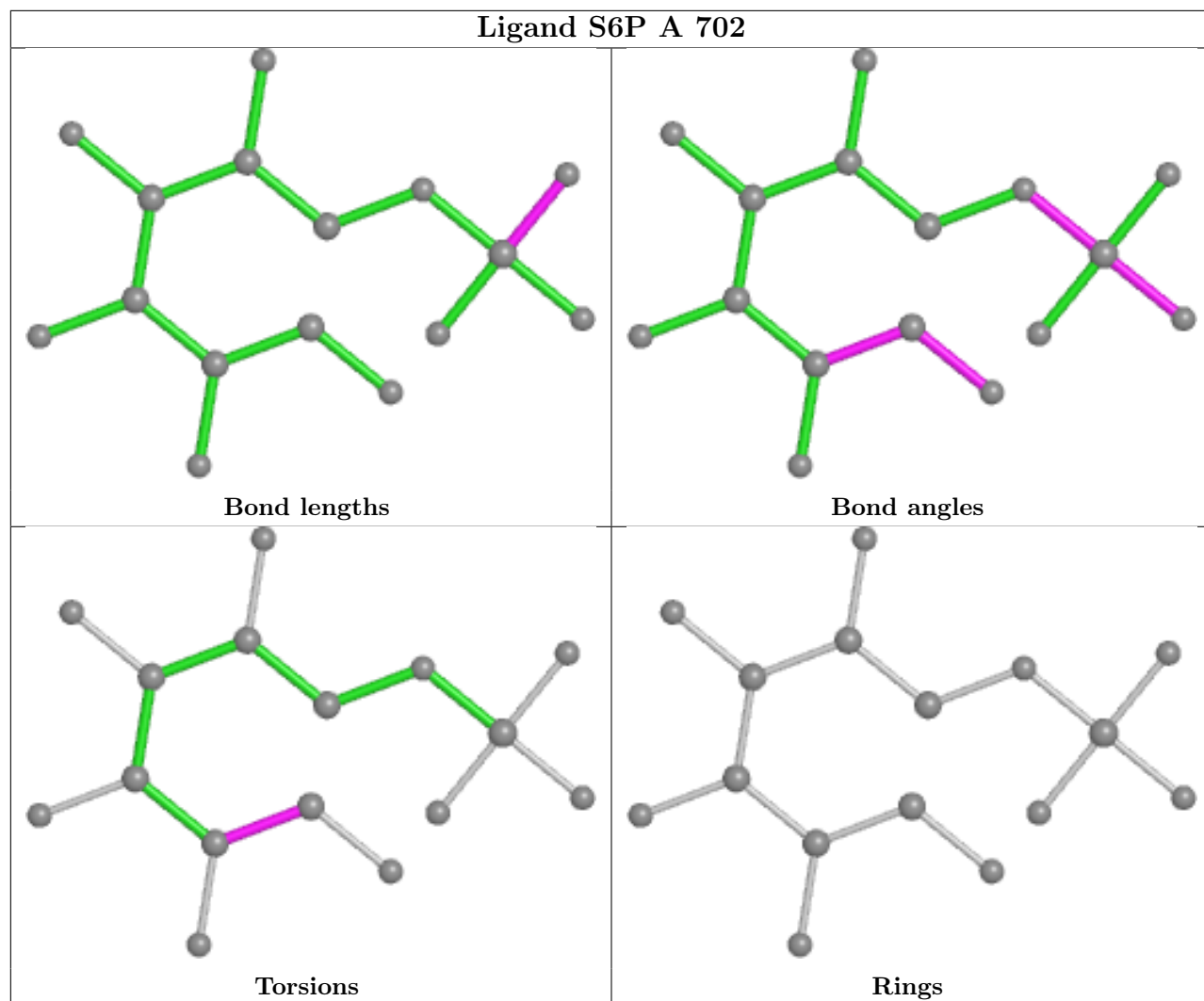
There are no ring outliers.

