Full wwPDB X-ray Structure Validation Report (i)

Oct 4, 2023 – 02:14 PM EDT

PDB ID	:	6P0P
Title	:	Human beta-tryptase co-crystal structure with 5-{4-[3-(aminomethyl)phenyl] piperidine-1-carbonyl}-2-(3'-{4-[3-(aminomethyl)phenyl]piperidine-1-carbonyl }-[1,1'-biphenyl]-3-yl)-2-hydroxy-2H-1,3,2-benzodioxaborol-2-uide
Authors	:	Giardina, S.F.; Pingle, M.R.; Werner, D.S.; Feinberg, P.B.; Foreman, K.W.; Bergstrom, D.E.; Arnold, L.D.; Barany, F.
Deposited on	:	2019-05-17
Resolution	:	2.55 Å(reported)

The following versions of software and data (see references ①) were used in the production of this report:

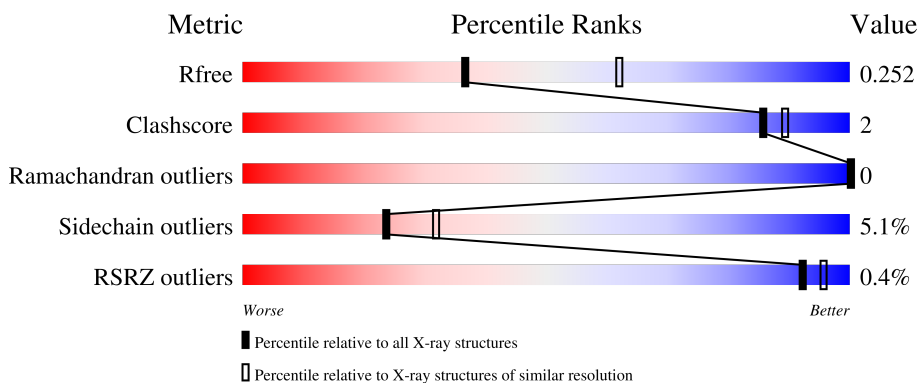|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & 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 2.55 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	Percentile Ranks	Value
Rfree		0.252
Clashscore		2
Ramachandran outliers		0
Sidechain outliers		5.1%
RSRZ outliers		0.4%

Worse ← → *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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 <=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	275	82%　　6%　12%
1	B	275	81%　　7%　12%

2 Entry composition ⓘ

There are 6 unique types of molecules in this entry. The entry contains 4128 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 Tryptase alpha/beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	243	Total	C	N	O	S	0	0	0
			1907	1221	334	340	12			
1	B	243	Total	C	N	O	S	0	0	0
			1905	1218	336	339	12			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	132	LYS	ASN	conflict	UNP Q15661
B	132	LYS	ASN	conflict	UNP Q15661

- Molecule 2 is (3'-{4-[3-(aminomethyl)phenyl]piperidine-1-carbonyl}[1,1'-biphenyl]-3-yl){4-[3-(aminomethyl)phenyl]piperidin-1-yl}[3,4-di(hydroxy-kappaO)phenyl]methanonato(2-)hydroxyborate(1-) (three-letter code: Y35) (formula: $C_{44}H_{46}BN_4O_5$) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	B	C	N	O	0	1
			108	2	88	8	10		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

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

- Molecule 4 is TRIETHYLENE GLYCOL (three-letter code: PGE) (formula: $C_6H_{14}O_4$).

PGE

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 10	C 6	O 4	0	0
4	B	1	Total 10	C 6	O 4	0	0

- Molecule 5 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).

MES
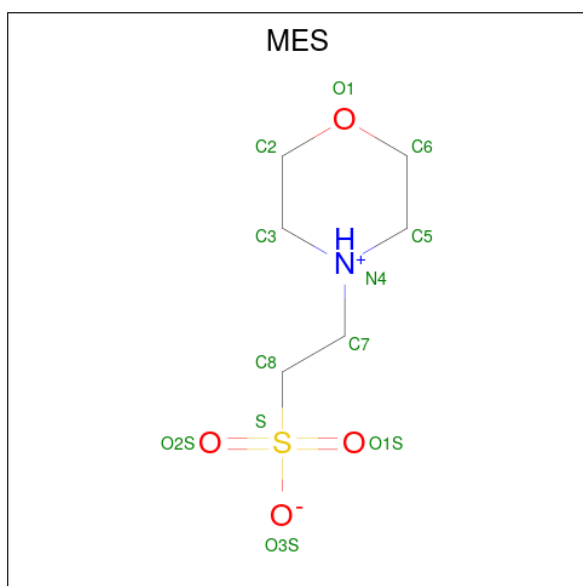
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total 12	C 6	N 1	O 4	S 1	0	0

