



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 24, 2023 – 08:54 AM EDT

PDB ID : 5USF
Title : Leishmania donovani tyrosyl-tRNA synthetase in complex with nanobody and inhibitor
Authors : Barros-Alvarez, X.; Hol, W.G.J.
Deposited on : 2017-02-13
Resolution : 2.75 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)
Xtrriage (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

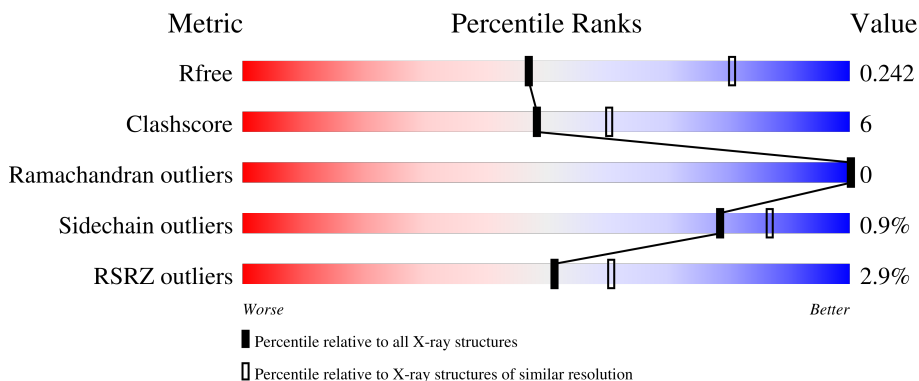
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

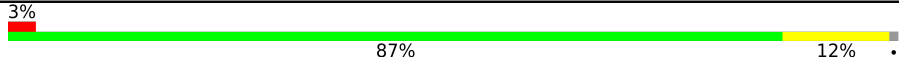

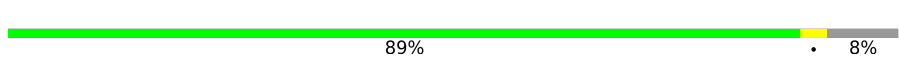

The reported resolution of this entry is 2.75 Å.

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	1235 (2.78-2.74)
Clashscore	141614	1277 (2.78-2.74)
Ramachandran outliers	138981	1257 (2.78-2.74)
Sidechain outliers	138945	1257 (2.78-2.74)
RSRZ outliers	127900	1207 (2.78-2.74)

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	686	 3% 87% 12% .
1	B	686	 3% 89% 10% .
2	C	128	 89% . 8%
2	D	128	 89% 5% 6%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12706 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 Tyrosyl-tRNA synthetase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	682	Total	C	N	O	S	0	0	0
			5225	3286	911	992	36			
1	B	680	Total	C	N	O	S	0	0	0
			5218	3283	910	989	36			

There are 14 discrepancies between the modelled and reference sequences:

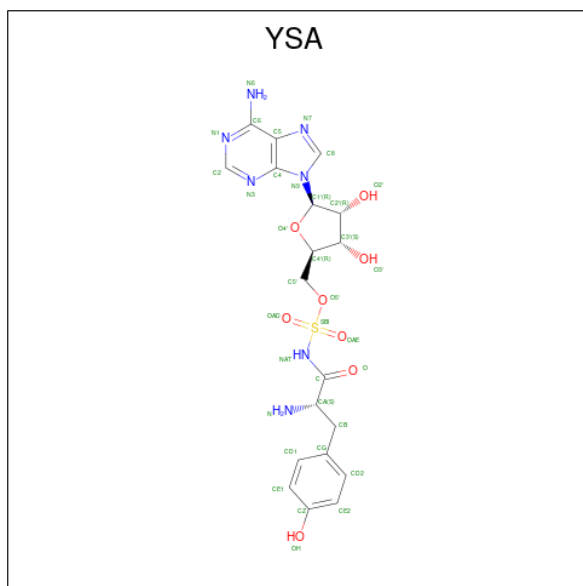
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP E9BC28
A	-2	PRO	-	expression tag	UNP E9BC28
A	-1	GLY	-	expression tag	UNP E9BC28
A	0	SER	-	expression tag	UNP E9BC28
A	5	GLU	ASP	conflict	UNP E9BC28
A	107	THR	MET	conflict	UNP E9BC28
A	681	ARG	LYS	conflict	UNP E9BC28
B	-3	GLY	-	expression tag	UNP E9BC28
B	-2	PRO	-	expression tag	UNP E9BC28
B	-1	GLY	-	expression tag	UNP E9BC28
B	0	SER	-	expression tag	UNP E9BC28
B	5	GLU	ASP	conflict	UNP E9BC28
B	107	THR	MET	conflict	UNP E9BC28
B	681	ARG	LYS	conflict	UNP E9BC28

- Molecule 2 is a protein called Immunoglobulin heavy chain variable region.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	118	Total	C	N	O	S	0	0	0
			910	566	164	176	4			
2	D	120	Total	C	N	O	S	0	0	0
			930	578	170	178	4			

- Molecule 3 is 5'-O-[N-(L-TYROSYL)SULFAMOYL]ADENOSINE (three-letter code: YSA)

(formula: C₁₉H₂₃N₇O₈S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	A	1	35	19	7	8	1	0	0
3	B	1	35	19	7	8	1	0	0