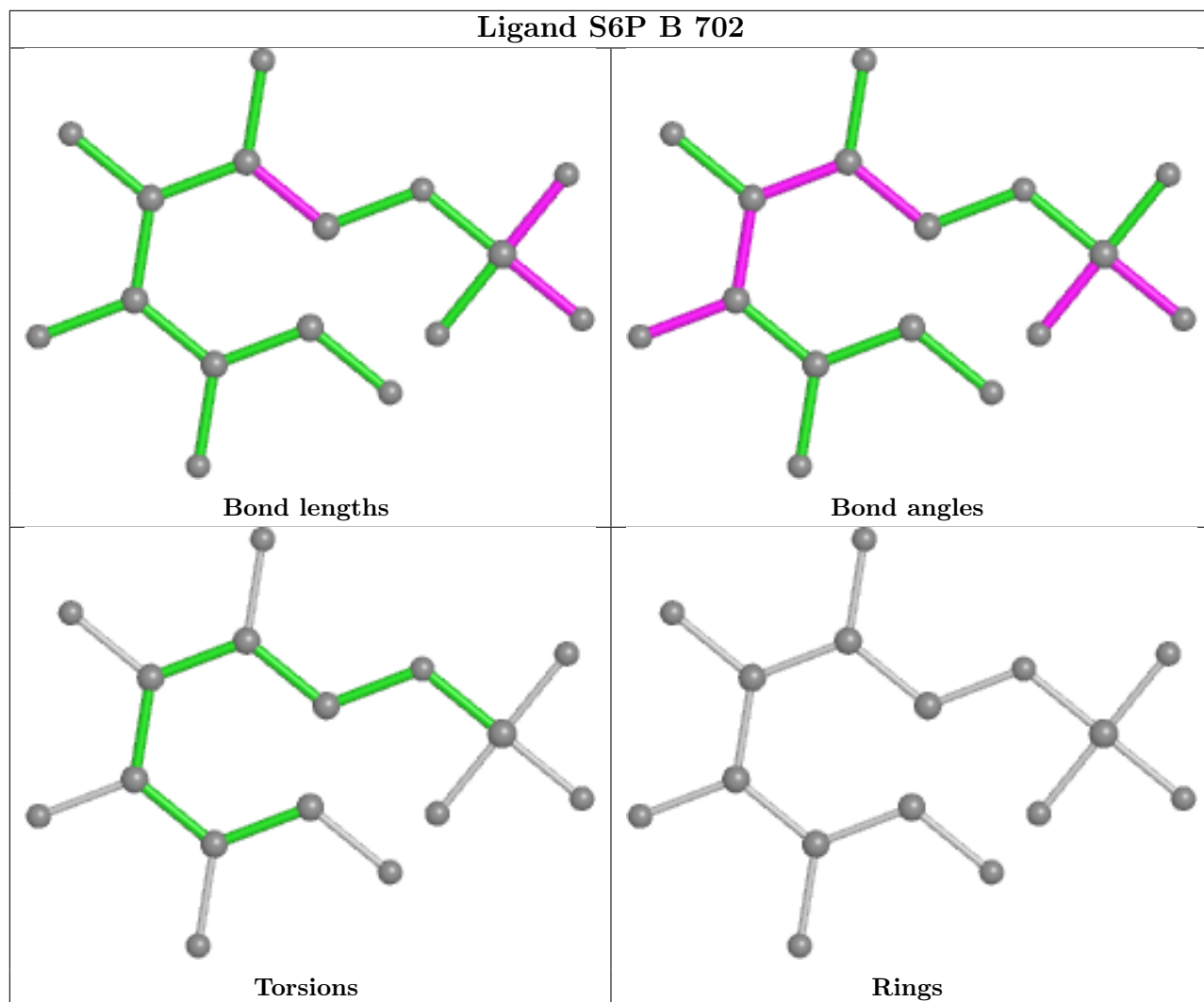
5 monomers are involved in 9 short contacts:

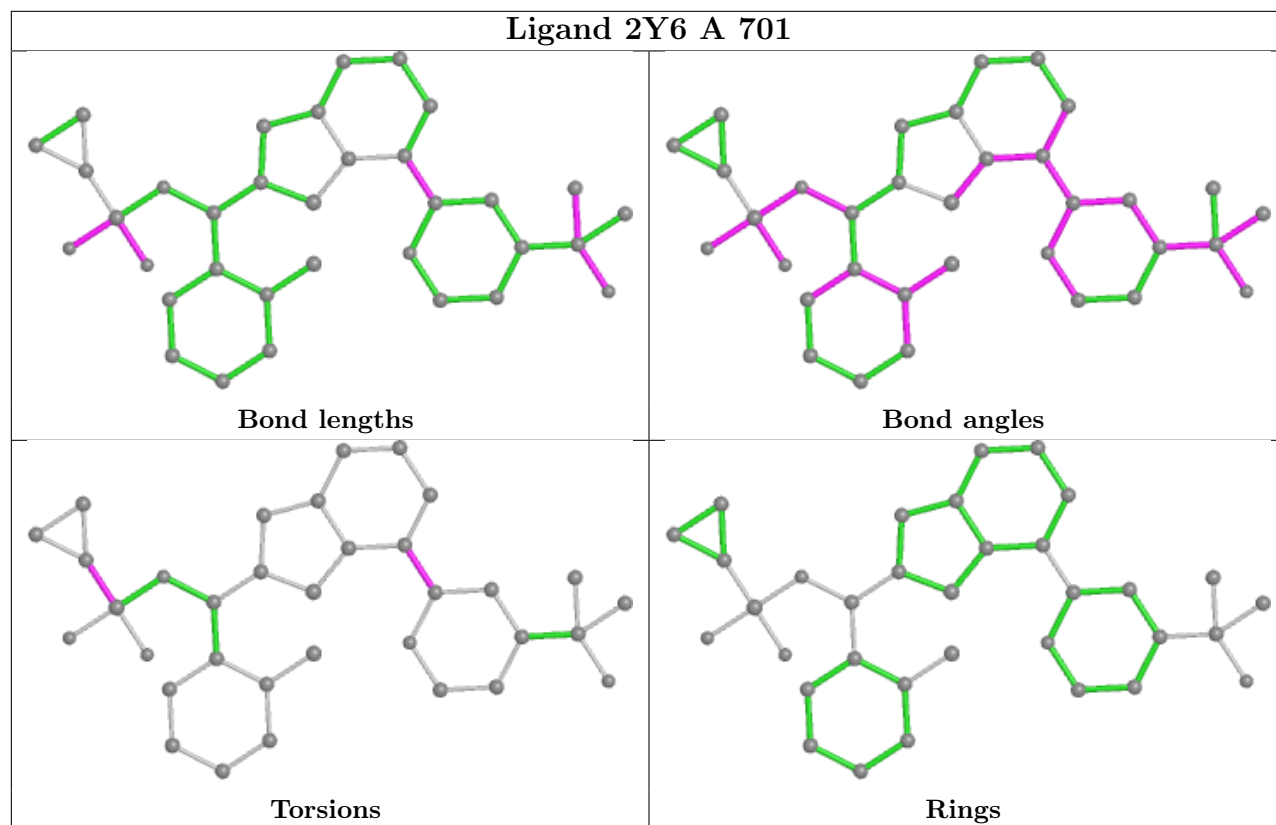
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	722	SO4	1	0
2	B	701	2Y6	4	0
3	A	702	S6P	1	0
3	B	702	S6P	1	0
2	A	701	2Y6	2	0

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	585/638 (91%)	-0.12	12 (2%) 63 58	37, 61, 104, 139	0
1	B	590/638 (92%)	-0.19	9 (1%) 73 70	34, 57, 86, 132	0
All	All	1175/1276 (92%)	-0.15	21 (1%) 68 64	34, 59, 96, 139	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	MET	7.0
1	B	2	PRO	5.1
1	B	66	GLN	4.2
1	A	1	MET	4.0
1	A	465	PHE	3.9
1	B	4	THR	3.8
1	A	2	PRO	3.4
1	A	430	THR	2.9
1	A	466	PHE	2.7
1	A	357	PHE	2.7
1	A	470	GLY	2.6
1	B	171	LYS	2.5
1	B	452	LEU	2.4
1	B	260	MET	2.4
1	A	264	SER	2.3
1	A	259	ARG	2.3
1	B	264	SER	2.2
1	A	449	LEU	2.2
1	A	404	ASP	2.2
1	A	69	SER	2.1
1	B	3	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 monosaccharides 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.