• Molecule 6 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	87	Total 87	O 87	0	0
6	B	74	Total 74	O 74	0	0

3 Residue-property plots ⓘ

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

• Molecule 1: Tryptase alpha/beta-1
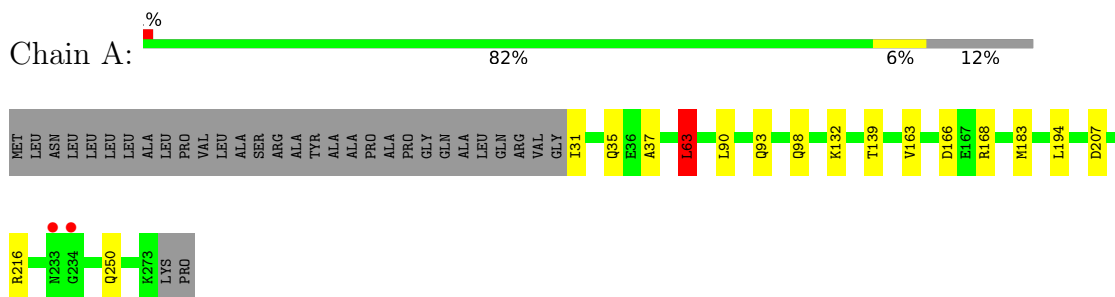
• Molecule 1: Tryptase alpha/beta-1
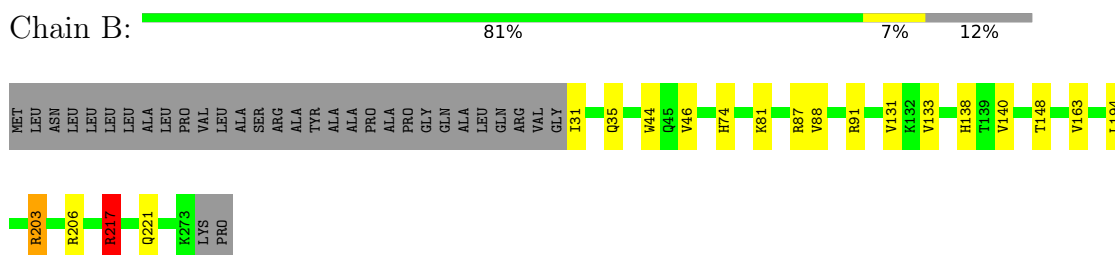
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	78.10Å 78.10Å 165.18Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.68 – 2.55 29.68 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.9 (29.68-2.55) 100.0 (29.68-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$< I/\sigma(I) >$ [1]	2.03 (at 2.54Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.180 , 0.249 0.187 , 0.252	Depositor DCC
R_{free} test set	1006 reflections (5.12%)	wwPDB-VP
Wilson B-factor (Å^2)	33.6	Xtriage
Anisotropy	0.103	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 25.1	EDS
L-test for twinning[2]	$< |L| > = 0.50, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.026 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	4128	wwPDB-VP
Average B, all atoms (Å^2)	33.0	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.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: Y35, PGE, SO4, MES

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	0.67	0/1971	0.86	2/2704 (0.1%)
1	B	0.66	0/1969	0.83	2/2701 (0.1%)
All	All	0.67	0/3940	0.84	4/5405 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	217	ARG	NE-CZ-NH2	6.38	123.49	120.30
1	A	63	LEU	CA-CB-CG	5.32	127.55	115.30
1	B	203	ARG	NE-CZ-NH2	5.25	122.93	120.30
1	A	207	ASP	CB-CG-OD1	5.12	122.90	118.30

There are no chirality outliers.

There are no planarity outliers.

