



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:23 PM UTC

PDB ID : 2Y00 / pdb_00002y00
Title : TURKEY BETA1 ADRENERGIC RECEPTOR WITH STABILISING MUTATIONS AND BOUND PARTIAL AGONIST DOBUTAMINE (CRYSTAL DOB92)
Authors : Warne, A.; Moukhametzianov, R.; Baker, J.G.; Nehme, R.; Edwards, P.C.; Leslie, A.G.W.; Schertler, G.F.X.; Tate, C.G.
Deposited on : 2010-11-30
Resolution : 2.50 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](#) ①) 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

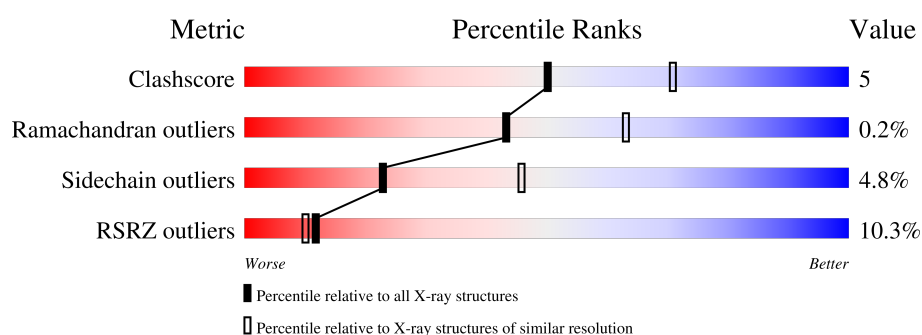
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	315	9% 78% 12% 9%
1	B	315	10% 80% 13% 5%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5052 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 BETA-1 ADRENERGIC RECEPTOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	0	0
			2269	1498	372	379	20			
1	B	298	Total	C	N	O	S	0	0	0
			2371	1560	396	395	20			

There are 86 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	MET	-	expression tag	UNP P07700
A	32	GLY	-	expression tag	UNP P07700
A	68	SER	ARG	engineered mutation	UNP P07700
A	90	VAL	MET	engineered mutation	UNP P07700
A	116	LEU	CYS	engineered mutation	UNP P07700
A	227	ALA	TYR	engineered mutation	UNP P07700
A	?	-	CYS	deletion	UNP P07700
A	?	-	GLU	deletion	UNP P07700
A	?	-	GLY	deletion	UNP P07700
A	?	-	ARG	deletion	UNP P07700
A	?	-	PHE	deletion	UNP P07700
A	?	-	TYR	deletion	UNP P07700
A	?	-	GLY	deletion	UNP P07700
A	?	-	SER	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	GLU	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	LEU	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700

Continued on next page...

Continued from previous page...

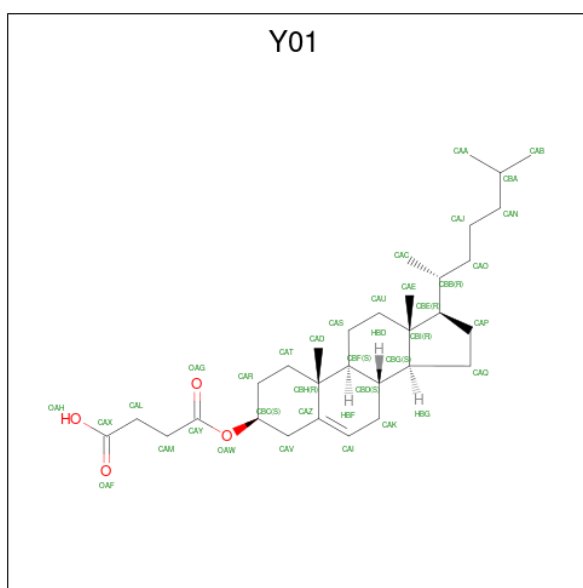
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	HIS	deletion	UNP P07700
A	?	-	GLN	deletion	UNP P07700
A	?	-	PRO	deletion	UNP P07700
A	?	-	ILE	deletion	UNP P07700
A	?	-	LEU	deletion	UNP P07700
A	?	-	GLY	deletion	UNP P07700
A	?	-	ASN	deletion	UNP P07700
A	?	-	GLY	deletion	UNP P07700
A	?	-	ARG	deletion	UNP P07700
A	282	LEU	ALA	engineered mutation	UNP P07700
A	327	ALA	PHE	engineered mutation	UNP P07700
A	338	MET	PHE	engineered mutation	UNP P07700
A	358	ALA	CYS	engineered mutation	UNP P07700
A	369	HIS	-	expression tag	UNP P07700
A	370	HIS	-	expression tag	UNP P07700
A	371	HIS	-	expression tag	UNP P07700
A	372	HIS	-	expression tag	UNP P07700
A	373	HIS	-	expression tag	UNP P07700
B	31	MET	-	expression tag	UNP P07700
B	32	GLY	-	expression tag	UNP P07700
B	68	SER	ARG	engineered mutation	UNP P07700
B	90	VAL	MET	engineered mutation	UNP P07700
B	116	LEU	CYS	engineered mutation	UNP P07700
B	227	ALA	TYR	engineered mutation	UNP P07700
B	?	-	CYS	deletion	UNP P07700
B	?	-	GLU	deletion	UNP P07700
B	?	-	GLY	deletion	UNP P07700
B	?	-	ARG	deletion	UNP P07700
B	?	-	PHE	deletion	UNP P07700
B	?	-	TYR	deletion	UNP P07700
B	?	-	GLY	deletion	UNP P07700
B	?	-	SER	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700
B	?	-	GLU	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	LEU	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	?	-	GLN	deletion	UNP P07700
B	?	-	HIS	deletion	UNP P07700
B	?	-	GLN	deletion	UNP P07700
B	?	-	PRO	deletion	UNP P07700
B	?	-	ILE	deletion	UNP P07700
B	?	-	LEU	deletion	UNP P07700
B	?	-	GLY	deletion	UNP P07700
B	?	-	ASN	deletion	UNP P07700
B	?	-	GLY	deletion	UNP P07700
B	?	-	ARG	deletion	UNP P07700
B	282	LEU	ALA	engineered mutation	UNP P07700
B	327	ALA	PHE	engineered mutation	UNP P07700
B	338	MET	PHE	engineered mutation	UNP P07700
B	358	ALA	CYS	engineered mutation	UNP P07700
B	369	HIS	-	expression tag	UNP P07700
B	370	HIS	-	expression tag	UNP P07700
B	371	HIS	-	expression tag	UNP P07700
B	372	HIS	-	expression tag	UNP P07700
B	373	HIS	-	expression tag	UNP P07700

- Molecule 2 is CHOLESTEROL HEMISUCCINATE (CCD ID: Y01) (formula: $C_{31}H_{50}O_4$).



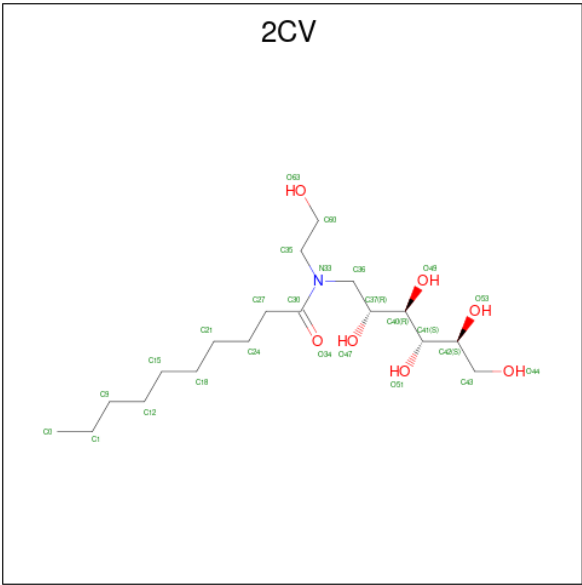
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total 35	C 31	O 4	0	0
2	A	1	Total 35	C 31	O 4	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			35	31	4		
2	B	1	Total	C	O	0	0
			35	31	4		

- Molecule 3 is HEGA-10 (CCD ID: 2CV) (formula: C₁₈H₃₇NO₇).



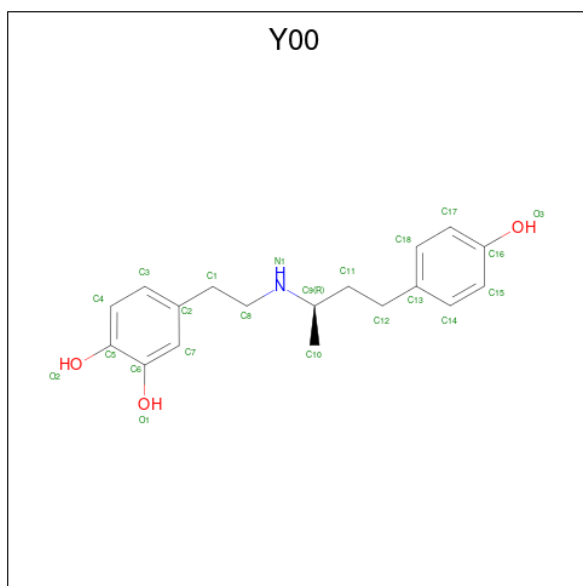
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			26	18	1	7		
3	A	1	Total	C			0	0
			5	5				
3	A	1	Total	C	N	O	0	0
			20	15	1	4		
3	A	1	Total	C	N	O	0	0
			26	18	1	7		
3	A	1	Total	C	N	O	0	0
			26	18	1	7		
3	B	1	Total	C	N	O	0	0
			20	15	1	4		
3	B	1	Total	C	N	O	0	0
			16	13	1	2		
3	B	1	Total	C	N	O	0	0
			16	13	1	2		
3	B	1	Total	C	N	O	0	0
			8	6	1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			26	18	1	7		

- Molecule 4 is DOBUTAMINE (CCD ID: Y00) (formula: $C_{18}H_{23}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			22	18	1	3		
4	B	1	Total	C	N	O	0	0
			22	18	1	3		

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Na	0	0
			1	1		

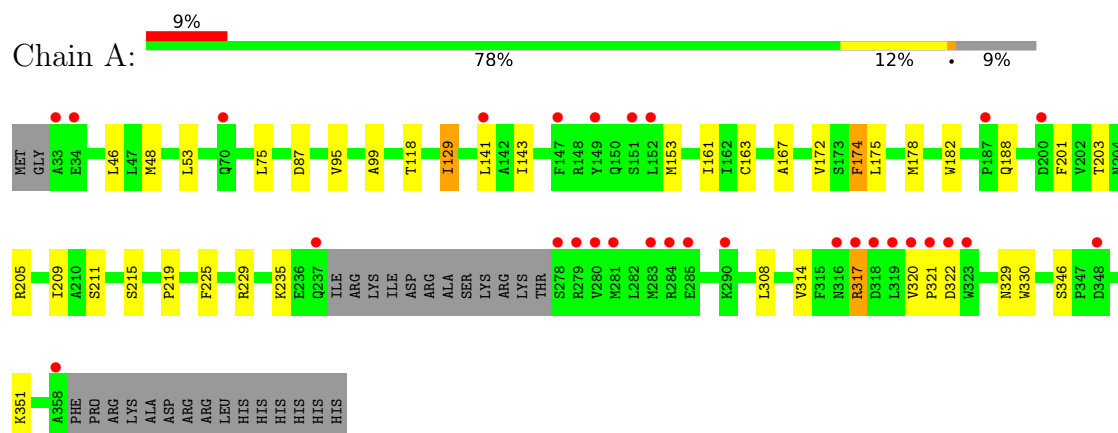
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	19	Total	O	0	0
			19	19		
6	B	19	Total	O	0	0
			19	19		