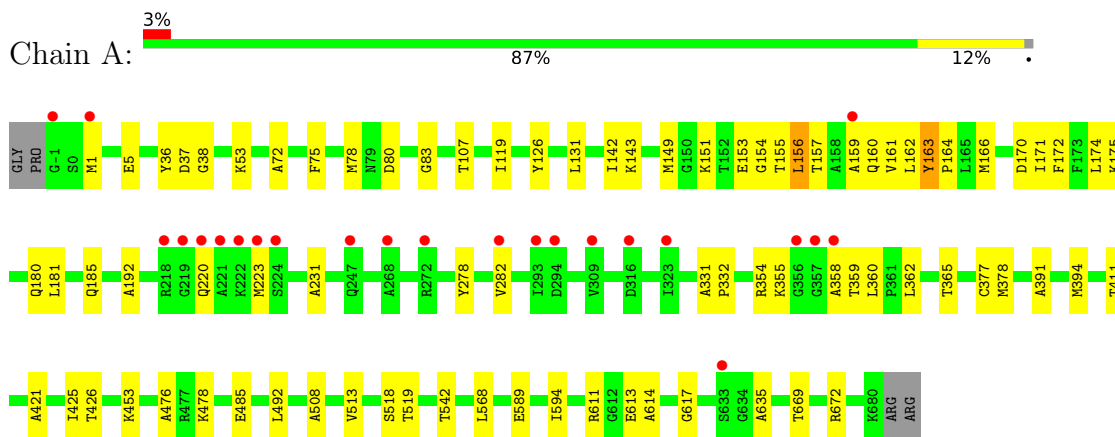
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	142	Total	O	0	0
			142	142		
4	B	148	Total	O	0	0
			148	148		
4	C	42	Total	O	0	0
			42	42		
4	D	21	Total	O	0	0
			21	21		

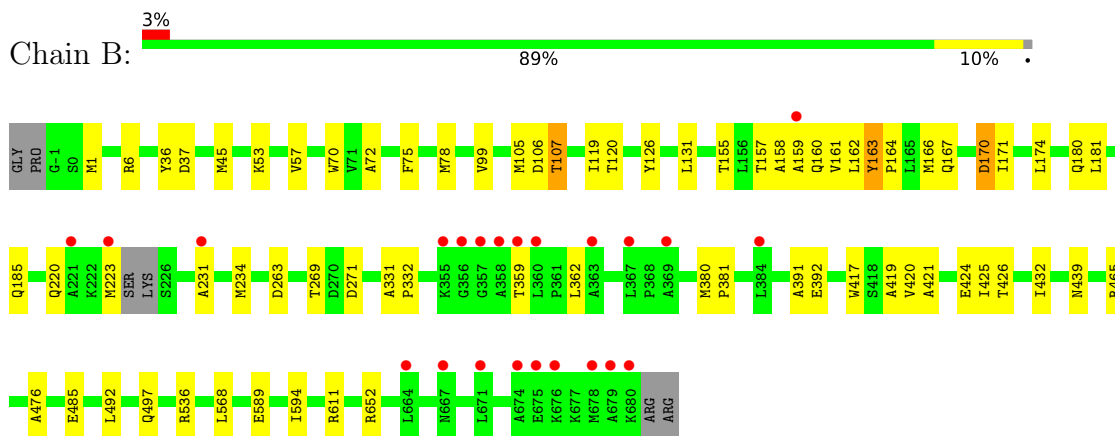
3 Residue-property plots [i](#)

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.

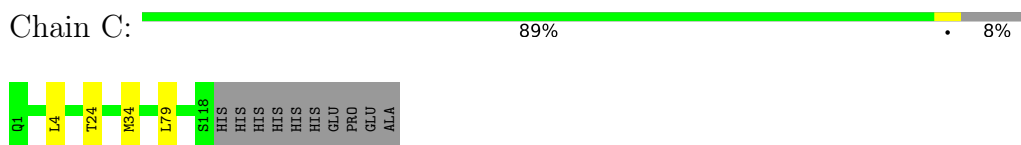
- Molecule 1: Tyrosyl-tRNA synthetase, putative




- Molecule 1: Tyrosyl-tRNA synthetase, putative



- Molecule 2: Immunoglobulin heavy chain variable region



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Chain D:  89% 5% 6%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	96.18Å 96.18Å 351.83Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	83.29 – 2.75 48.09 – 2.75	Depositor EDS
% Data completeness (in resolution range)	99.8 (83.29-2.75) 99.8 (48.09-2.75)	Depositor EDS
R_{merge}	0.21	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.77Å)	Xtrriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.189 , 0.244 0.190 , 0.242	Depositor DCC
R_{free} test set	2311 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	57.1	Xtrriage
Anisotropy	0.051	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 42.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.059 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12706	wwPDB-VP
Average B, all atoms (Å ²)	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.86% 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: YSA

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	0.55	0/5314	0.74	3/7202 (0.0%)
1	B	0.53	0/5306	0.74	5/7188 (0.1%)
2	C	0.52	0/928	0.71	0/1254
2	D	0.52	0/950	0.72	0/1284
All	All	0.54	0/12498	0.74	8/16928 (0.0%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	611	ARG	NE-CZ-NH2	6.68	123.64	120.30
1	A	360	LEU	N-CA-C	-6.58	93.22	111.00
1	B	170	ASP	C-N-CA	-5.82	107.15	121.70
1	B	536	ARG	NE-CZ-NH1	5.81	123.21	120.30
1	B	611	ARG	NE-CZ-NH1	-5.74	117.43	120.30
1	B	170	ASP	O-C-N	-5.66	113.64	122.70
1	A	156	LEU	N-CA-C	5.62	126.17	111.00
1	A	154	GLY	N-CA-C	-5.26	99.94	113.10

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	5225	0	5244	88	0
1	B	5218	0	5247	53	0
2	C	910	0	883	2	0
2	D	930	0	897	4	0
3	A	35	0	23	2	0
3	B	35	0	22	0	0
4	A	142	0	0	2	0
4	B	148	0	0	0	0
4	C	42	0	0	0	0
4	D	21	0	0	0	0
All	All	12706	0	12316	147	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 6.