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	1907	0	1828	3	0
1	B	1905	0	1826	9	0
2	A	108	0	0	4	0
3	A	5	0	0	0	0
3	B	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	10	0	14	0	0
4	B	10	0	14	3	0
5	B	12	0	13	0	0
6	A	87	0	0	0	0
6	B	74	0	0	4	0
All	All	4128	0	3695	17	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 2.

All (17) 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:63:LEU:HD13	1:A:139:THR:HG22	1.78	0.65
2:A:301[B]:Y35:C23	2:A:301[B]:Y35:O3	2.45	0.64
1:B:133:VAL:HG13	1:B:138:HIS:HB3	1.86	0.57
1:B:74:HIS:HB2	4:B:304:PGE:H4	1.92	0.51
2:A:301[A]:Y35:C23	2:A:301[A]:Y35:O3	2.54	0.50
2:A:301[A]:Y35:C19	2:A:301[A]:Y35:O2	2.58	0.49
1:B:74:HIS:CB	4:B:304:PGE:H4	2.43	0.49
4:B:304:PGE:H5	6:B:428:HOH:O	2.12	0.49
1:B:217:ARG:CD	6:B:454:HOH:O	2.64	0.46
2:A:301[A]:Y35:C15	2:A:301[A]:Y35:C10	2.94	0.45
1:B:217:ARG:HD2	6:B:454:HOH:O	2.19	0.42
1:B:44:TRP:CD2	1:B:140:VAL:HB	2.55	0.42
1:B:46:VAL:HG13	1:B:88:VAL:HG13	2.02	0.42
1:B:203:ARG:NH2	6:B:408:HOH:O	2.53	0.42
1:A:31:ILE:O	1:A:163:VAL:HA	2.20	0.40
1:A:37:ALA:O	1:A:93:GLN:NE2	2.44	0.40
1:B:31:ILE:O	1:B:163:VAL:HA	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	241/275 (88%)	232 (96%)	9 (4%)	0	100	100
1	B	241/275 (88%)	232 (96%)	9 (4%)	0	100	100
All	All	482/550 (88%)	464 (96%)	18 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	205/231 (89%)	194 (95%)	11 (5%)	22	29
1	B	205/231 (89%)	195 (95%)	10 (5%)	25	34
All	All	410/462 (89%)	389 (95%)	21 (5%)	24	32

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	63	LEU
1	A	90	LEU
1	A	98	GLN
1	A	132	LYS
1	A	166	ASP
1	A	168	ARG
1	A	183	MET
1	A	194	LEU
1	A	216	ARG
1	A	250	GLN
1	B	35	GLN
1	B	81	LYS
1	B	87	ARG
1	B	91	ARG

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Mol	Chain	Res	Type
1	B	131	VAL
1	B	148	THR
1	B	194	LEU
1	B	206	ARG
1	B	217	ARG
1	B	221	GLN

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

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 monosaccharides in this entry.

5.6   Ligand geometry ⓘ

8 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	#$|Z| > 2$
4	PGE	A	303	-	9,9,9	0.64	0	8,8,8	0.62	0
4	PGE	B	304	-	9,9,9	0.72	0	8,8,8	1.34	1 (12%)
5	MES	B	303	-	12,12,12	1.78	1 (8%)	14,16,16	2.05	2 (14%)
3	SO4	B	302	-	4,4,4	0.39	0	6,6,6	0.18	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	#|Z| > 2	Counts	RMSZ	#|Z| > 2
2	Y35	A	301[B]	-	57,61,61	0.66	1 (1%)	82,88,88	1.55	17 (20%)
3	SO4	B	301	-	4,4,4	0.49	0	6,6,6	0.40	0
2	Y35	A	301[A]	-	57,61,61	0.69	1 (1%)	82,88,88	1.88	21 (25%)
3	SO4	A	302	-	4,4,4	0.52	0	6,6,6	0.43	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
4	PGE	A	303	-	-	4/7/7/7	-
4	PGE	B	304	-	-	5/7/7/7	-
5	MES	B	303	-	-	1/6/14/14	0/1/1/1
2	Y35	A	301[B]	-	-	9/38/68/68	0/8/8/8
2	Y35	A	301[A]	-	-	2/38/68/68	0/8/8/8

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	303	MES	C8-S	-5.44	1.69	1.77
2	A	301[B]	Y35	C17-C16	3.22	1.47	1.39
2	A	301[A]	Y35	C17-C16	3.11	1.47	1.39