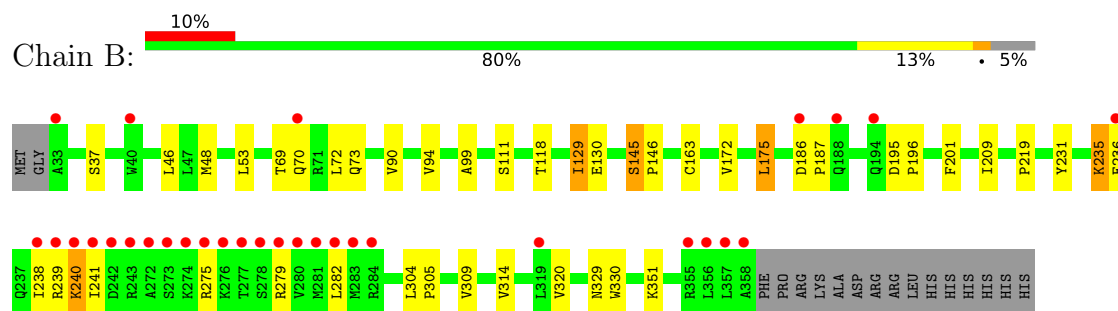
3 Residue-property plots

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: BETA-1 ADRENERGIC RECEPTOR



• Molecule 1: BETA-1 ADRENERGIC RECEPTOR



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	90.00Å 60.50Å 101.90Å 90.00° 110.20° 90.00°	Depositor
Resolution (Å)	95.65 – 2.50 95.63 – 2.50	Depositor EDS
% Data completeness (in resolution range)	93.7 (95.65-2.50) 93.6 (95.63-2.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.94 (at 2.51Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.226 , 0.256 0.228 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	32.5	Xtriage
Anisotropy	0.191	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 59.1	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	0.91	EDS
Total number of atoms	5052	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.70% 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: 2CV, Y01, Y00, NA

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	0.75	1/2323 (0.0%)	0.96	4/3167 (0.1%)
1	B	0.75	0/2426	0.93	2/3303 (0.1%)
All	All	0.75	1/4749 (0.0%)	0.95	6/6470 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	VAL	CA-CB	5.50	1.57	1.54

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	145	SER	CA-C-N	7.79	128.20	119.32
1	B	145	SER	C-N-CA	7.79	128.20	119.32
1	A	322	ASP	N-CA-C	6.14	117.64	111.07
1	A	174	PHE	N-CA-C	5.52	116.97	111.07
1	A	346	SER	CA-C-N	5.11	124.56	119.24
1	A	346	SER	C-N-CA	5.11	124.56	119.24

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	2269	0	2349	23	0
1	B	2371	0	2471	24	0
2	A	70	0	98	2	0
2	B	70	0	98	2	0
3	A	103	0	146	5	0
3	B	86	0	122	6	0
4	A	22	0	22	3	0
4	B	22	0	20	1	0
5	A	1	0	0	0	0
6	A	19	0	0	1	0
6	B	19	0	0	2	0
All	All	5052	0	5326	55	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 5.

All (55) 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:163:CYS:SG	3:B:505:2CV:H601	2.17	0.85
1:B:175:LEU:HB2	6:B:2010:HOH:O	1.77	0.81
3:B:501:2CV:H601	3:B:501:2CV:H272	1.68	0.75
1:A:174:PHE:O	1:A:178:MET:HG2	1.90	0.72
1:A:87:ASP:OD1	6:A:2003:HOH:O	2.07	0.72
2:A:402:Y01:HAC1	2:A:402:Y01:HAE2	1.70	0.71
1:B:235:LYS:O	1:B:238:ILE:HG13	1.94	0.68
1:B:239:ARG:O	1:B:240:LYS:HB2	1.94	0.67
1:B:48:MET:HE1	1:B:330:TRP:CZ3	2.30	0.67
3:A:505:2CV:H602	3:A:505:2CV:H37	1.77	0.66
1:B:209:ILE:HD11	1:B:314:VAL:HG11	1.78	0.65
1:A:209:ILE:HD11	1:A:314:VAL:HG11	1.82	0.62
1:B:329:ASN:OD1	4:B:601:Y00:H122	2.00	0.61
1:B:241:ILE:HD12	1:B:282:LEU:HD23	1.84	0.59
1:A:129:ILE:HG13	1:A:219:PRO:HB2	1.84	0.59
1:A:48:MET:HE2	1:A:99:ALA:HB2	1.83	0.59
3:B:501:2CV:H272	3:B:501:2CV:C60	2.33	0.58
1:A:205:ARG:NH1	1:A:314:VAL:O	2.38	0.57
1:A:163:CYS:SG	3:A:505:2CV:H601	2.45	0.56
1:B:186:ASP:OD1	1:B:187:PRO:HD2	2.06	0.56
1:B:129:ILE:HG13	1:B:219:PRO:HB2	1.88	0.55
1:A:182:TRP:CD1	1:A:182:TRP:H	2.26	0.53
1:B:118:THR:HG21	1:B:201:PHE:CE1	2.44	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ILE:HG12	2:A:401:Y01:HBC	1.94	0.50
1:B:304:LEU:N	1:B:305:PRO:CD	2.75	0.49
1:B:145:SER:N	1:B:146:PRO:HD3	2.28	0.49
1:A:330:TRP:NE1	4:A:601:Y00:H17	2.28	0.48
1:B:241:ILE:HD11	1:B:279:ARG:HG3	1.95	0.48
1:A:329:ASN:OD1	4:A:601:Y00:H121	2.13	0.48
1:A:205:ARG:HG2	1:A:314:VAL:HG13	1.97	0.46
1:B:69:THR:HB	1:B:72:LEU:HD12	1.98	0.46
3:A:501:2CV:H272	3:A:501:2CV:C60	2.46	0.45
1:B:130:GLU:HG2	2:B:401:Y01:HAC3	1.99	0.45
2:B:402:Y01:HAA1	3:B:505:2CV:H01C	1.99	0.44
1:A:48:MET:HE1	1:A:330:TRP:CZ3	2.52	0.44
1:A:320:VAL:HA	1:A:321:PRO:HD3	1.89	0.44
1:A:118:THR:HG21	1:A:201:PHE:CE1	2.53	0.43
3:A:505:2CV:H271	3:A:505:2CV:H352	1.74	0.43
1:B:239:ARG:O	1:B:240:LYS:CB	2.63	0.43
1:B:70:GLN:HA	1:B:73:GLN:OE1	2.18	0.43
1:B:90:VAL:HA	1:B:94:VAL:HB	2.00	0.43
1:A:308:LEU:HD23	1:A:308:LEU:HA	1.83	0.43
1:B:48:MET:HE2	1:B:99:ALA:HB2	2.01	0.43
1:B:48:MET:HE1	1:B:330:TRP:CH2	2.53	0.43
1:B:175:LEU:N	6:B:2010:HOH:O	2.39	0.42
1:A:225:PHE:O	1:A:229:ARG:HG2	2.20	0.42
1:A:211:SER:O	1:A:215:SER:HB2	2.20	0.42
1:A:75:LEU:HD13	1:A:153:MET:HB3	2.02	0.42
1:A:182:TRP:O	1:A:203:THR:HA	2.19	0.41
1:A:317:ARG:H	1:A:317:ARG:HE	1.68	0.41
3:B:505:2CV:O47	3:B:505:2CV:H602	2.21	0.41
1:B:231:TYR:HD1	3:B:502:2CV:H182	1.86	0.41
1:B:195:ASP:HA	1:B:196:PRO:HD3	1.94	0.40
1:A:167:ALA:HB2	3:A:505:2CV:H181	2.03	0.40
1:A:330:TRP:HE1	4:A:601:Y00:H17	1.87	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	282/315 (90%)	274 (97%)	8 (3%)	0	100	100
1	B	296/315 (94%)	282 (95%)	13 (4%)	1 (0%)	36	55
All	All	578/630 (92%)	556 (96%)	21 (4%)	1 (0%)	43	63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	240	LYS

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	247/273 (90%)	236 (96%)	11 (4%)	24	49
1	B	258/273 (94%)	245 (95%)	13 (5%)	22	44
All	All	505/546 (92%)	481 (95%)	24 (5%)	23	46

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	LEU
1	A	53	LEU
1	A	129	ILE
1	A	141	LEU
1	A	143	ILE
1	A	172	VAL
1	A	175	LEU
1	A	188	GLN
1	A	235	LYS
1	A	317	ARG
1	A	351	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	37	SER
1	B	46	LEU
1	B	53	LEU
1	B	111	SER
1	B	129	ILE
1	B	172	VAL
1	B	175	LEU
1	B	235	LYS
1	B	236	GLU
1	B	275	ARG
1	B	309	VAL
1	B	320	VAL
1	B	351	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	286	HIS
1	B	237	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 1 is monoatomic - leaving 16 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
2	Y01	A	402	-	38,38,38	1.48	3 (7%)	57,57,57	1.48	9 (15%)
3	2CV	B	502	-	15,15,25	0.90	1 (6%)	16,16,30	0.40	0
3	2CV	A	501	-	25,25,25	0.86	0	29,30,30	1.24	3 (10%)
4	Y00	A	601	-	23,23,23	1.22	1 (4%)	28,30,30	0.99	1 (3%)
3	2CV	A	504	-	25,25,25	0.64	0	29,30,30	1.49	2 (6%)
3	2CV	A	505	-	25,25,25	0.82	0	29,30,30	0.96	2 (6%)
3	2CV	A	502	-	4,4,25	0.53	0	3,3,30	0.36	0
3	2CV	B	505	-	25,25,25	0.78	0	29,30,30	0.76	2 (6%)
2	Y01	A	401	-	38,38,38	1.34	2 (5%)	57,57,57	1.93	18 (31%)
3	2CV	B	504	-	7,7,25	0.80	0	7,7,30	0.26	0
3	2CV	B	503	-	15,15,25	0.70	0	16,16,30	0.62	0
4	Y00	B	601	-	23,23,23	1.06	1 (4%)	28,30,30	1.43	1 (3%)
2	Y01	B	402	-	38,38,38	1.37	2 (5%)	57,57,57	1.57	13 (22%)
2	Y01	B	401	-	38,38,38	1.30	3 (7%)	57,57,57	1.96	14 (24%)
3	2CV	A	503	-	19,19,25	0.62	0	21,21,30	0.49	0
3	2CV	B	501	-	19,19,25	0.55	0	21,21,30	0.92	1 (4%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	Y01	A	402	-	-	12/19/77/77	0/4/4/4
3	2CV	B	502	-	-	4/16/16/34	-
3	2CV	A	501	-	-	14/34/34/34	-
4	Y00	A	601	-	-	4/11/11/11	0/2/2/2
3	2CV	A	504	-	-	22/34/34/34	-
3	2CV	A	505	-	-	16/34/34/34	-
3	2CV	A	502	-	-	0/2/2/34	-
3	2CV	B	505	-	-	11/34/34/34	-
2	Y01	A	401	-	-	11/19/77/77	0/4/4/4
3	2CV	B	504	-	-	0/5/5/34	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	2CV	B	503	-	-	1/16/16/34	-
4	Y00	B	601	-	-	2/11/11/11	0/2/2/2
2	Y01	B	402	-	-	10/19/77/77	0/4/4/4
2	Y01	B	401	-	-	9/19/77/77	0/4/4/4
3	2CV	A	503	-	-	9/22/22/34	-
3	2CV	B	501	-	-	7/22/22/34	-

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	402	Y01	CAK-CAI	-5.46	1.39	1.50
2	A	402	Y01	CAK-CAI	-5.12	1.39	1.50
4	A	601	Y00	C5-C6	4.88	1.48	1.40
2	A	401	Y01	CAK-CAI	-4.87	1.40	1.50
2	B	401	Y01	CAK-CAI	-4.53	1.41	1.50
4	B	601	Y00	C5-C6	4.26	1.47	1.40
2	A	402	Y01	CAI-CAZ	3.59	1.40	1.33
2	A	401	Y01	CAI-CAZ	3.52	1.40	1.33
2	B	401	Y01	CAI-CAZ	3.43	1.40	1.33
2	B	402	Y01	CAI-CAZ	2.67	1.38	1.33
2	A	402	Y01	CBH-CAZ	2.63	1.57	1.52
3	B	502	2CV	C27-C30	2.40	1.56	1.51
2	B	401	Y01	CAV-CAZ	2.28	1.56	1.51