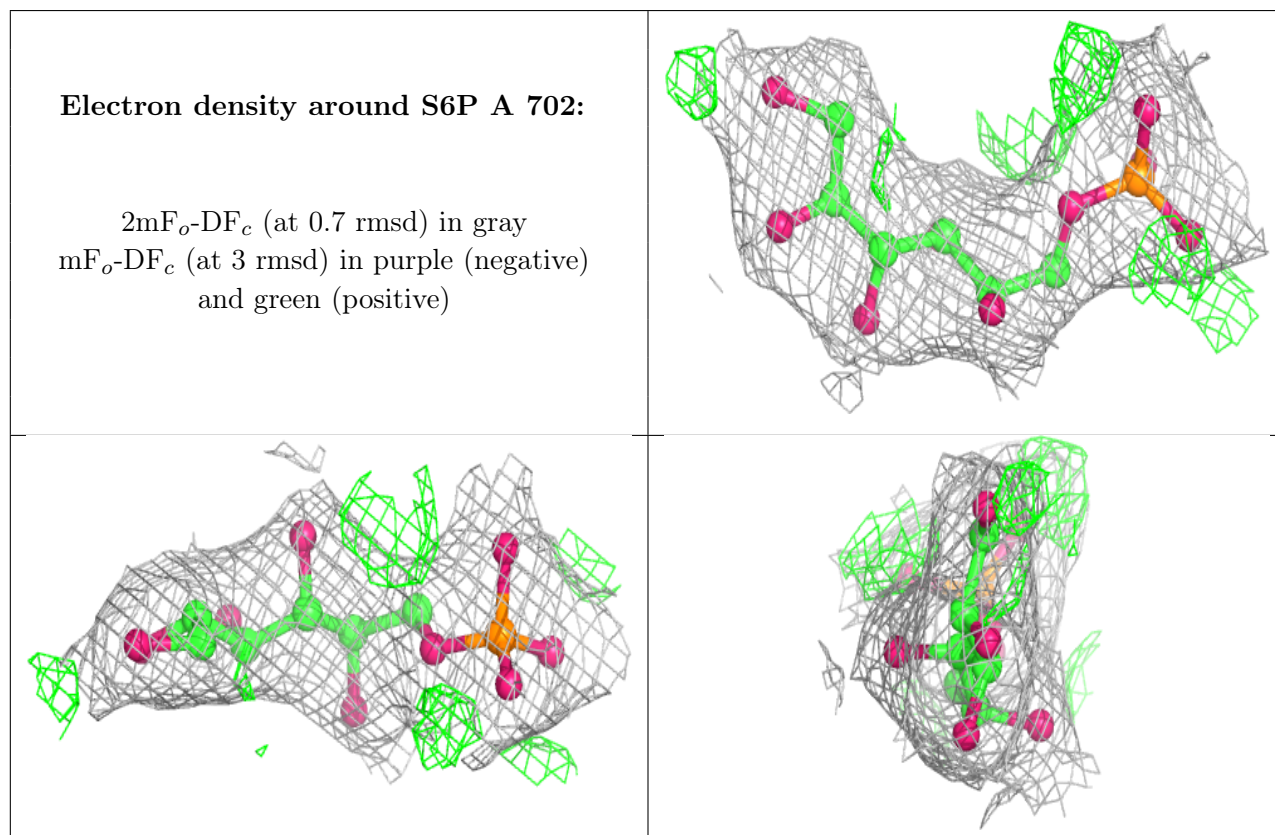
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	IOD	A	711	1/1	0.68	0.12	84,84,84,84	1
4	IOD	B	711	1/1	0.81	0.16	112,112,112,112	1
4	IOD	B	712	1/1	0.81	0.14	90,90,90,90	1
6	SO4	B	723	5/5	0.83	0.27	86,92,111,115	0
6	SO4	B	721	5/5	0.84	0.21	78,82,97,106	0
4	IOD	A	712	1/1	0.85	0.08	92,92,92,92	1
4	IOD	A	715	1/1	0.86	0.07	89,89,89,89	1
4	IOD	B	715	1/1	0.86	0.10	88,88,88,88	1
4	IOD	B	718	1/1	0.87	0.11	88,88,88,88	1
5	GOL	B	720	6/6	0.87	0.17	47,53,57,67	0
4	IOD	B	716	1/1	0.87	0.10	84,84,84,84	1
4	IOD	B	717	1/1	0.87	0.21	97,97,97,97	1
4	IOD	B	714	1/1	0.90	0.07	93,93,93,93	1
4	IOD	A	710	1/1	0.90	0.21	106,106,106,106	1
4	IOD	A	708	1/1	0.90	0.08	98,98,98,98	1
4	IOD	A	709	1/1	0.90	0.14	98,98,98,98	1