All (147) 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:78:MET:CE	1:A:166:MET:HE3	1.54	1.35
1:A:78:MET:CE	1:A:166:MET:CE	2.28	1.12
1:A:78:MET:SD	1:A:166:MET:CE	2.39	1.11
1:A:78:MET:HE1	1:A:166:MET:CE	1.81	1.07
1:A:611:ARG:HB2	1:A:617:GLY:O	1.57	1.05
1:A:78:MET:HE1	1:A:166:MET:HE3	1.10	1.04
1:A:78:MET:SD	1:A:166:MET:HE1	2.01	1.01
1:B:160:GLN:O	1:B:164:PRO:HD2	1.65	0.95
1:A:589:GLU:OE1	1:A:589:GLU:N	2.01	0.93
1:A:354:ARG:HG3	1:A:355:LYS:HD3	1.52	0.88
1:A:519:THR:HA	1:A:542:THR:HG21	1.55	0.88
1:B:155:THR:HG22	1:B:155:THR:O	1.77	0.84
1:A:613:GLU:OE1	1:A:614:ALA:N	2.08	0.83
1:B:159:ALA:HB3	1:B:476:ALA:HB1	1.65	0.80
1:A:378:MET:HE2	1:A:394:MET:HG2	1.65	0.79
1:A:37:ASP:HA	1:A:181:LEU:HD11	1.69	0.75
1:A:78:MET:HE3	1:A:166:MET:HE3	1.68	0.75
1:A:391:ALA:CB	1:A:568:LEU:HD23	2.18	0.74
1:A:425:ILE:HG22	1:A:426:THR:HG23	1.69	0.74
1:A:519:THR:HA	1:A:542:THR:CG2	2.16	0.73
1:B:391:ALA:CB	1:B:568:LEU:HD23	2.18	0.73
1:A:278:TYR:O	1:A:282:VAL:HG12	1.90	0.71
1:B:159:ALA:CB	1:B:476:ALA:HB1	2.21	0.71
1:A:377:CYS:HB2	1:A:513:VAL:HG11	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37:ASP:HA	1:B:181:LEU:HD11	1.73	0.71
1:A:354:ARG:HG3	1:A:355:LYS:CD	2.20	0.71
1:A:37:ASP:OD1	1:A:181:LEU:HG	1.91	0.70
1:A:155:THR:HG22	1:A:156:LEU:N	2.07	0.69
1:A:611:ARG:CB	1:A:617:GLY:O	2.39	0.68
1:B:391:ALA:HB2	1:B:568:LEU:HD23	1.75	0.68
1:A:391:ALA:HB2	1:A:568:LEU:HD23	1.74	0.67
1:B:37:ASP:OD1	1:B:181:LEU:HG	1.94	0.67
1:B:589:GLU:O	1:B:594:ILE:HD13	1.93	0.67
1:B:170:ASP:O	1:B:171:ILE:C	2.25	0.67
1:A:613:GLU:CD	1:A:614:ALA:H	1.96	0.67
1:A:589:GLU:O	1:A:594:ILE:HD13	1.94	0.66
1:A:159:ALA:HB3	1:A:476:ALA:O	1.94	0.66
1:A:37:ASP:HA	1:A:181:LEU:CD1	2.25	0.66
1:A:143:LYS:HB3	1:A:153:GLU:HG3	1.76	0.66
1:A:155:THR:HG22	1:A:156:LEU:H	1.63	0.64
1:B:106:ASP:O	1:B:107:THR:HG22	1.97	0.63
1:A:157:THR:HG23	1:A:160:GLN:HB2	1.79	0.63
1:B:37:ASP:HA	1:B:181:LEU:CD1	2.29	0.63
1:A:355:LYS:HE3	4:A:926:HOH:O	1.99	0.62
1:A:170:ASP:O	1:A:171:ILE:C	2.30	0.62
1:A:142:ILE:HG21	1:A:161:VAL:HG13	1.81	0.61
1:A:611:ARG:HB2	1:A:617:GLY:C	2.22	0.60
1:A:155:THR:OG1	4:A:801:HOH:O	2.00	0.59
1:B:159:ALA:HB3	1:B:476:ALA:O	2.02	0.59
1:B:167:GLN:O	1:B:170:ASP:HB2	2.02	0.59
1:A:411:THR:HG22	1:A:453:LYS:HB2	1.85	0.58
1:B:45:MET:HE2	1:B:234:MET:HG3	1.85	0.58
1:B:45:MET:HE2	1:B:99:VAL:HG11	1.86	0.58
1:B:589:GLU:O	1:B:594:ILE:CD1	2.51	0.57
1:B:417:TRP:O	1:B:420:VAL:HG22	2.03	0.57
1:A:83:GLY:HA2	1:A:362:LEU:CD2	2.34	0.57
1:B:425:ILE:HG22	1:B:426:THR:HG23	1.86	0.56
1:A:611:ARG:NH2	1:A:635:ALA:O	2.36	0.56
1:A:149:MET:HE2	1:A:160:GLN:HG2	1.88	0.56
1:B:162:LEU:HG	1:B:166:MET:SD	2.45	0.56
1:A:1:MET:CE	1:A:5:GLU:HB3	2.36	0.55
1:A:172:PHE:CD1	1:A:172:PHE:N	2.73	0.55
1:A:589:GLU:O	1:A:594:ILE:CD1	2.56	0.54
1:B:359:THR:HG22	1:B:362:LEU:HB2	1.89	0.53
1:B:163:TYR:HB3	1:B:164:PRO:CD	2.38	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:THR:O	1:A:478:LYS:HE2	2.08	0.53
1:B:57:VAL:HG11	1:B:105:MET:CE	2.39	0.53
1:B:155:THR:O	1:B:155:THR:CG2	2.49	0.53
1:A:80:ASP:HB3	1:A:362:LEU:HD13	1.90	0.52
1:A:181:LEU:HD23	1:A:185:GLN:HG3	1.91	0.52
1:B:159:ALA:HB3	1:B:476:ALA:C	2.30	0.52
1:B:159:ALA:HB3	1:B:476:ALA:CB	2.37	0.52
1:B:1:MET:HG2	1:B:6:ARG:HG3	1.91	0.51
1:B:380:MET:HE3	1:B:381:PRO:HD2	1.92	0.51
1:A:589:GLU:H	1:A:589:GLU:CD	2.03	0.51
1:A:149:MET:HE3	1:A:163:TYR:CD2	2.46	0.51
1:A:78:MET:SD	1:A:166:MET:HE2	2.44	0.50
1:B:181:LEU:HD23	1:B:185:GLN:HG3	1.92	0.50
1:A:142:ILE:CG2	1:A:161:VAL:HG13	2.41	0.50