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	Y01	OAW-CBC-CAV	5.58	119.54	108.04
4	B	601	Y00	C8-N1-C9	5.44	122.15	113.98
2	B	401	Y01	CBC-CAV-CAZ	-5.35	103.55	111.45
2	B	401	Y01	OAW-CBC-CAR	5.27	120.82	108.37
2	B	401	Y01	OAW-CBC-CAV	5.21	118.76	108.04
3	A	504	2CV	C37-C40-C41	5.17	120.42	112.48
2	A	402	Y01	OAW-CAY-CAM	5.15	122.62	111.48
2	B	402	Y01	CAV-CAZ-CBH	4.90	122.69	116.42
2	A	401	Y01	CAR-CBC-CAV	-4.53	104.68	110.97
2	A	401	Y01	CAV-CAZ-CBH	4.11	121.68	116.42
2	A	402	Y01	CAV-CAZ-CBH	4.07	121.63	116.42
2	B	402	Y01	OAW-CAY-CAM	4.01	120.15	111.48
2	A	401	Y01	OAW-CBC-CAR	4.01	117.84	108.37
3	A	504	2CV	C42-C41-C40	-3.73	106.75	112.48

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	501	2CV	C35-N33-C36	-3.71	111.94	116.14
4	A	601	Y00	C8-N1-C9	3.60	119.38	113.98
2	B	401	Y01	CAR-CBC-CAV	-3.58	105.99	110.97
2	A	401	Y01	OAW-CAY-CAM	3.43	118.89	111.48
2	B	402	Y01	OAW-CBC-CAV	-3.40	101.03	108.04
2	B	401	Y01	CAC-CBB-CBE	-3.38	107.81	112.88
2	B	402	Y01	CAV-CAZ-CAI	-3.38	115.99	120.57
2	B	401	Y01	CAO-CBB-CBE	3.34	117.25	110.33
2	A	401	Y01	CAC-CBB-CBE	-3.25	108.00	112.88
2	B	401	Y01	CAT-CAR-CBC	-3.16	105.19	110.33
2	A	402	Y01	CAK-CBD-CBF	3.02	113.21	109.72
2	A	401	Y01	CAT-CBH-CBF	3.02	112.73	108.74
3	A	505	2CV	C37-C40-C41	2.92	116.97	112.48
2	B	402	Y01	OAW-CBC-CAR	2.91	115.25	108.37
2	B	402	Y01	CAQ-CBG-CBI	-2.87	100.46	103.84
2	B	402	Y01	CBG-CBI-CBE	-2.83	96.85	100.10
2	B	401	Y01	OAW-CAY-CAM	2.82	117.59	111.48
2	A	401	Y01	CBF-CBD-CBG	2.81	112.76	109.09
2	B	401	Y01	CAP-CBE-CBB	2.77	116.37	112.18
2	A	401	Y01	CAO-CBB-CBE	2.75	116.03	110.33
2	A	402	Y01	CAV-CAZ-CAI	-2.71	116.90	120.57
2	A	402	Y01	OAW-CAY-OAG	-2.60	117.62	123.70
2	A	401	Y01	CBC-CAV-CAZ	-2.53	107.72	111.45
2	A	401	Y01	OAF-CAX-CAL	-2.51	115.15	123.09
2	A	401	Y01	CAP-CBE-CBB	2.50	115.96	112.18
3	B	501	2CV	C35-N33-C36	-2.49	113.33	116.14
2	B	401	Y01	CAU-CBI-CBE	-2.44	113.01	116.60
2	B	401	Y01	CAV-CAZ-CBH	2.43	119.53	116.42
2	B	402	Y01	CAP-CBE-CBB	-2.38	108.58	112.18
2	B	402	Y01	OAW-CAY-OAG	-2.37	118.17	123.70
2	A	402	Y01	CBG-CBI-CBE	-2.37	97.38	100.10
2	A	401	Y01	CBG-CBI-CBE	-2.32	97.44	100.10
2	A	401	Y01	CBI-CBE-CBB	-2.32	115.92	119.50
2	B	401	Y01	CBH-CAZ-CAI	-2.31	119.56	122.93
3	A	505	2CV	C35-N33-C36	2.24	118.68	116.14
3	B	505	2CV	C42-C41-C40	2.22	115.88	112.48
2	B	401	Y01	OAF-CAX-CAL	-2.20	116.10	123.09
2	A	401	Y01	CAU-CBI-CBE	-2.18	113.39	116.60
2	A	401	Y01	CAD-CBH-CBF	-2.18	109.21	111.66
2	A	402	Y01	CAU-CBI-CBE	-2.17	113.40	116.60
3	A	501	2CV	O51-C41-C42	2.17	113.87	108.93
2	A	402	Y01	CAD-CBH-CAZ	2.15	111.67	108.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	402	Y01	CAK-CBD-CBF	2.13	112.18	109.72
2	A	401	Y01	CAE-CBI-CAU	2.12	113.73	110.61
3	A	501	2CV	C37-C40-C41	2.08	115.67	112.48
2	A	402	Y01	CAQ-CBG-CBD	-2.07	115.80	119.10
3	B	505	2CV	C35-N33-C36	2.06	118.47	116.14
2	B	402	Y01	CAR-CBC-CAV	2.04	113.81	110.97
2	B	402	Y01	OAF-CAX-CAL	-2.03	116.64	123.09
2	B	402	Y01	CAQ-CBG-CBD	-2.01	115.89	119.10
2	B	401	Y01	CAL-CAM-CAY	-2.01	107.47	113.44
2	A	401	Y01	CBH-CAZ-CAI	-2.01	119.99	122.93

There are no chirality outliers.

All (132) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	402	Y01	OAG-CAY-OAW-CBC
2	A	402	Y01	CAM-CAY-OAW-CBC
2	B	402	Y01	OAG-CAY-OAW-CBC
3	A	501	2CV	C37-C36-N33-C30
3	A	501	2CV	C37-C36-N33-C35
3	A	501	2CV	N33-C36-C37-O47
3	A	501	2CV	C36-C37-C40-C41
3	A	501	2CV	C36-C37-C40-O49
3	A	501	2CV	O47-C37-C40-C41
3	A	501	2CV	O47-C37-C40-O49
3	A	501	2CV	C37-C40-C41-C42
3	A	501	2CV	C37-C40-C41-O51
3	A	501	2CV	O49-C40-C41-C42
3	A	501	2CV	O49-C40-C41-O51
3	A	503	2CV	C36-C37-C40-O49
3	A	504	2CV	N33-C36-C37-C40
3	A	504	2CV	N33-C36-C37-O47
3	A	504	2CV	C36-C37-C40-C41
3	A	504	2CV	C36-C37-C40-O49
3	A	504	2CV	O47-C37-C40-C41
3	A	504	2CV	O47-C37-C40-O49
3	A	504	2CV	C37-C40-C41-C42
3	A	504	2CV	C37-C40-C41-O51
3	A	504	2CV	O49-C40-C41-C42
3	A	504	2CV	O49-C40-C41-O51
3	A	504	2CV	O51-C41-C42-C43
3	A	505	2CV	N33-C36-C37-C40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	A	505	2CV	N33-C36-C37-O47
3	A	505	2CV	C36-C37-C40-C41
3	A	505	2CV	C36-C37-C40-O49
3	B	501	2CV	N33-C36-C37-C40
3	B	501	2CV	N33-C36-C37-O47
3	B	505	2CV	C37-C40-C41-C42
3	B	505	2CV	C37-C40-C41-O51
3	B	505	2CV	O53-C42-C43-O44
4	A	601	Y00	C12-C11-C9-C10
2	A	401	Y01	CAR-CBC-OAW-CAY
2	B	401	Y01	CAR-CBC-OAW-CAY
2	B	402	Y01	CAR-CBC-OAW-CAY
2	A	402	Y01	CAC-CBB-CBE-CBI
3	B	502	2CV	C21-C24-C27-C30
3	A	505	2CV	N33-C35-C60-O63
3	B	505	2CV	N33-C35-C60-O63
2	B	402	Y01	CAM-CAY-OAW-CBC
3	B	505	2CV	C41-C42-C43-O44
3	A	504	2CV	C21-C24-C27-C30
3	A	504	2CV	N33-C35-C60-O63
2	A	402	Y01	CAO-CBB-CBE-CAP
3	A	504	2CV	C40-C41-C42-C43
3	B	505	2CV	O49-C40-C41-O51
2	A	401	Y01	CAC-CBB-CBE-CAP
2	B	401	Y01	CAX-CAL-CAM-CAY
3	A	504	2CV	O51-C41-C42-O53
3	A	504	2CV	C40-C41-C42-O53
3	A	503	2CV	O47-C37-C40-O49
2	A	401	Y01	CAC-CBB-CBE-CBI
2	A	401	Y01	CAO-CBB-CBE-CBI
2	B	401	Y01	CAO-CBB-CBE-CBI
3	A	504	2CV	C41-C42-C43-O44
3	B	505	2CV	O49-C40-C41-C42
2	A	402	Y01	CAC-CBB-CBE-CAP
2	B	401	Y01	CAN-CAJ-CAO-CBB
2	A	401	Y01	CAN-CAJ-CAO-CBB
3	A	505	2CV	O47-C37-C40-O49
2	B	401	Y01	CAC-CBB-CBE-CAP
2	A	401	Y01	CAO-CBB-CBE-CAP
3	A	504	2CV	O53-C42-C43-O44
2	A	402	Y01	CAX-CAL-CAM-CAY
2	B	401	Y01	CAC-CBB-CBE-CBI

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	B	501	2CV	N33-C35-C60-O63
3	A	505	2CV	C37-C40-C41-O51
3	A	504	2CV	C9-C12-C15-C18
3	A	504	2CV	C18-C21-C24-C27
2	B	402	Y01	CAJ-CAN-CBA-CAB
2	A	401	Y01	CAX-CAL-CAM-CAY
2	A	401	Y01	CAJ-CAN-CBA-CAB
3	A	505	2CV	C37-C40-C41-C42
3	A	505	2CV	O47-C37-C40-C41
3	B	505	2CV	C21-C24-C27-C30
3	B	502	2CV	C9-C12-C15-C18
3	A	503	2CV	C15-C12-C9-C1
2	A	401	Y01	CAJ-CAN-CBA-CAA
2	B	401	Y01	CAJ-CAN-CBA-CAA
2	B	401	Y01	CAJ-CAN-CBA-CAB
2	B	401	Y01	CAO-CBB-CBE-CAP
2	B	402	Y01	CAV-CBC-OAW-CAY
2	A	402	Y01	CAJ-CAO-CBB-CBE
3	A	501	2CV	N33-C35-C60-O63
2	B	402	Y01	CAJ-CAN-CBA-CAA
3	A	504	2CV	C0-C1-C9-C12
3	B	505	2CV	C15-C12-C9-C1
2	B	402	Y01	CAO-CAJ-CAN-CBA
2	A	402	Y01	CAO-CBB-CBE-CBI
3	B	501	2CV	C60-C35-N33-C36
3	B	501	2CV	O47-C37-C40-O49
3	A	503	2CV	C21-C24-C27-C30
3	A	503	2CV	C18-C21-C24-C27
4	B	601	Y00	C8-C1-C2-C3
3	A	503	2CV	C0-C1-C9-C12
4	B	601	Y00	C8-C1-C2-C7
3	A	504	2CV	C15-C12-C9-C1
4	A	601	Y00	C12-C11-C9-N1
3	B	501	2CV	C60-C35-N33-C30
3	A	503	2CV	C9-C12-C15-C18
3	A	505	2CV	C9-C12-C15-C18
3	A	505	2CV	C15-C12-C9-C1
3	B	502	2CV	N33-C35-C60-O63
3	A	505	2CV	C21-C24-C27-C30
2	A	402	Y01	CAJ-CAO-CBB-CAC
3	A	503	2CV	N33-C36-C37-O47
3	B	501	2CV	C36-C37-C40-O49