4	IOD	B	710	1/1	0.91	0.19	91,91,91,91	1
4	IOD	A	703	1/1	0.92	0.07	84,84,84,84	0
4	IOD	B	709	1/1	0.92	0.10	95,95,95,95	1
5	GOL	B	719	6/6	0.92	0.18	64,76,77,84	0
4	IOD	B	706	1/1	0.95	0.10	65,65,65,65	1
4	IOD	B	707	1/1	0.95	0.04	93,93,93,93	0
4	IOD	B	713	1/1	0.95	0.04	95,95,95,95	1
4	IOD	A	713	1/1	0.96	0.04	73,73,73,73	1
4	IOD	B	708	1/1	0.96	0.05	74,74,74,74	1
4	IOD	A	714	1/1	0.97	0.05	66,66,66,66	1
3	S6P	A	702	16/16	0.97	0.25	33,36,40,41	0

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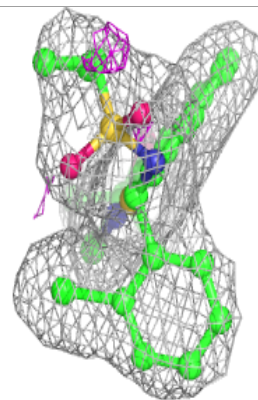
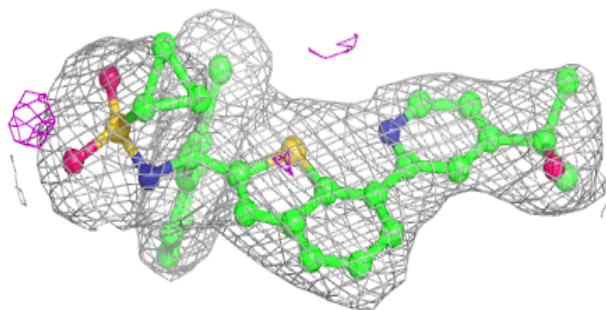
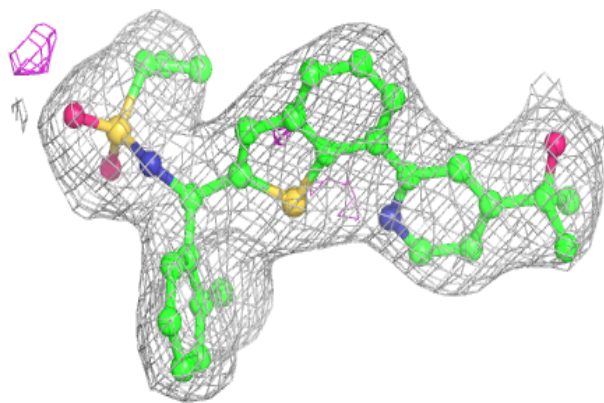
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	IOD	B	703	1/1	0.97	0.09	69,69,69,69	0