1:A:83:GLY:HA2	1:A:362:LEU:HD22	1.93	0.49
1:A:162:LEU:O	1:A:166:MET:HG3	2.12	0.49
1:A:155:THR:CG2	1:A:156:LEU:H	2.22	0.49
1:B:392:GLU:OE2	1:B:652:ARG:NH2	2.45	0.49
1:A:391:ALA:HB2	1:A:568:LEU:CD2	2.42	0.48
1:A:72:ALA:HB1	1:A:75:PHE:HB2	1.96	0.48
1:B:45:MET:CE	1:B:234:MET:HG3	2.44	0.48
1:A:107:THR:HG22	1:A:107:THR:O	2.13	0.48
1:A:161:VAL:O	1:A:164:PRO:HG2	2.14	0.48
1:A:354:ARG:C	1:A:355:LYS:HD2	2.33	0.48
1:A:391:ALA:CB	1:A:568:LEU:CD2	2.89	0.47
1:B:391:ALA:CB	1:B:568:LEU:CD2	2.91	0.47
1:B:72:ALA:HB1	1:B:75:PHE:HB2	1.95	0.47
1:A:223:MET:HB2	1:A:231:ALA:HB2	1.97	0.47
1:A:365:THR:O	1:A:478:LYS:CE	2.62	0.47
1:B:157:THR:HG22	1:B:158:ALA:O	2.13	0.47
1:B:223:MET:HB2	1:B:231:ALA:HB2	1.96	0.47
1:A:508:ALA:O	1:A:513:VAL:HG22	2.14	0.47
1:B:159:ALA:CB	1:B:476:ALA:O	2.63	0.47
2:D:119:HIS:O	2:D:120:HIS:CG	2.67	0.47
1:A:611:ARG:CD	1:A:617:GLY:O	2.63	0.47
1:A:613:GLU:CG	1:A:614:ALA:N	2.78	0.47
2:C:4:LEU:HD23	2:C:24:THR:HG22	1.97	0.47
1:A:358:ALA:O	1:A:359:THR:OG1	2.29	0.47
1:A:163:TYR:OH	3:A:701:YSA:N	2.48	0.46
1:A:613:GLU:O	1:A:614:ALA:HB3	2.16	0.45
2:D:4:LEU:HD23	2:D:24:THR:HG22	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:GLN:O	1:A:164:PRO:HD2	2.16	0.45
1:A:174:LEU:O	1:A:175:LYS:HB2	2.16	0.45
1:B:57:VAL:HG11	1:B:105:MET:HE1	1.97	0.45
1:B:75:PHE:HA	1:B:78:MET:HE3	1.99	0.44
1:A:151:LYS:HD2	1:A:156:LEU:HD11	2.00	0.44
1:B:331:ALA:HB3	1:B:332:PRO:HD3	1.99	0.43
1:B:380:MET:HE1	1:B:439:ASN:HB3	1.99	0.43
1:B:391:ALA:HB2	1:B:568:LEU:CD2	2.44	0.43
1:B:131:LEU:HD13	1:B:421:ALA:HB2	2.01	0.43
1:B:120:THR:HG23	1:B:465:ARG:HB3	1.99	0.43
1:A:669:THR:HG22	1:A:672:ARG:NH2	2.34	0.43
1:B:419:ALA:O	1:B:424:GLU:HG2	2.18	0.43
1:A:425:ILE:HG22	1:A:426:THR:N	2.34	0.43
1:A:1:MET:HE1	1:A:5:GLU:HB3	2.00	0.42
1:A:163:TYR:C	1:A:163:TYR:CD1	2.93	0.42
1:B:70:TRP:CZ3	1:B:174:LEU:HD21	2.54	0.42
1:B:269:THR:HG22	1:B:271:ASP:H	1.84	0.42
1:A:149:MET:CE	1:A:160:GLN:HG2	2.49	0.42
1:B:161:VAL:HG23	1:B:162:LEU:N	2.35	0.42
1:A:80:ASP:HB3	1:A:362:LEU:CD1	2.49	0.42
1:A:119:ILE:HG23	1:A:126:TYR:CD2	2.55	0.42
1:A:354:ARG:O	1:A:355:LYS:HD2	2.19	0.42
1:B:485:GLU:HG2	1:B:492:LEU:HD12	2.01	0.42
1:B:57:VAL:HB	1:B:105:MET:CE	2.50	0.41
2:D:18:LEU:HB2	2:D:83:MET:HE3	2.03	0.41
1:A:485:GLU:HG2	1:A:492:LEU:HD12	2.03	0.41
1:B:159:ALA:HB3	1:B:476:ALA:CA	2.49	0.41
1:A:171:ILE:HD12	1:A:192:ALA:HB2	2.02	0.41
1:B:492:LEU:HD22	1:B:497:GLN:HB2	2.03	0.41
1:A:149:MET:HE2	1:A:160:GLN:CG	2.51	0.41
1:A:131:LEU:HD13	1:A:421:ALA:HB2	2.03	0.41
1:A:142:ILE:HG21	1:A:161:VAL:CG1	2.48	0.41
1:B:420:VAL:HG12	1:B:432:ILE:HD12	2.03	0.41
1:A:38:GLY:HA3	3:A:701:YSA:CD2	2.51	0.41
1:A:613:GLU:O	1:A:614:ALA:CB	2.68	0.41
1:B:119:ILE:HG23	1:B:126:TYR:CD2	2.55	0.41
1:A:331:ALA:HB3	1:A:332:PRO:HD3	2.01	0.40
1:A:611:ARG:O	1:A:617:GLY:HA2	2.21	0.40
1:A:518:SER:O	1:A:542:THR:HG22	2.21	0.40
2:C:34:MET:HB3	2:C:79:LEU:HD22	2.04	0.40
2:D:119:HIS:O	2:D:120:HIS:CB	2.69	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	680/686 (99%)	662 (97%)	18 (3%)	0	100	100
1	B	676/686 (98%)	650 (96%)	26 (4%)	0	100	100
2	C	116/128 (91%)	114 (98%)	2 (2%)	0	100	100
2	D	118/128 (92%)	117 (99%)	1 (1%)	0	100	100
All	All	1590/1628 (98%)	1543 (97%)	47 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	552/558 (99%)	547 (99%)	5 (1%)	78	87
1	B	552/558 (99%)	545 (99%)	7 (1%)	69	81
2	C	97/106 (92%)	97 (100%)	0	100	100
2	D	99/106 (93%)	99 (100%)	0	100	100
All	All	1300/1328 (98%)	1288 (99%)	12 (1%)	78	87