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
3	A	505	2CV	O51-C41-C42-C43
2	A	401	Y01	CAM-CAL-CAX-OAH
2	B	402	Y01	CAM-CAL-CAX-OAF
2	A	402	Y01	CAM-CAL-CAX-OAF
4	A	601	Y00	C11-C12-C13-C14
2	A	401	Y01	CAM-CAL-CAX-OAF
2	B	402	Y01	CAM-CAL-CAX-OAH
3	B	505	2CV	C9-C12-C15-C18
4	A	601	Y00	C11-C12-C13-C18
2	A	402	Y01	CAM-CAL-CAX-OAH
2	A	402	Y01	CAL-CAM-CAY-OAW
3	B	502	2CV	C0-C1-C9-C12
3	A	505	2CV	O51-C41-C42-O53
3	A	505	2CV	C40-C41-C42-C43
3	A	501	2CV	C21-C24-C27-C30
3	B	503	2CV	C15-C18-C21-C24
3	B	505	2CV	C15-C18-C21-C24
3	A	505	2CV	C40-C41-C42-O53
3	A	501	2CV	N33-C36-C37-C40
2	B	402	Y01	CAJ-CAO-CBB-CBE
3	A	503	2CV	N33-C36-C37-C40

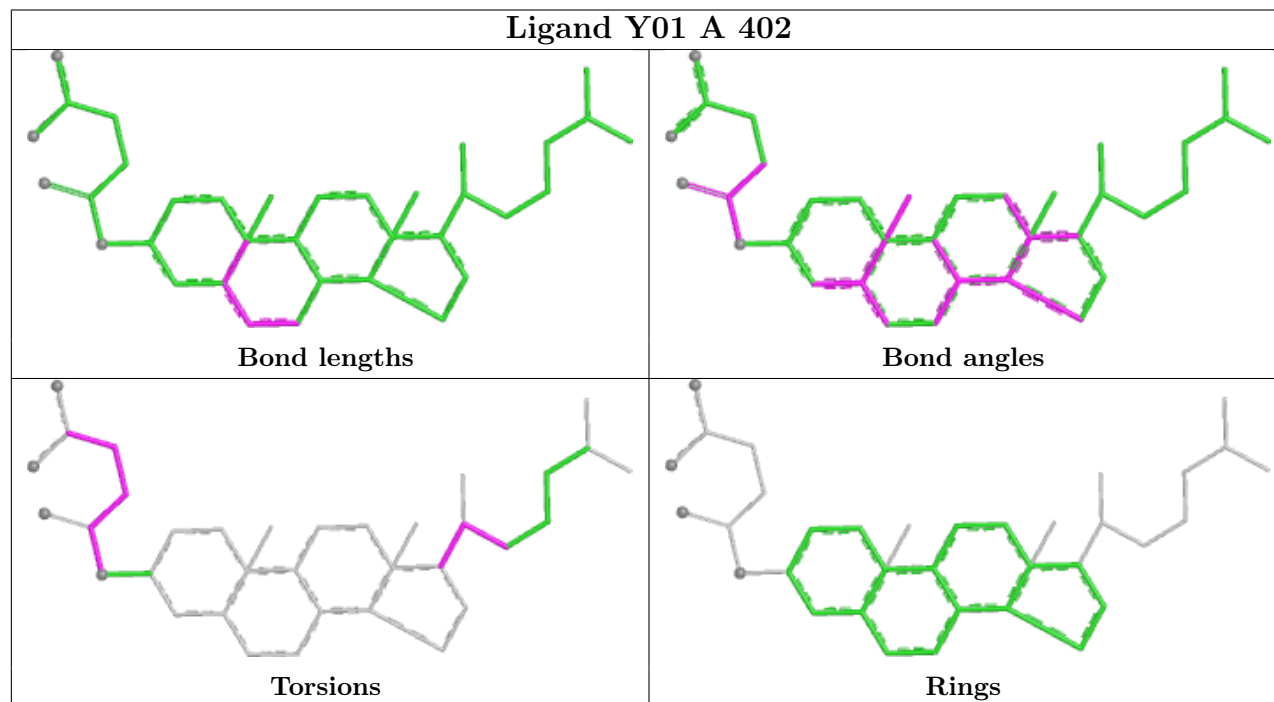
There are no ring outliers.

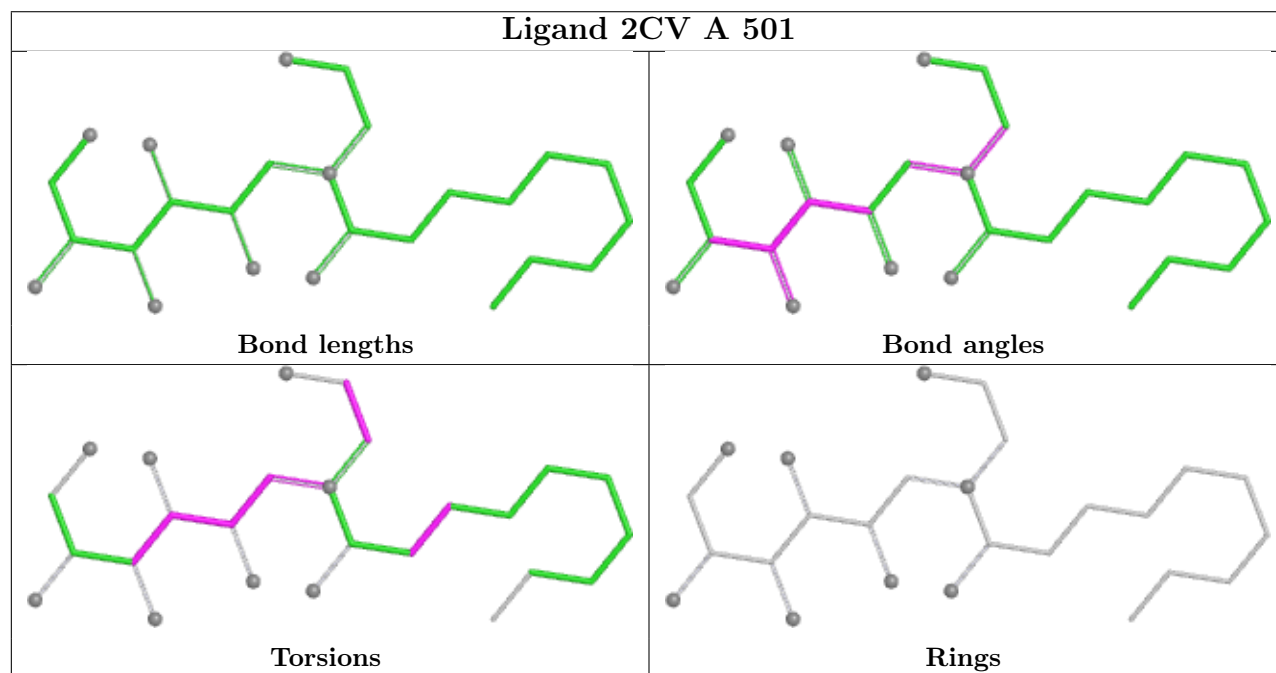
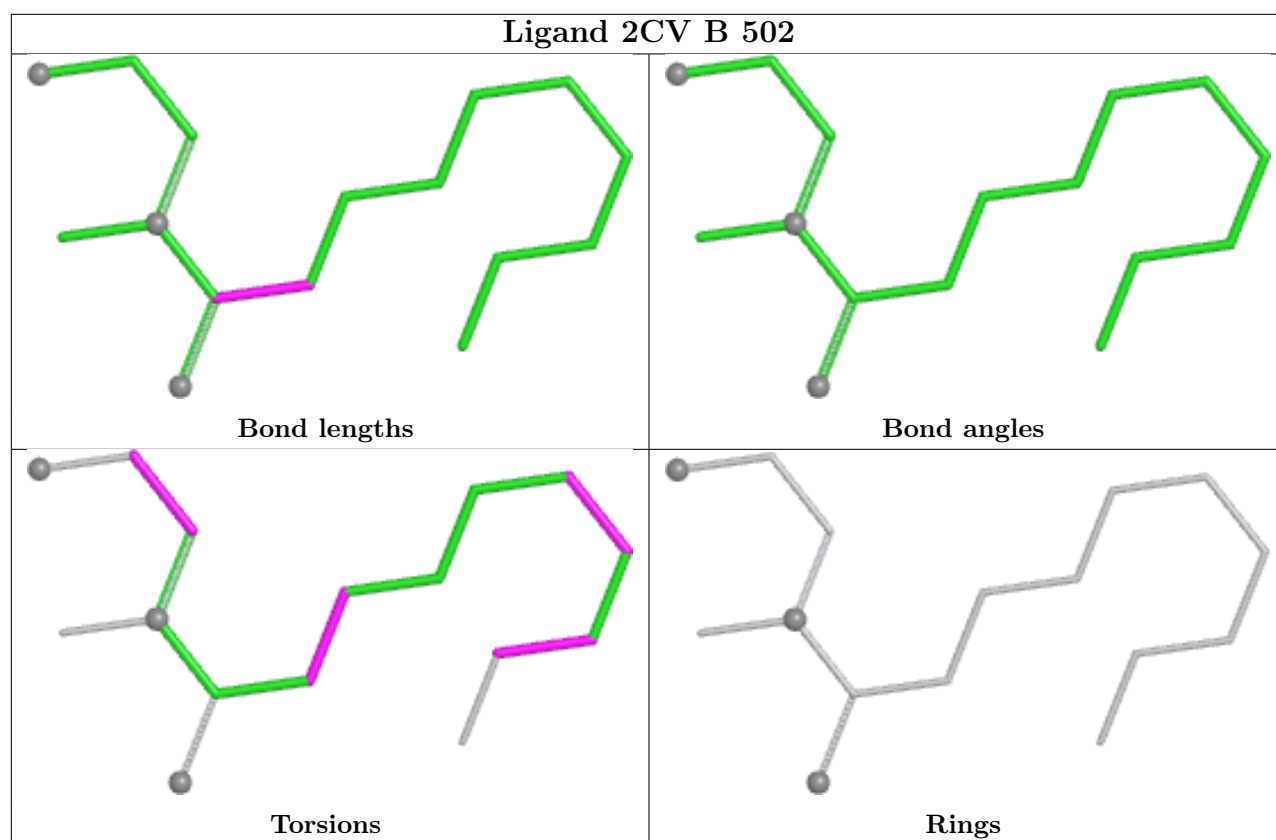
11 monomers are involved in 18 short contacts:

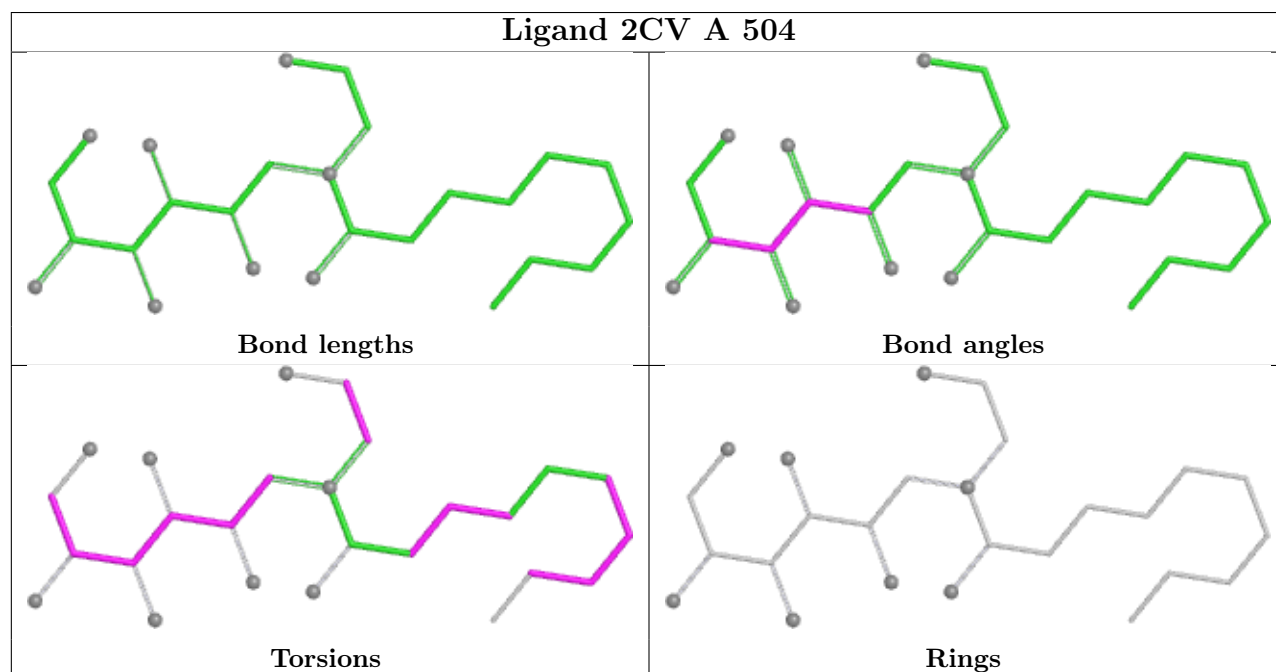
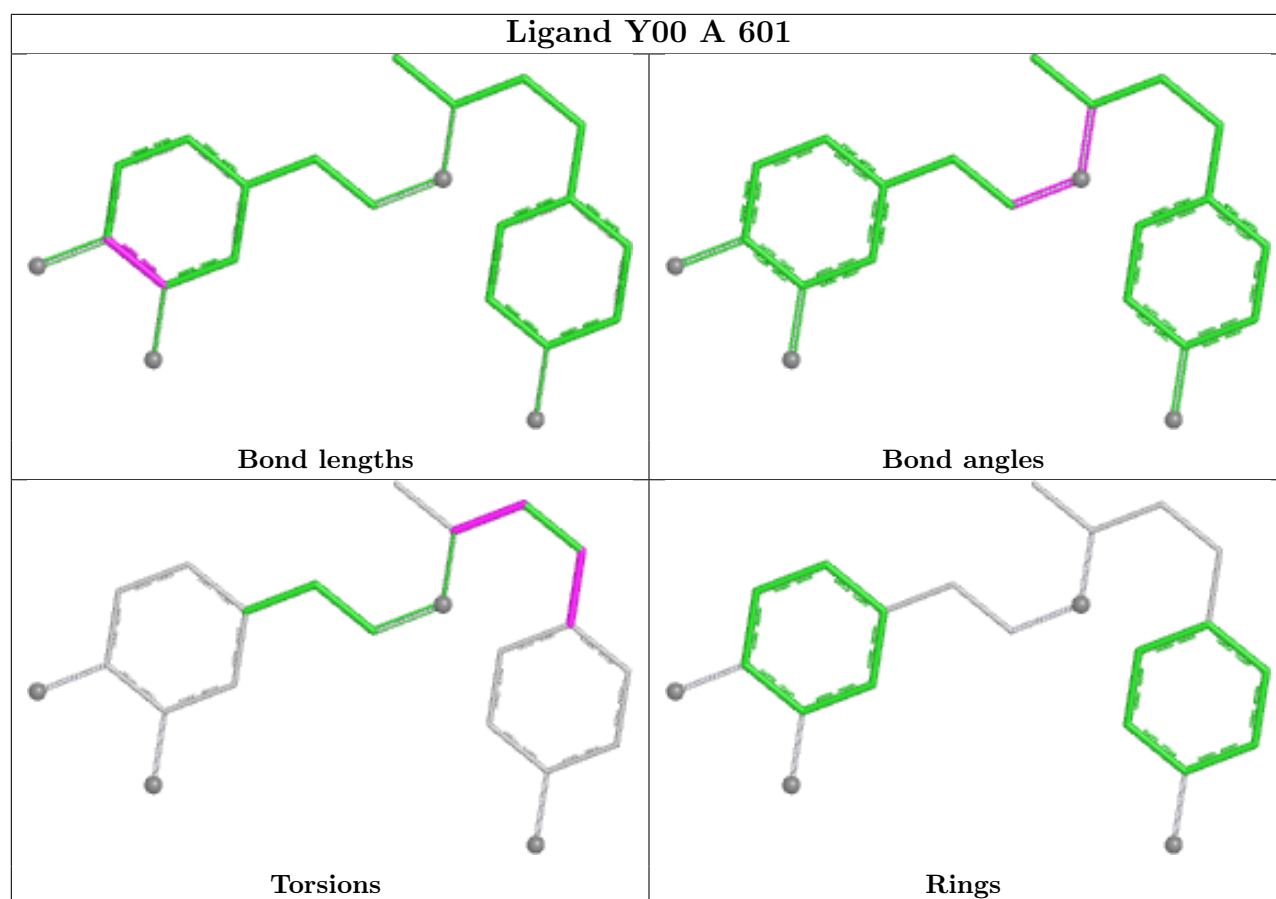
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	402	Y01	1	0
3	B	502	2CV	1	0
3	A	501	2CV	1	0
4	A	601	Y00	3	0
3	A	505	2CV	4	0
3	B	505	2CV	3	0
2	A	401	Y01	1	0
4	B	601	Y00	1	0
2	B	402	Y01	1	0
2	B	401	Y01	1	0
3	B	501	2CV	2	0

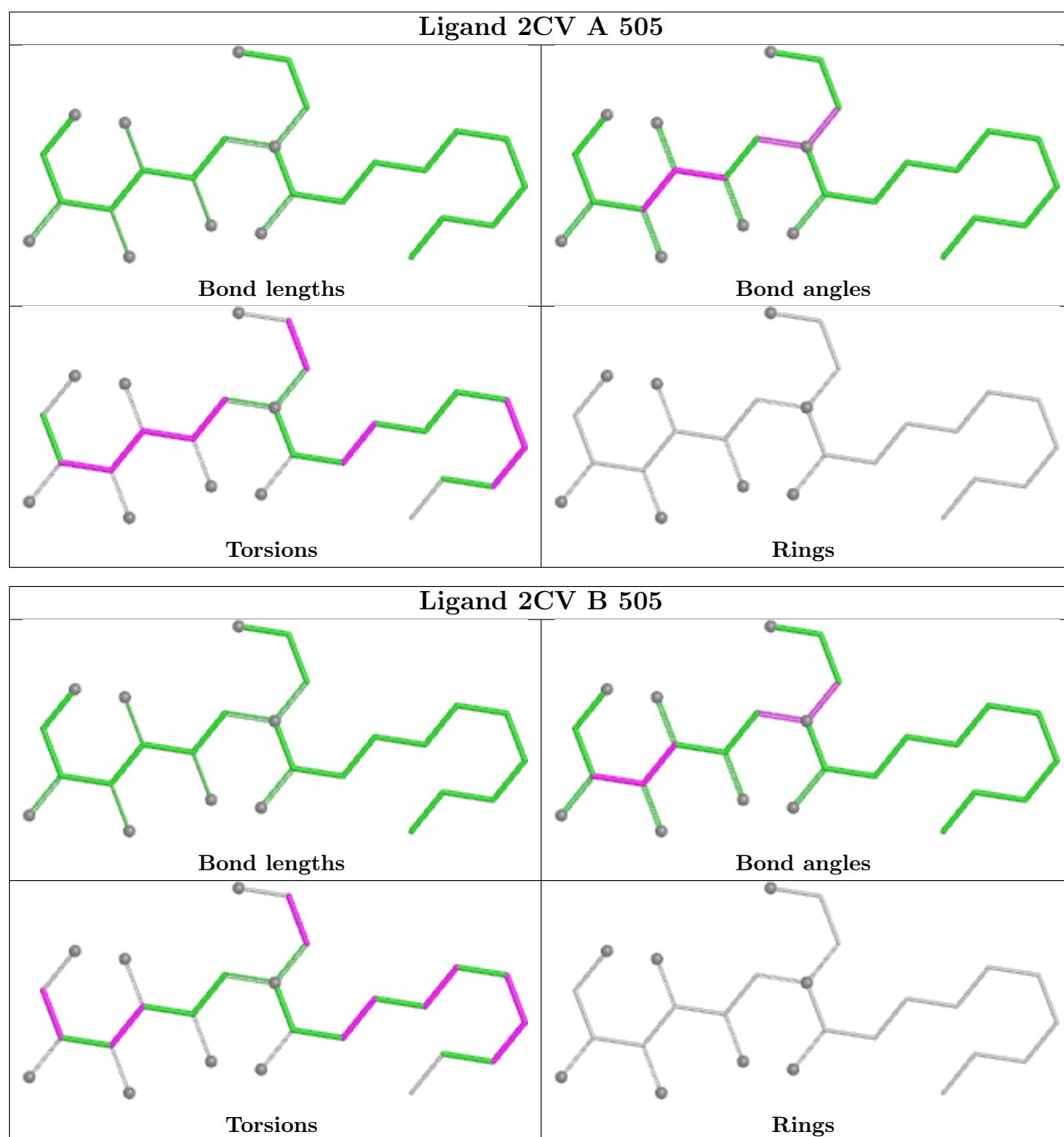
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is