All (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	303	MES	O3S-S-C8	5.71	115.00	105.77
2	A	301[A]	Y35	C19-C18-C23	5.09	122.15	116.22
2	A	301[A]	Y35	C9-C10-N2	-4.94	103.32	110.82
2	A	301[B]	Y35	C34-C35-N3	-4.92	103.34	110.82
2	A	301[B]	Y35	O3-B-O4	4.66	121.58	109.55
2	A	301[A]	Y35	C25-C24-C22	-4.27	113.96	121.36
2	A	301[B]	Y35	C19-C18-C23	4.08	120.98	116.22
2	A	301[A]	Y35	C12-C11-N2	-3.92	104.87	110.82
2	A	301[A]	Y35	C34-C35-N3	-3.70	105.20	110.82
2	A	301[A]	Y35	B-O4-C16	-3.63	104.16	106.72
2	A	301[A]	Y35	C29-C24-C22	3.56	126.75	120.86
2	A	301[A]	Y35	C28-C30-N3	3.47	123.13	118.72
2	A	301[A]	Y35	C23-C22-C24	3.41	126.51	120.86
2	A	301[A]	Y35	O3-B-O2	3.38	118.30	109.55

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301[A]	Y35	C22-C23-C18	-3.25	119.05	122.00
2	A	301[B]	Y35	C32-C31-N3	-3.24	105.90	110.82
5	B	303	MES	O3S-S-O2S	-3.23	103.37	111.27
2	A	301[B]	Y35	C9-C10-N2	-3.02	106.23	110.82
2	A	301[A]	Y35	C21-C22-C24	-3.00	116.17	121.36
2	A	301[A]	Y35	C44-C14-C15	2.92	122.69	119.24
2	A	301[A]	Y35	O2-C17-C43	2.80	131.34	127.83
2	A	301[B]	Y35	C25-C24-C22	-2.70	116.67	121.36
2	A	301[A]	Y35	C37-C36-C33	2.67	125.89	120.73
2	A	301[B]	Y35	C20-C19-C18	-2.64	118.78	122.55
2	A	301[A]	Y35	C20-C21-C22	2.60	123.83	120.56
2	A	301[B]	Y35	O3-B-O2	2.56	116.18	109.55
2	A	301[A]	Y35	O2-C17-C16	-2.56	107.60	110.52
2	A	301[B]	Y35	O2-C17-C43	2.55	131.02	127.83
2	A	301[B]	Y35	C28-C30-N3	2.49	121.87	118.72
2	A	301[B]	Y35	C21-C22-C24	-2.43	117.14	121.36
2	A	301[B]	Y35	C22-C23-C18	-2.42	119.81	122.00
2	A	301[A]	Y35	C32-C31-N3	-2.39	107.19	110.82
2	A	301[B]	Y35	C44-C14-C15	2.38	122.05	119.24
2	A	301[A]	Y35	C29-C28-C30	2.38	125.44	120.14
2	A	301[A]	Y35	O3-B-O4	2.35	115.62	109.55
2	A	301[B]	Y35	C7-C6-C8	2.33	125.23	120.73
2	A	301[B]	Y35	O2-C17-C16	-2.32	107.87	110.52
2	A	301[A]	Y35	C20-C19-C18	-2.29	119.28	122.55
4	B	304	PGE	O2-C3-C4	2.14	120.06	110.39
2	A	301[B]	Y35	C23-C22-C24	2.12	124.36	120.86
2	A	301[B]	Y35	C11-C12-C8	2.04	113.45	111.04

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301[B]	Y35	O3-B-C18-C23
5	B	303	MES	N4-C7-C8-S
4	A	303	PGE	O2-C3-C4-O3
2	A	301[B]	Y35	C23-C22-C24-C29
2	A	301[B]	Y35	C23-C22-C24-C25
2	A	301[B]	Y35	C21-C22-C24-C29
2	A	301[B]	Y35	C21-C22-C24-C25
4	A	303	PGE	O1-C1-C2-O2
4	B	304	PGE	O1-C1-C2-O2
4	B	304	PGE	O2-C3-C4-O3