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	36	TYR
1	A	53	LYS
1	A	163	TYR
1	A	180	GLN
1	A	220	GLN
1	B	36	TYR
1	B	53	LYS
1	B	107	THR
1	B	163	TYR
1	B	180	GLN
1	B	220	GLN
1	B	263	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

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	YSA	B	701	-	35,38,38	0.75	0	40,56,56	0.85	2 (5%)
3	YSA	A	701	-	35,38,38	0.80	0	40,56,56	1.16	4 (10%)

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	YSA	B	701	-	-	9/18/39/39	0/4/4/4
3	YSA	A	701	-	-	3/18/39/39	0/4/4/4

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	YSA	CB-CA-C	3.94	118.19	108.97
3	A	701	YSA	C-CA-N	-2.80	98.58	109.40
3	A	701	YSA	C-NAT-SBI	-2.50	120.56	124.61
3	A	701	YSA	C5-C6-N6	2.40	124.00	120.35
3	B	701	YSA	C5-C6-N6	2.36	123.93	120.35
3	B	701	YSA	C-NAT-SBI	2.28	128.30	124.61

There are no chirality outliers.

All (12) torsion outliers are listed below:

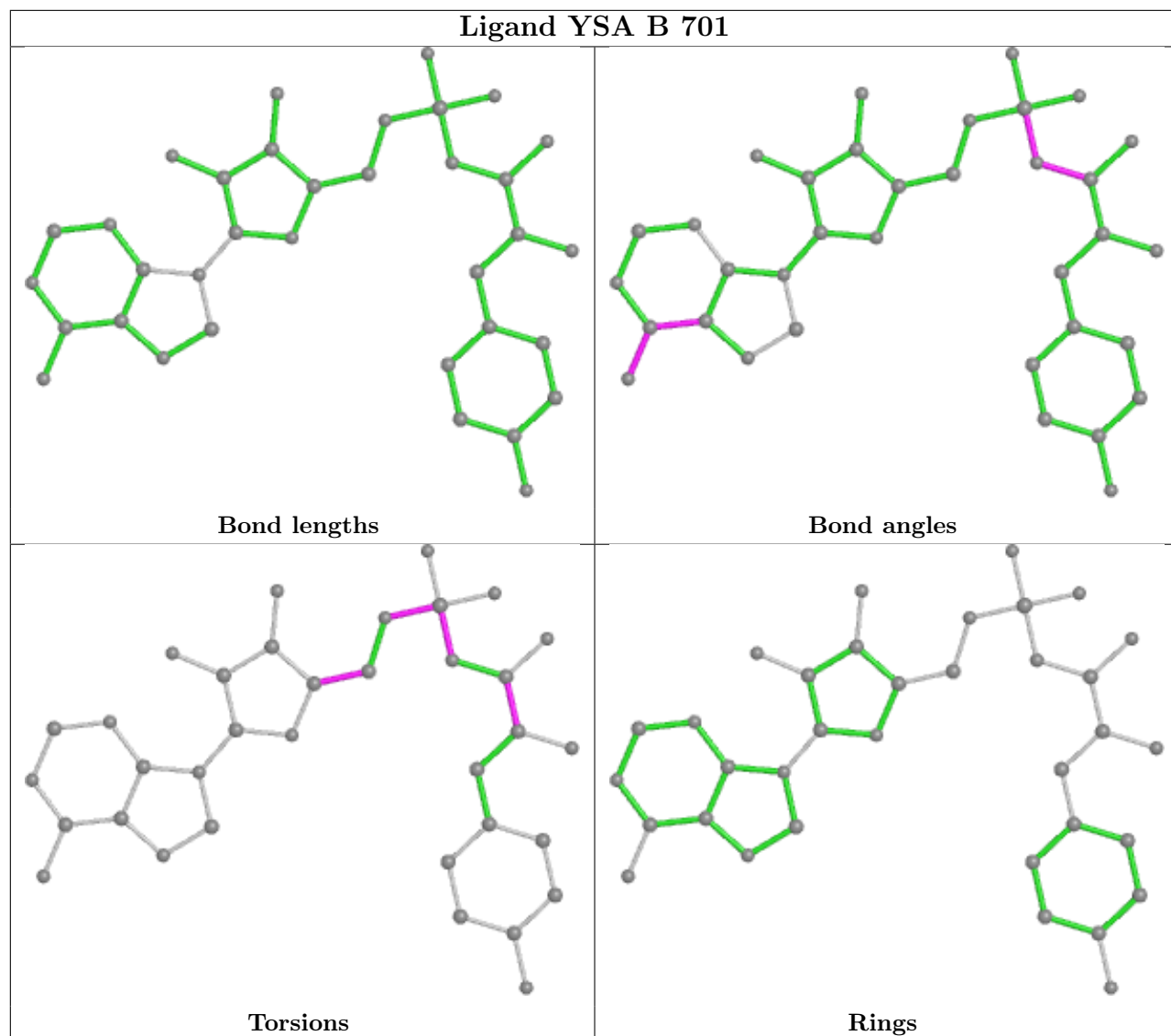
Mol	Chain	Res	Type	Atoms
3	A	701	YSA	O-C-CA-CB
3	A	701	YSA	NAT-C-CA-CB
3	B	701	YSA	O-C-CA-CB
3	B	701	YSA	NAT-C-CA-CB
3	B	701	YSA	C-NAT-SBI-OAD
3	B	701	YSA	C-NAT-SBI-OAE
3	B	701	YSA	C5'-O5'-SBI-NAT
3	B	701	YSA	C5'-O5'-SBI-OAD
3	B	701	YSA	O4'-C4'-C5'-O5'
3	B	701	YSA	C3'-C4'-C5'-O5'
3	A	701	YSA	N-CA-CB-CG
3	B	701	YSA	C5'-O5'-SBI-OAE