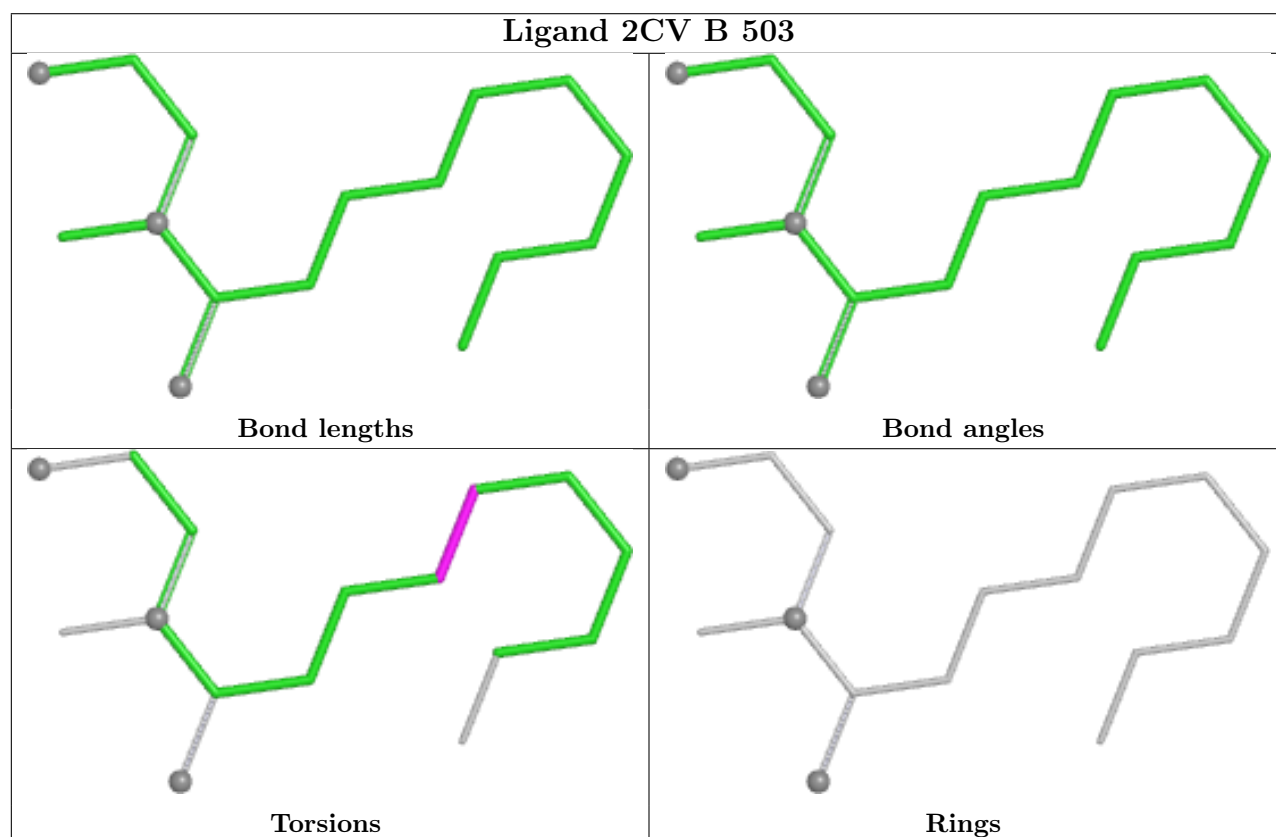
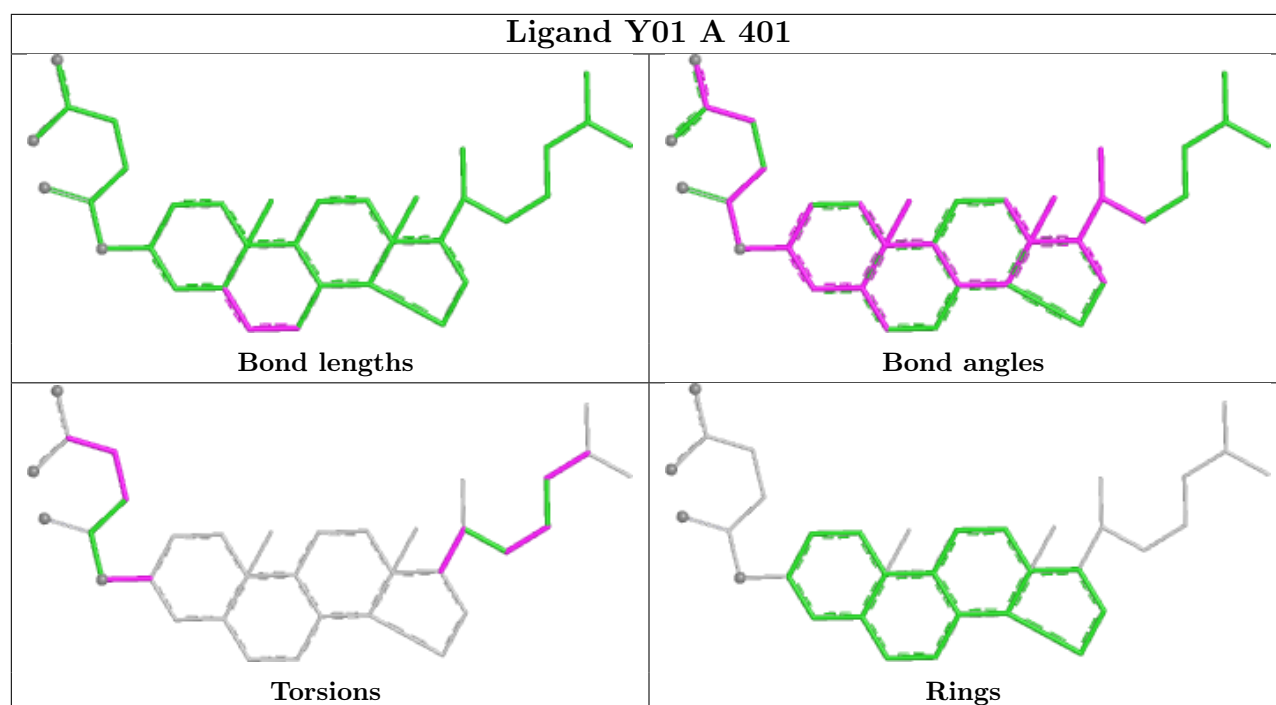
within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question 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.

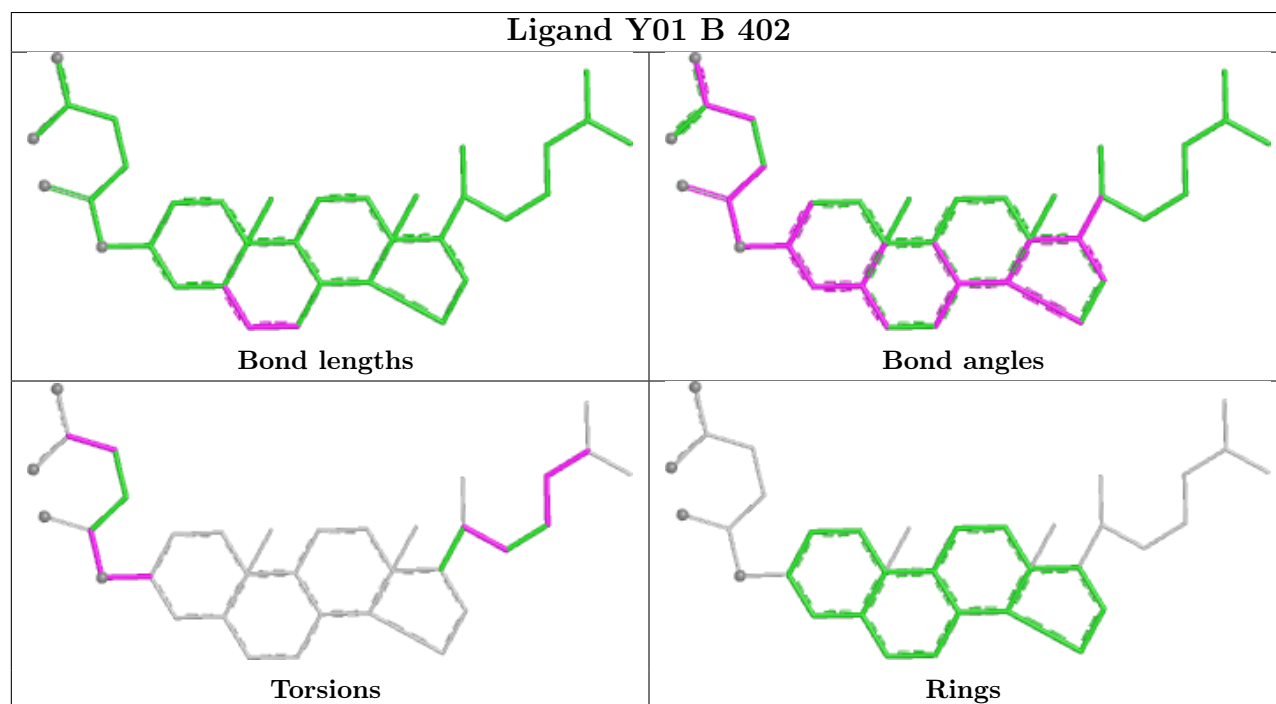
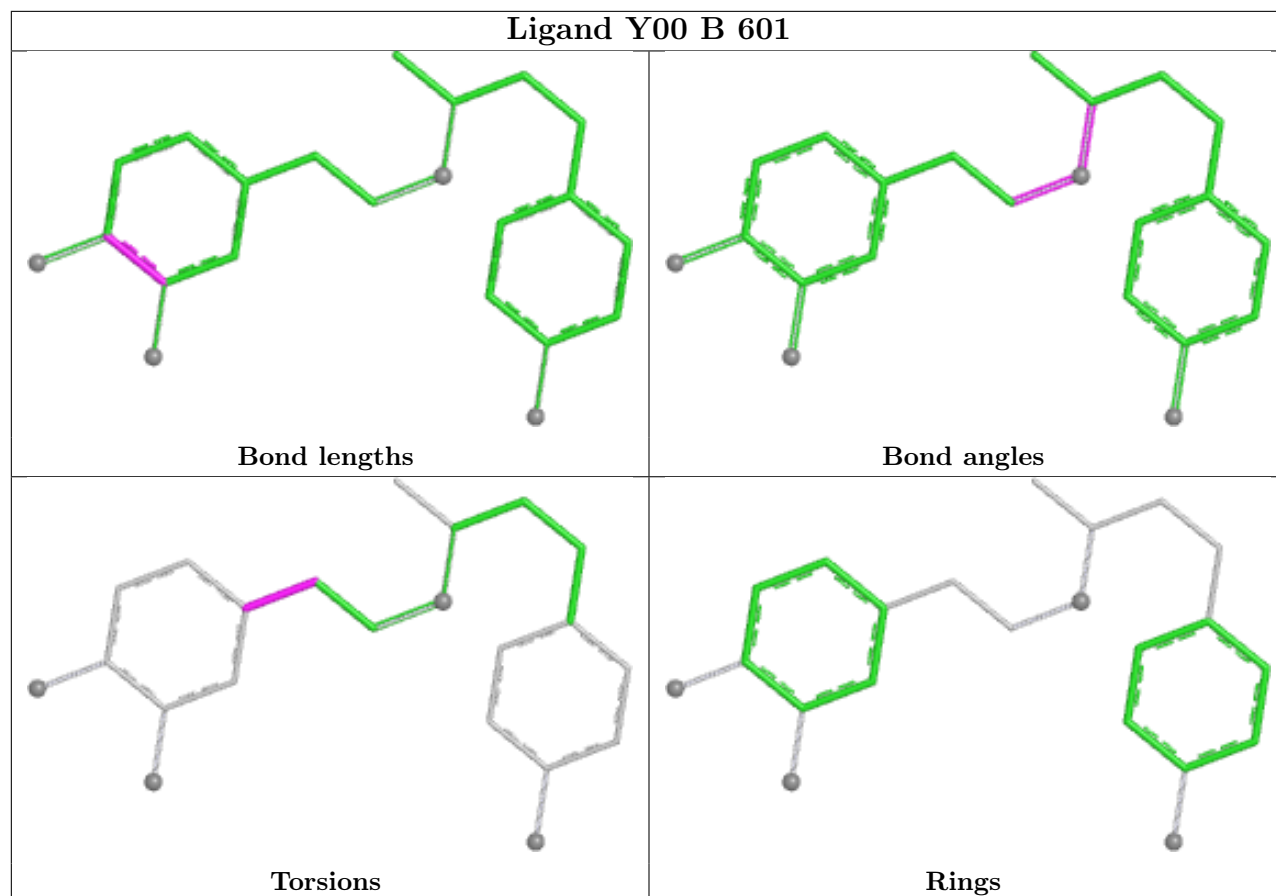