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Mol	Chain	Res	Type	Atoms
4	A	303	PGE	C4-C3-O2-C2
4	B	304	PGE	C1-C2-O2-C3
4	B	304	PGE	O3-C5-C6-O4
4	B	304	PGE	C3-C4-O3-C5
4	A	303	PGE	O3-C5-C6-O4
2	A	301[A]	Y35	O3-B-C18-C23
2	A	301[B]	Y35	O3-B-C18-C19
2	A	301[B]	Y35	N1-C1-C2-C7
2	A	301[A]	Y35	O4-B-C18-C23
2	A	301[B]	Y35	O2-B-C18-C19
2	A	301[B]	Y35	O2-B-C18-C23

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	304	PGE	3	0
2	A	301[B]	Y35	1	0
2	A	301[A]	Y35	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.

Ligand Y35 A 301 (B)

Bond lengths

Bond angles

Torsions

Rings

Ligand Y35 A 301 (A)

Bond lengths

Bond angles

Torsions

Rings
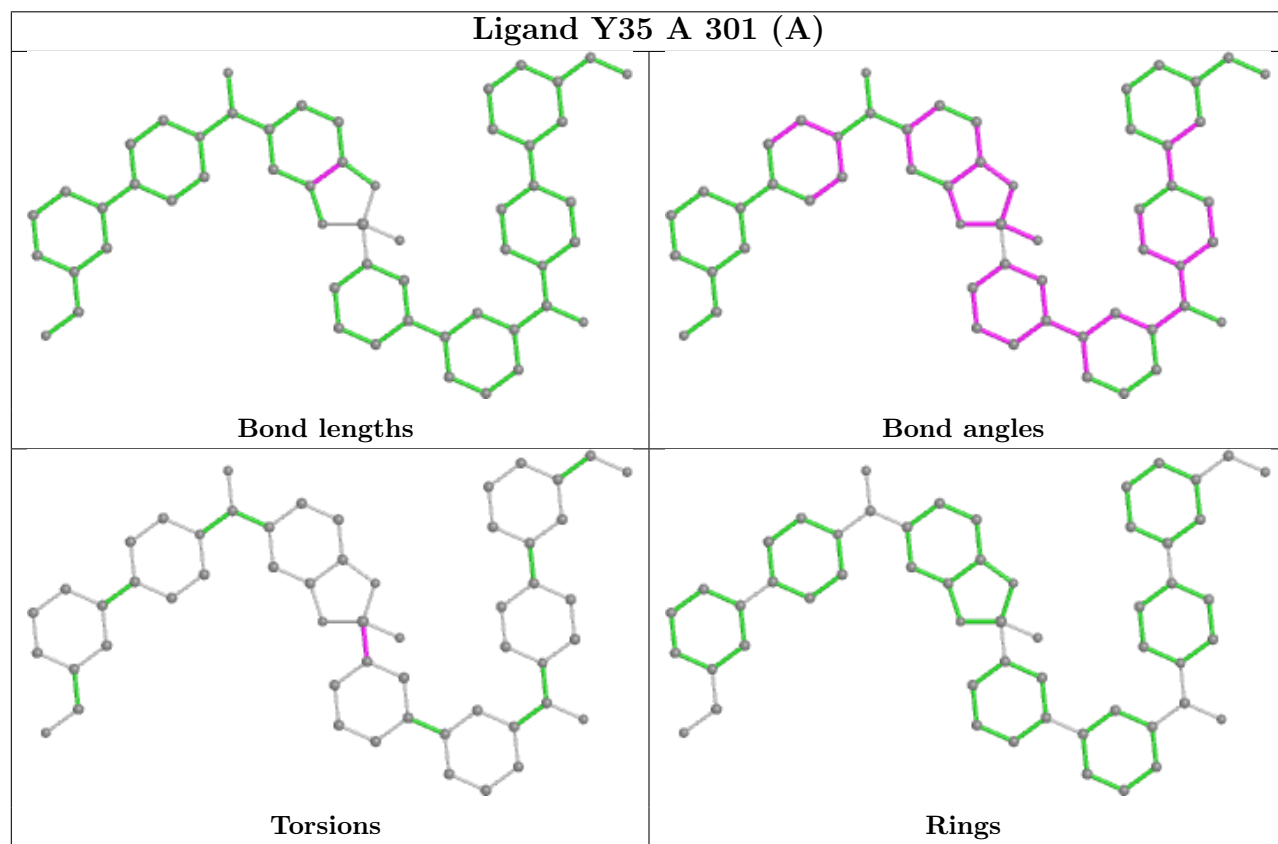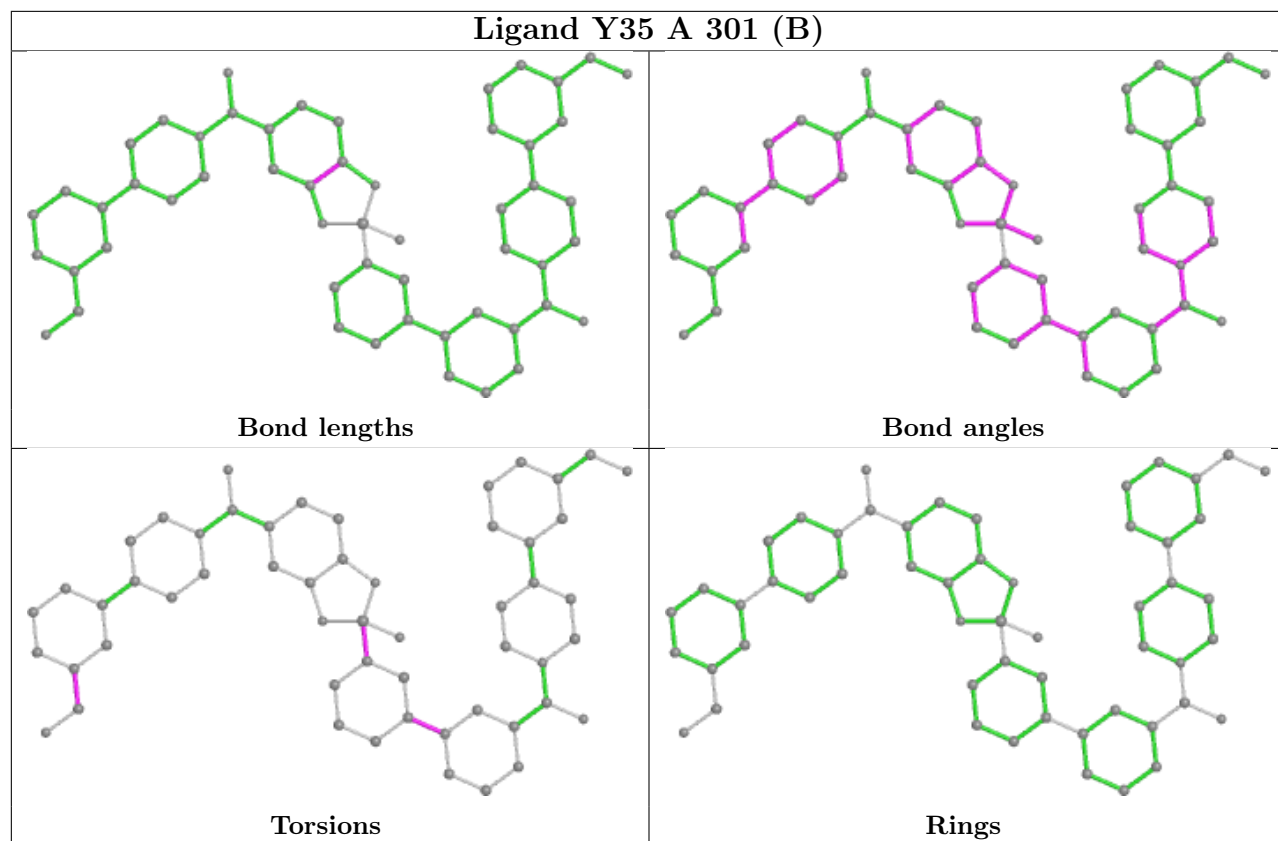
5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	243/275 (88%)	-0.50	2 (0%)	86	89	21, 29, 48, 67	0
1	B	243/275 (88%)	-0.40	0	100	100	20, 32, 53, 70	0
All	All	486/550 (88%)	-0.45	2 (0%)	92	96	20, 31, 51, 70	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	234	GLY	2.6
1	A	233	ASN	2.1