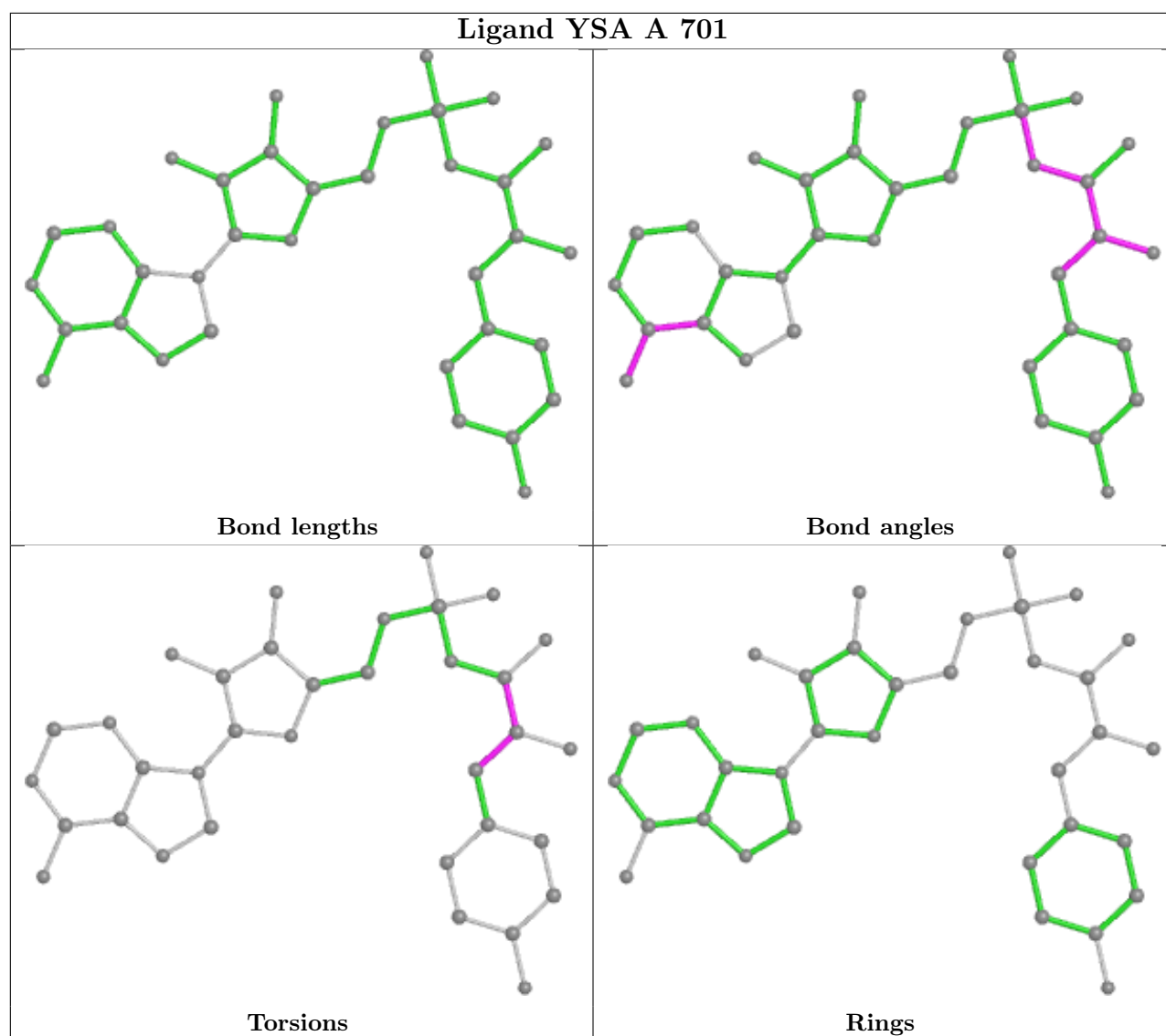
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	701	YSA	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	682/686 (99%)	0.14	23 (3%) 45 53	37, 64, 104, 153	0
1	B	680/686 (99%)	0.07	23 (3%) 45 53	38, 64, 114, 177	0
2	C	118/128 (92%)	-0.31	0 100 100	33, 49, 69, 83	0
2	D	120/128 (93%)	-0.27	0 100 100	36, 51, 82, 123	0
All	All	1600/1628 (98%)	0.05	46 (2%) 51 61	33, 62, 106, 177	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	675	GLU	8.3
1	B	359	THR	8.2
1	A	356	GLY	6.9
1	A	357	GLY	6.5
1	B	363	ALA	5.7
1	A	223	MET	5.0
1	A	222	LYS	5.0
1	B	221	ALA	4.4
1	B	676	LYS	4.1
1	B	680	LYS	4.1
1	B	358	ALA	3.9
1	B	674	ALA	3.9
1	B	679	ALA	3.9
1	B	671	LEU	3.8