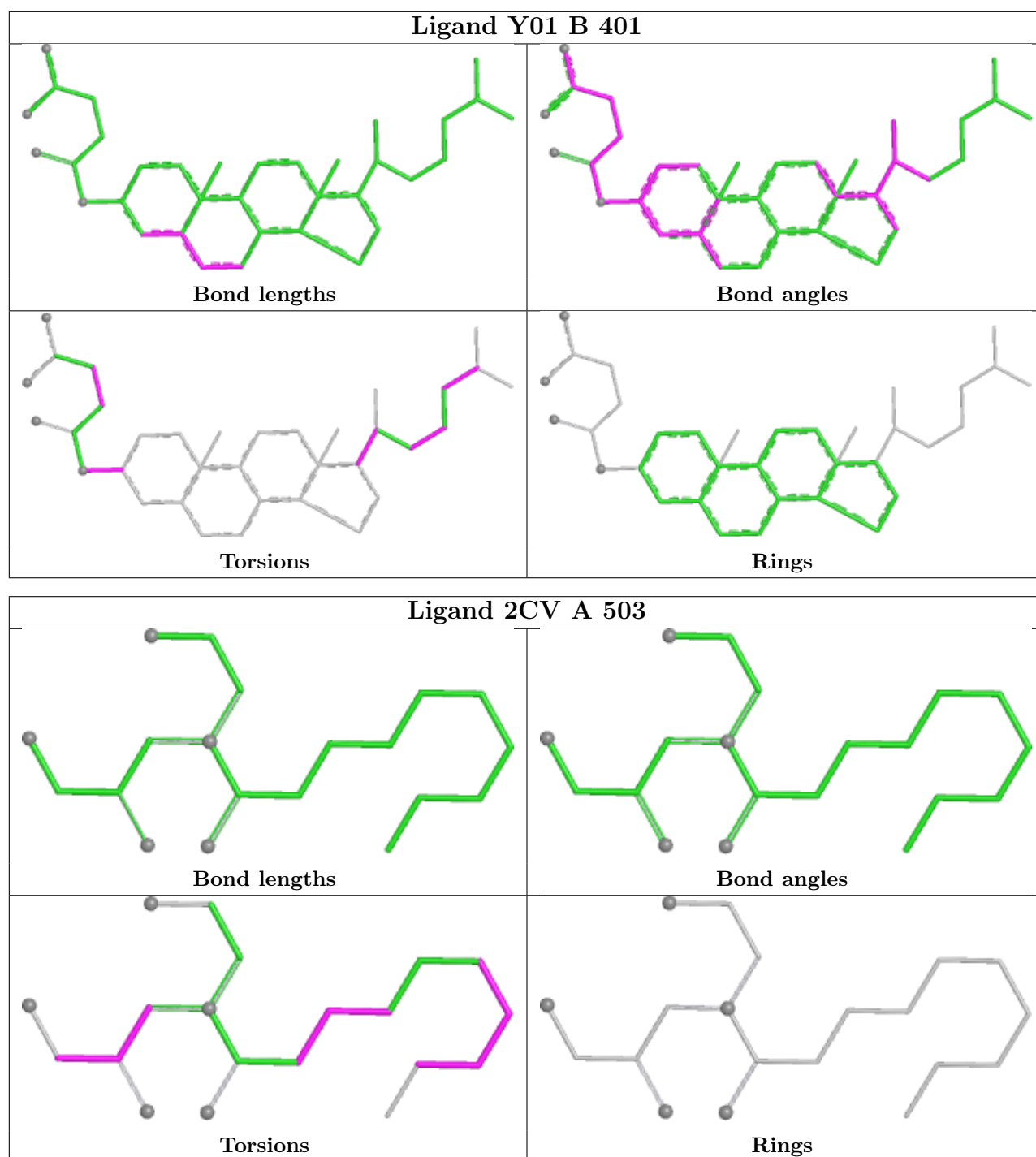


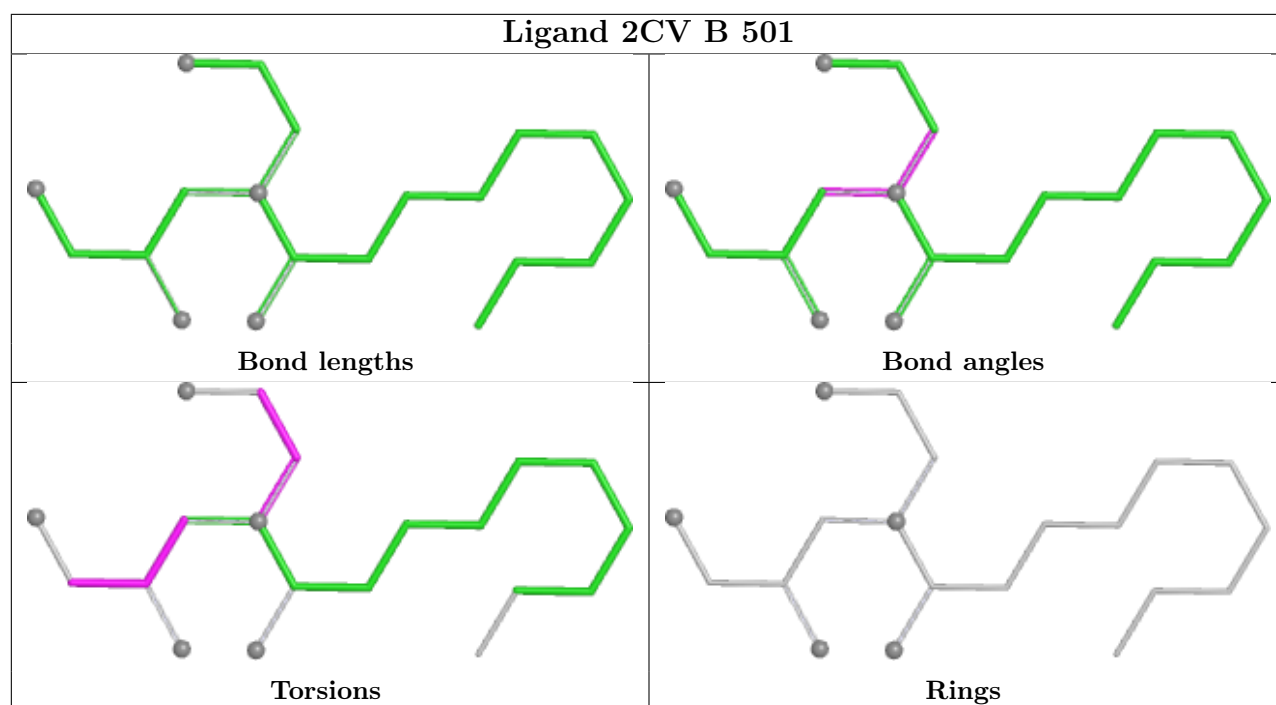












5.7 Other polymers [i](#)

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	286/315 (90%)	0.51	29 (10%)	12 10	10, 32, 76, 101	0
1	B	298/315 (94%)	0.50	31 (10%)	11 10	10, 30, 84, 99	0
All	All	584/630 (92%)	0.50	60 (10%)	12 10	10, 31, 79, 101	0

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	277	THR	6.9
1	B	241	ILE	6.6
1	B	280	VAL	6.6
1	A	358	ALA	6.5
1	B	281	MET	5.8
1	A	147	PHE	5.6
1	B	358	ALA	5.2
1	B	272	ALA	5.1
1	B	242	ASP	4.6
1	A	278	SER	4.5
1	A	318	ASP	4.5
1	B	278	SER	4.4
1	B	236	GLU	4.3
1	B	273	SER	4.0
1	B	275	ARG	3.9
1	B	239	ARG	3.8
1	B	279	ARG	3.8
1	B	40	TRP	3.7
1	A	319	LEU	3.6
1	B	284	ARG	3.6
1	A	316	ASN	3.6
1	A	280	VAL	3.4
1	A	281	MET	3.4
1	B	274	LYS	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	321	PRO	3.4
1	B	186	ASP	3.3
1	A	34	GLU	3.3
1	B	188	GLN	3.1
1	A	33	ALA	3.1
1	A	284	ARG	3.1
1	B	357	LEU	3.1
1	B	243	ARG	3.1
1	A	317	ARG	3.0
1	A	283	MET	2.9
1	B	276	LYS	2.9
1	B	238	ILE	2.8
1	A	200	ASP	2.8
1	A	320	VAL	2.8
1	B	282	LEU	2.7
1	A	348	ASP	2.7
1	A	279	ARG	2.6
1	A	151	SER	2.6
1	B	33	ALA	2.6
1	B	355	ARG	2.6
1	A	237	GLN	2.5
1	B	283	MET	2.5
1	B	70	GLN	2.5
1	A	187	PRO	2.4
1	B	194	GLN	2.4
1	A	322	ASP	2.4
1	A	141	LEU	2.3
1	A	152	LEU	2.2
1	B	240	LYS	2.2
1	B	319	LEU	2.2
1	A	149	TYR	2.2
1	A	70	GLN	2.2
1	B	356	LEU	2.1
1	A	290	LYS	2.1
1	A	285	GLU	2.1
1	A	323	TRP	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 ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

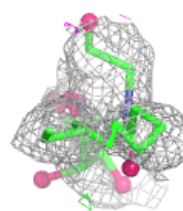
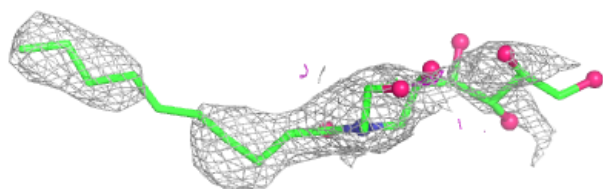
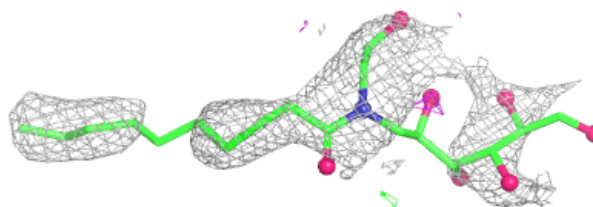
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	2CV	B	505	26/26	0.72	0.24	59,90,103,105	0
3	2CV	B	504	8/26	0.75	0.22	30,47,56,60	0
3	2CV	A	505	26/26	0.75	0.22	57,93,108,109	0
3	2CV	A	504	26/26	0.76	0.24	43,77,85,86	0
3	2CV	A	502	5/26	0.77	0.26	39,40,43,44	0
3	2CV	A	503	20/26	0.80	0.17	53,81,98,98	0
3	2CV	B	503	16/26	0.80	0.25	79,84,103,107	0
3	2CV	B	502	16/26	0.81	0.22	23,73,88,90	0
2	Y01	A	402	35/35	0.81	0.22	55,67,99,101	0
5	NA	A	1359	1/1	0.81	0.13	40,40,40,40	0
3	2CV	A	501	26/26	0.90	0.13	14,54,75,79	0
4	Y00	B	601	22/22	0.92	0.10	21,30,37,39	0
2	Y01	B	401	35/35	0.92	0.10	10,25,46,50	0
2	Y01	B	402	35/35	0.93	0.12	27,35,84,86	0
2	Y01	A	401	35/35	0.93	0.10	18,26,50,58	0
3	2CV	B	501	20/26	0.94	0.12	16,47,60,65	0
4	Y00	A	601	22/22	0.94	0.11	27,35,50,59	0

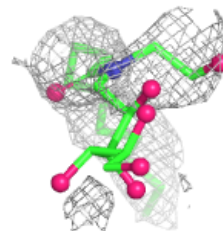
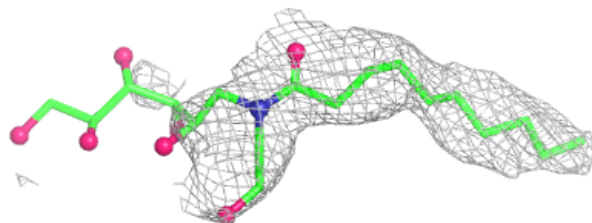
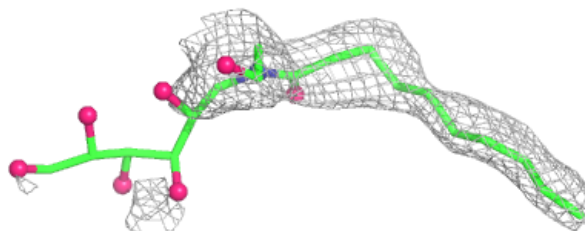
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 2CV B 505:

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

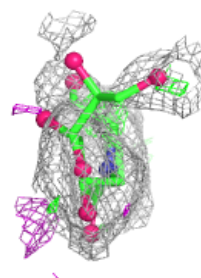
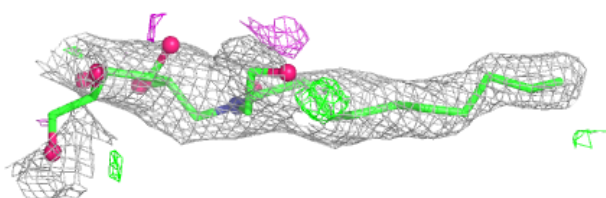
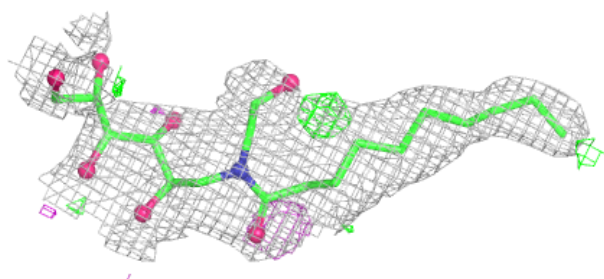
**Electron density around 2CV A 505:**