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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.
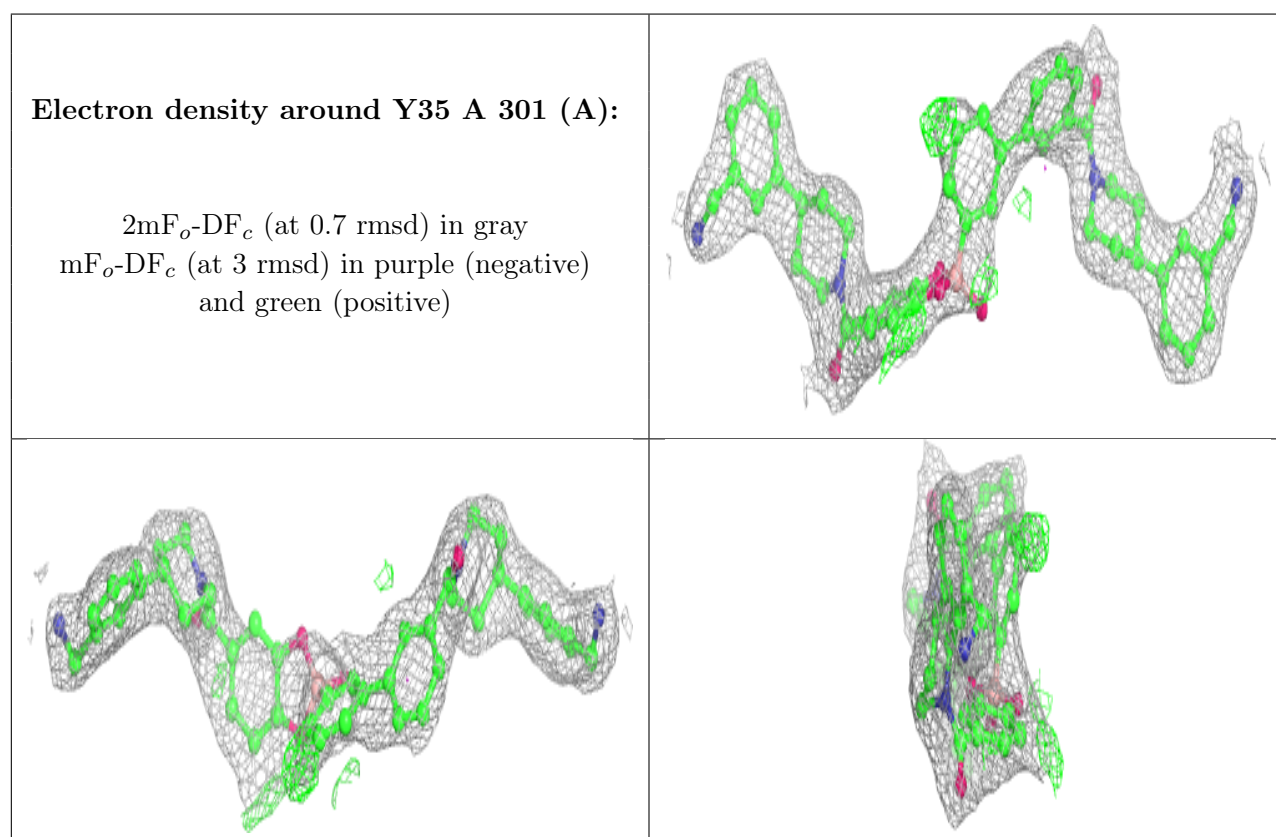
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
4	PGE	B	304	10/10	0.77	0.35	52,64,82,83	0
4	PGE	A	303	10/10	0.85	0.29	50,73,78,79	0
2	Y35	A	301[A]	54/54	0.90	0.18	25,33,45,46	54

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($Å^2$)	Q<0.9
2	Y35	A	301[B]	54/54	0.90	0.18	29,36,51,53	54
3	SO4	B	301	5/5	0.96	0.10	49,53,53,58	0
5	MES	B	303	12/12	0.96	0.13	49,63,66,67	0
3	SO4	B	302	5/5	0.98	0.16	58,58,62,62	0
3	SO4	A	302	5/5	0.98	0.08	44,45,48,52	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 Y35 A 301 (A):

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

Electron density around Y35 A 301 (B):

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

6.5 Other polymers ⓘ

There are no such residues in this entry.