1	A	268	ALA	3.5
1	A	220	GLN	3.5
1	A	221	ALA	3.3
1	B	678	MET	3.2
1	B	223	MET	3.2
1	A	294	ASP	3.1
1	B	367	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	219	GLY	2.8
1	A	159	ALA	2.7
1	B	357	GLY	2.7
1	A	218	ARG	2.6
1	A	282	VAL	2.6
1	A	309	VAL	2.5
1	A	247	GLN	2.5
1	B	355	LYS	2.5
1	A	358	ALA	2.4
1	B	369	ALA	2.4
1	B	667	ASN	2.4
1	B	664	LEU	2.4
1	A	1	MET	2.3
1	A	272	ARG	2.3
1	B	384	LEU	2.3
1	A	316	ASP	2.3
1	B	360	LEU	2.2
1	A	-1	GLY	2.2
1	A	633	SER	2.2
1	A	224	SER	2.2
1	A	293	ILE	2.2
1	A	323	ILE	2.1
1	B	231	ALA	2.1
1	B	159	ALA	2.0
1	B	356	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](#)

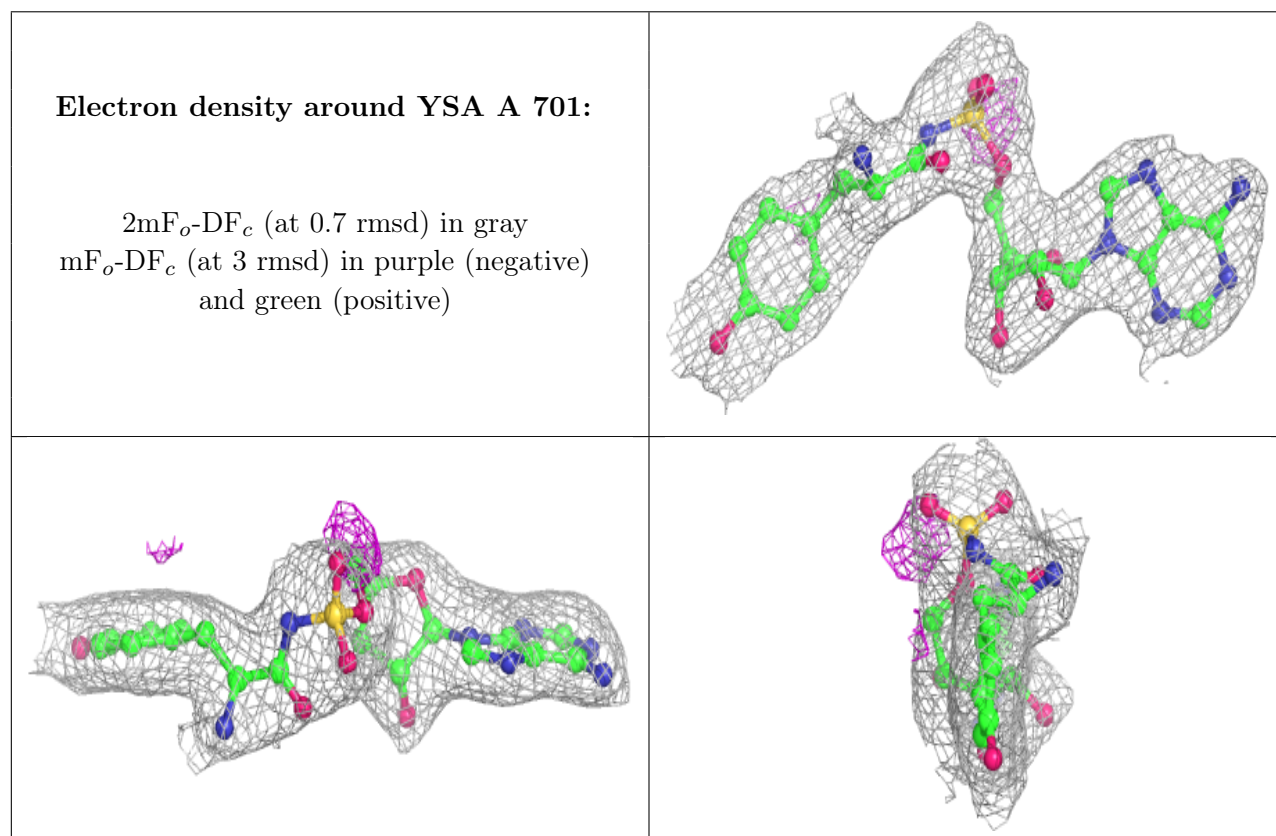
There are no monosaccharides in this entry.