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

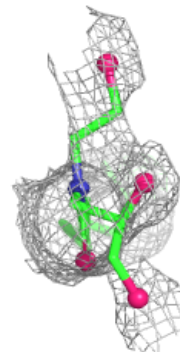
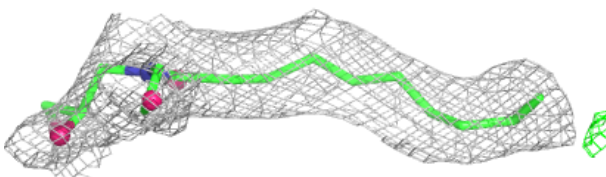
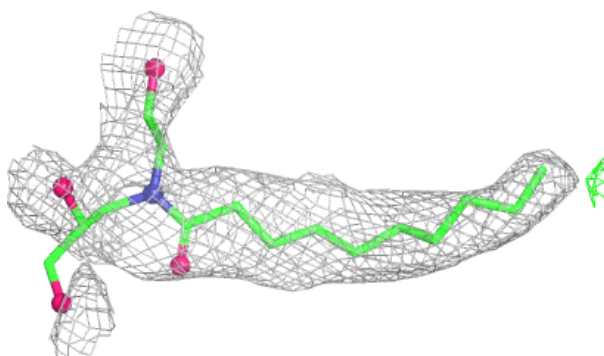


Electron density around 2CV A 504:

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

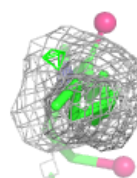
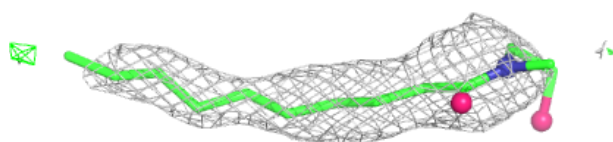
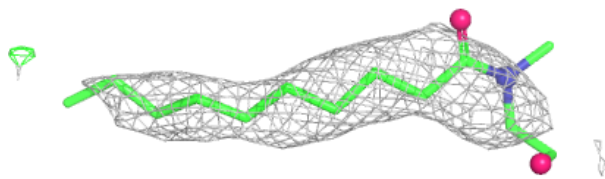
**Electron density around 2CV A 503:**

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

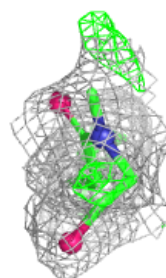
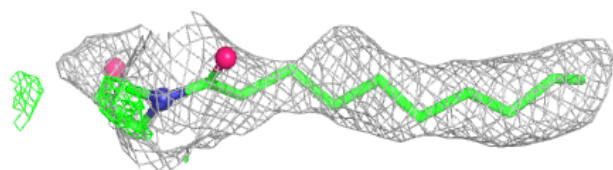
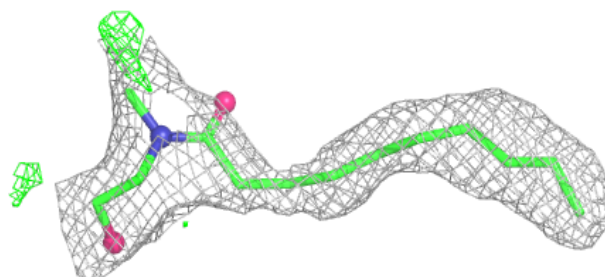


Electron density around 2CV B 503:

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

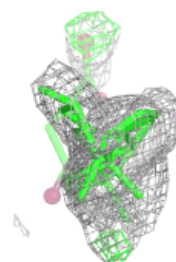
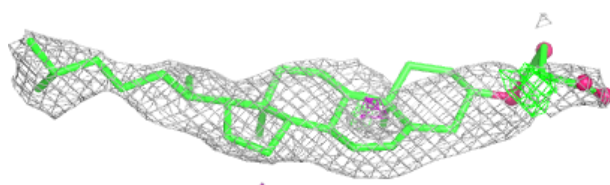
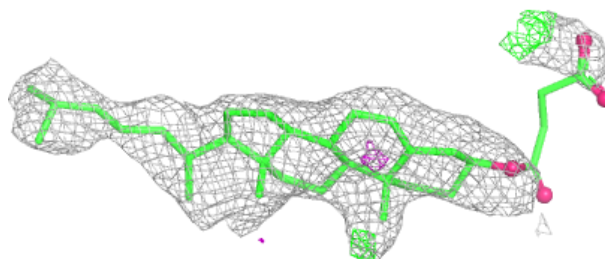
**Electron density around 2CV B 502:**

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

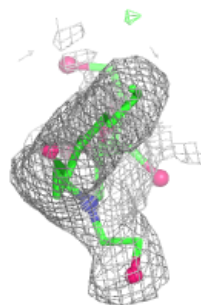
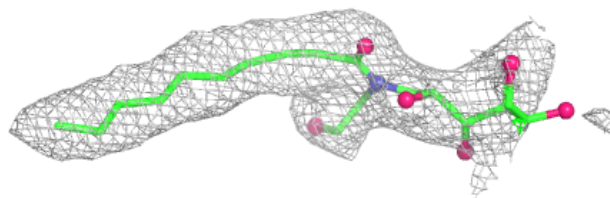
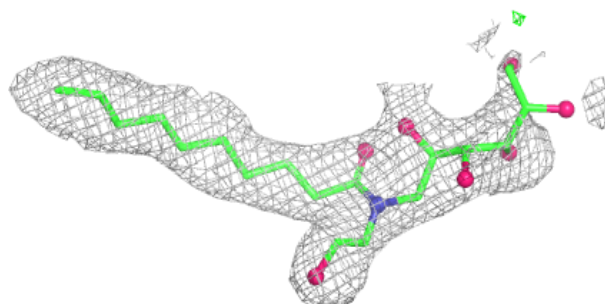


Electron density around Y01 A 402:

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

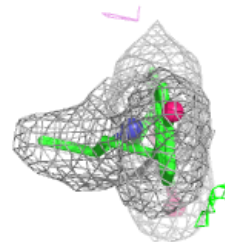
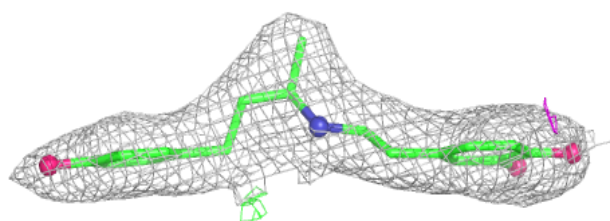
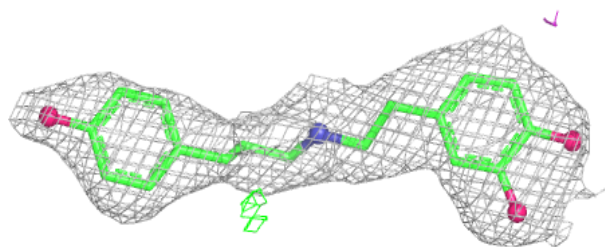
**Electron density around 2CV A 501:**

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

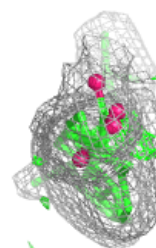
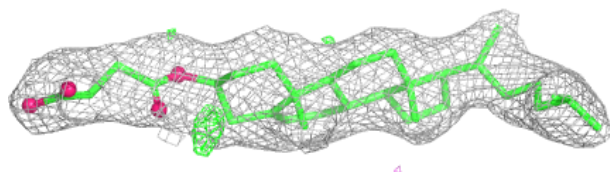
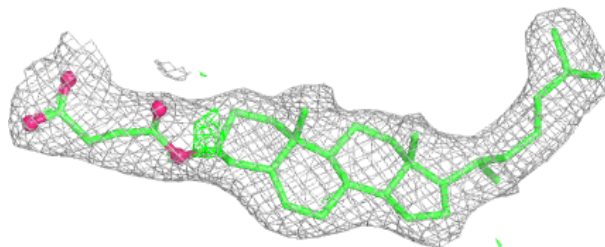


Electron density around Y00 B 601:

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

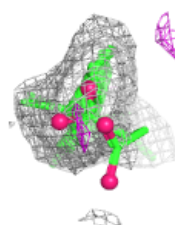
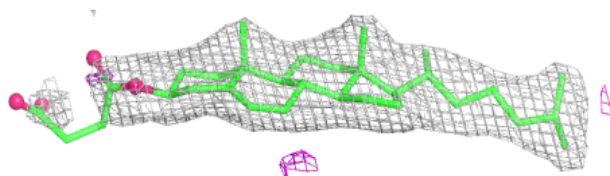
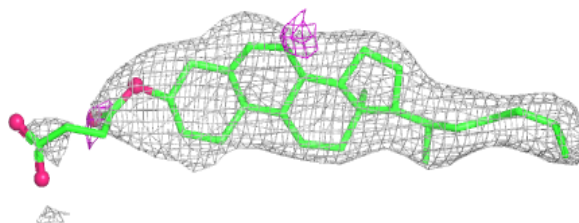
**Electron density around Y01 B 401:**

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

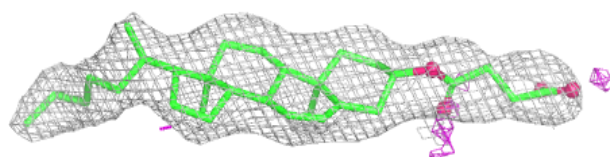
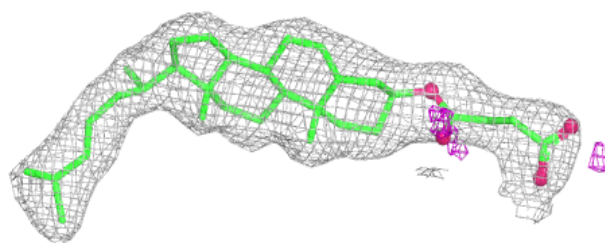


Electron density around Y01 B 402:

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

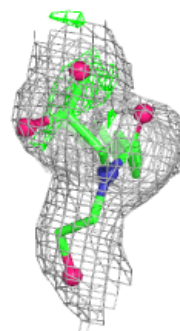
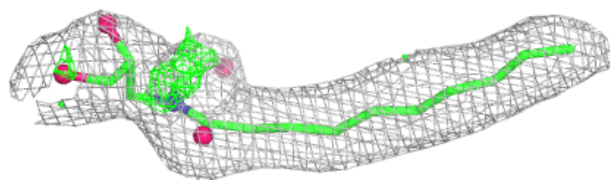
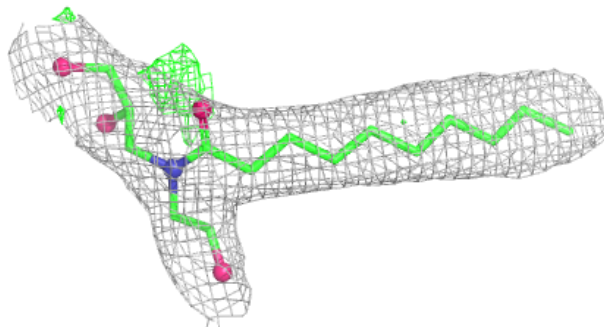
**Electron density around Y01 A 401:**

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

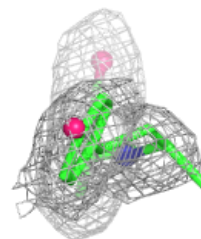
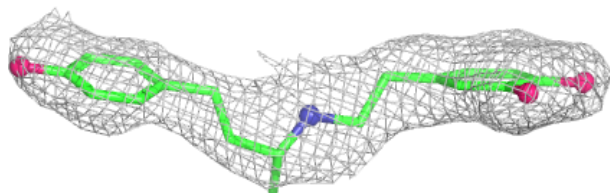
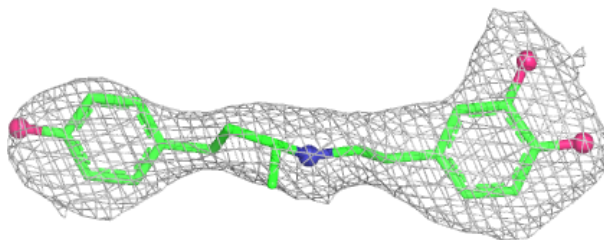


Electron density around 2CV B 501:

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

**Electron density around Y00 A 601:**

$2mF_o-DF_c$ (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.