2	2Y6	B	701	34/34	0.97	0.15	36,43,47,53	0
6	SO4	B	722	5/5	0.97	0.19	36,37,40,41	5
4	IOD	A	706	1/1	0.97	0.06	99,99,99,99	0
4	IOD	A	707	1/1	0.98	0.07	66,66,66,66	1
2	2Y6	A	701	34/34	0.98	0.13	35,43,49,51	0
4	IOD	A	705	1/1	0.98	0.06	64,64,64,64	1
3	S6P	B	702	16/16	0.98	0.26	31,33,38,42	0
4	IOD	A	704	1/1	0.99	0.05	74,74,74,74	0
4	IOD	B	705	1/1	0.99	0.05	68,68,68,68	1
4	IOD	B	704	1/1	1.00	0.05	69,69,69,69	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.

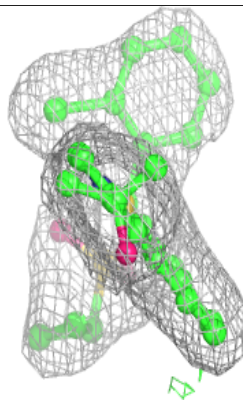
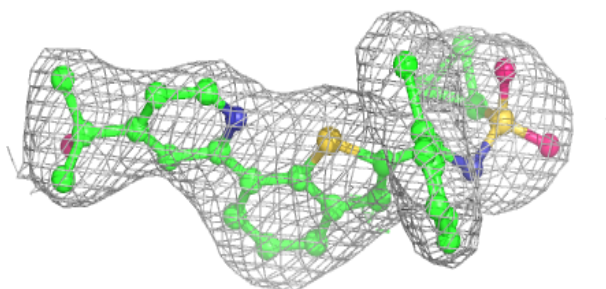
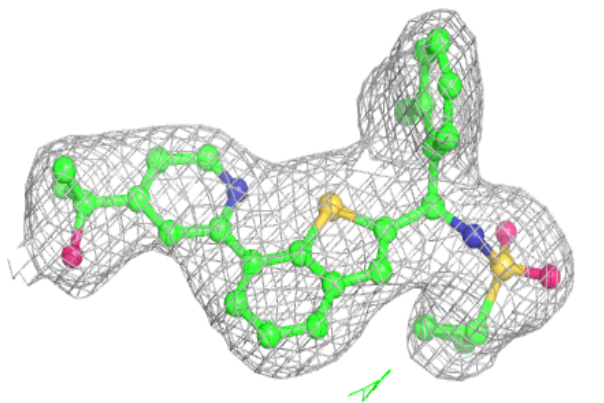


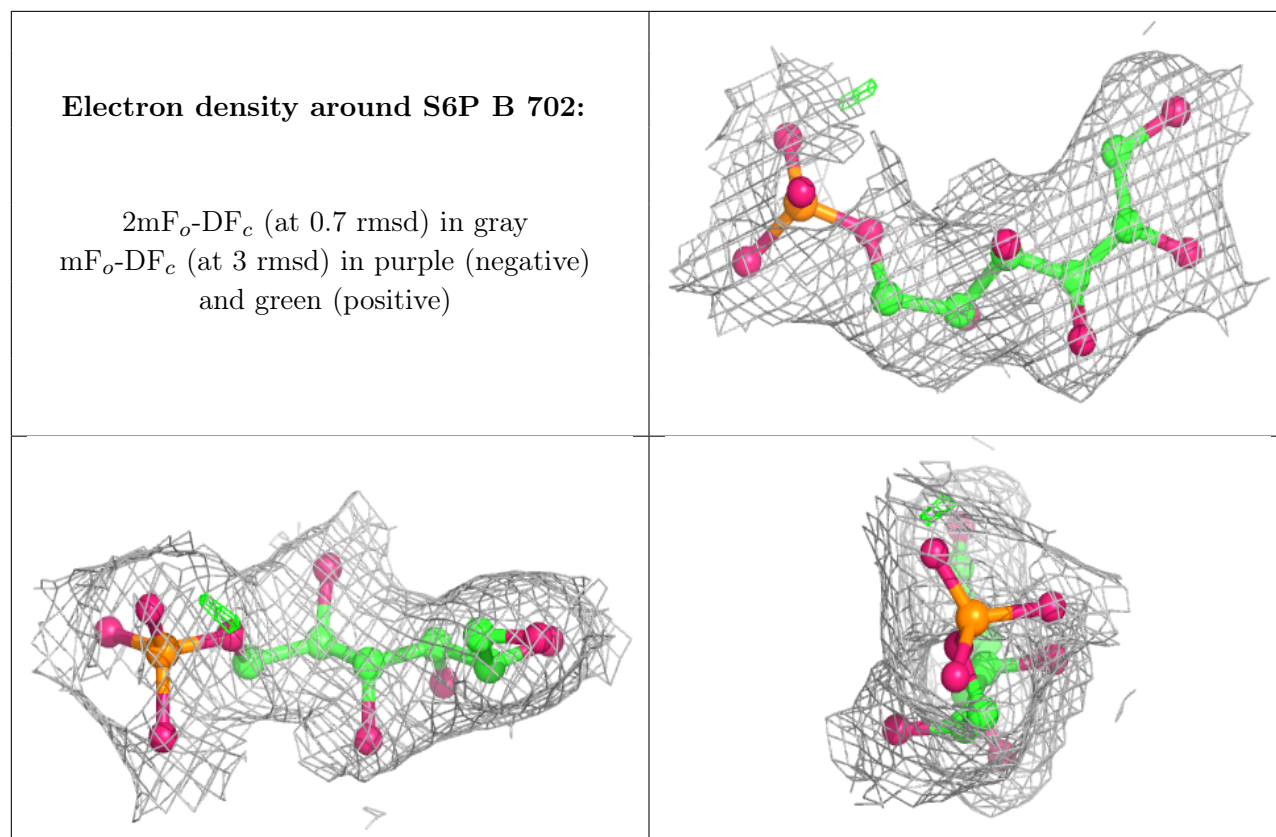
Electron density around 2Y6 B 701:

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

**Electron density around 2Y6 A 701:**

$2mF_o-DF_c$ (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.