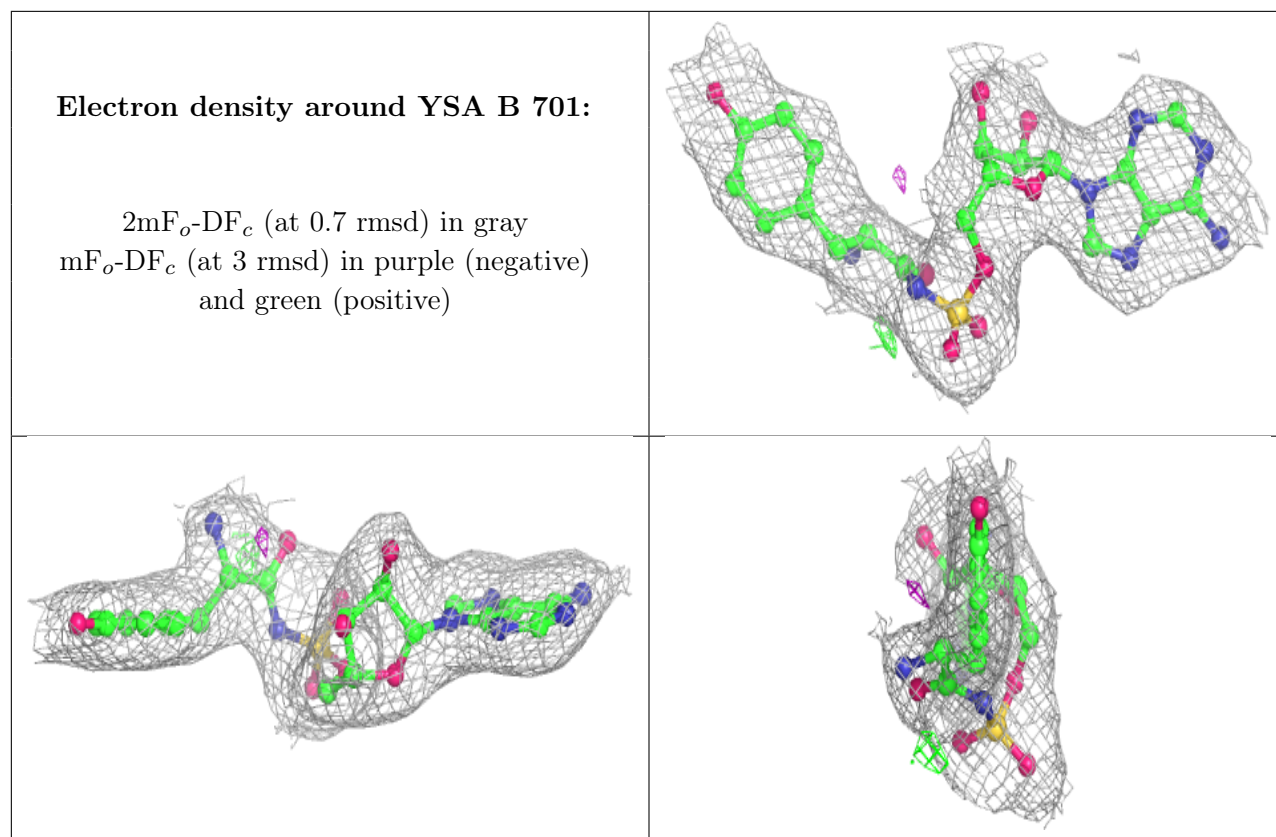
6.4 Ligands [i](#)

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(\AA^2)	Q<0.9
3	YSA	A	701	35/35	0.96	0.14	36,52,57,60	0
3	YSA	B	701	35/35	0.97	0.14	36,50,57,65	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 [i](#)

There are no such residues in this entry.