



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 06:01 AM UTC

PDB ID : 4M48 / pdb_00004m48
Title : X-ray structure of dopamine transporter elucidates antidepressant mechanism
Authors : Gouaux, E.; Penmatsa, A.; Wang, K.
Deposited on : 2013-08-06
Resolution : 2.96 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

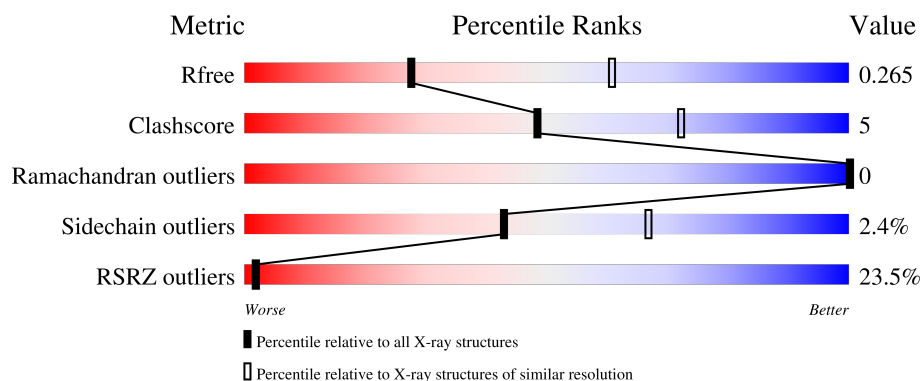
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.96 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	543	25% 86% 12% .
2	L	237	13% 74% 16% 10%
3	H	240	24% 72% 17% . 10%

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 7496 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 Transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	532	Total	C	N	O	S	0	1	0
			4184	2809	644	713	18			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	MET	-	initiating methionine	UNP Q9NB97
A	74	ALA	VAL	engineered mutation	UNP Q9NB97
A	275	ALA	VAL	engineered mutation	UNP Q9NB97
A	311	ALA	VAL	engineered mutation	UNP Q9NB97
A	415	ALA	LEU	engineered mutation	UNP Q9NB97
A	538	LEU	GLY	engineered mutation	UNP Q9NB97
A	602	LEU	-	expression tag	UNP Q9NB97
A	603	VAL	-	expression tag	UNP Q9NB97
A	604	PRO	-	expression tag	UNP Q9NB97
A	605	ARG	-	expression tag	UNP Q9NB97

- Molecule 2 is a protein called 9D5 antibody, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	214	Total	C	N	O	S	0	0	0
			1629	1013	272	336	8			

- Molecule 3 is a protein called 9D5 antibody, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	215	Total	C	N	O	S	0	0	0
			1600	1010	269	313	8			

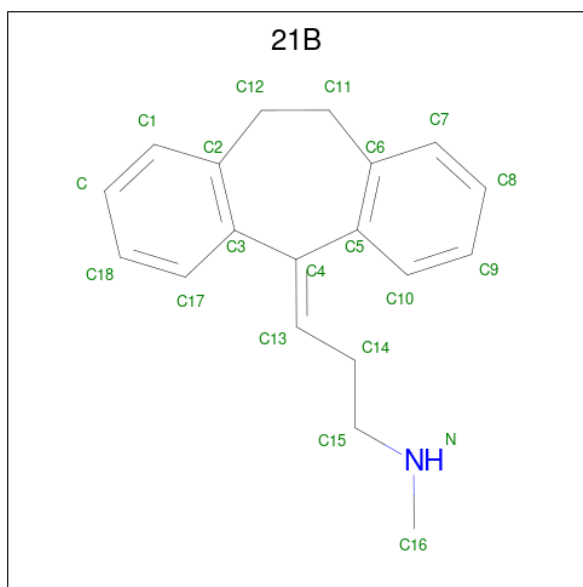
- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Na	0	0
			2	2		

- Molecule 5 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

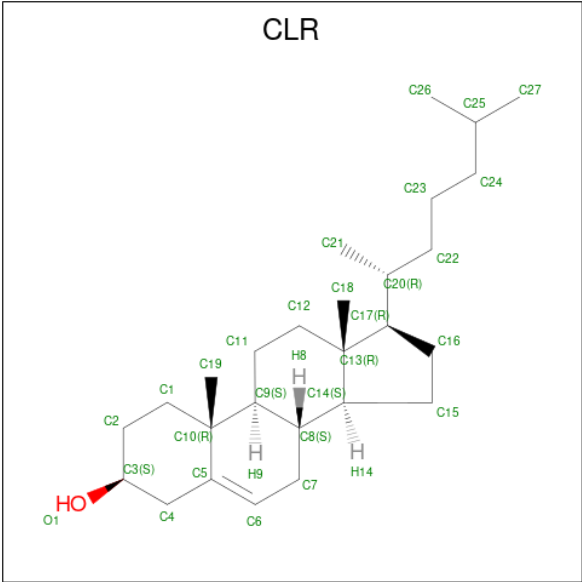
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Cl	0	0
			1	1		

- Molecule 6 is Nortriptyline (CCD ID: 21B) (formula: C₁₉H₂₁N).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	N	0	0
			20	19	1		

- Molecule 7 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			28	27	1		

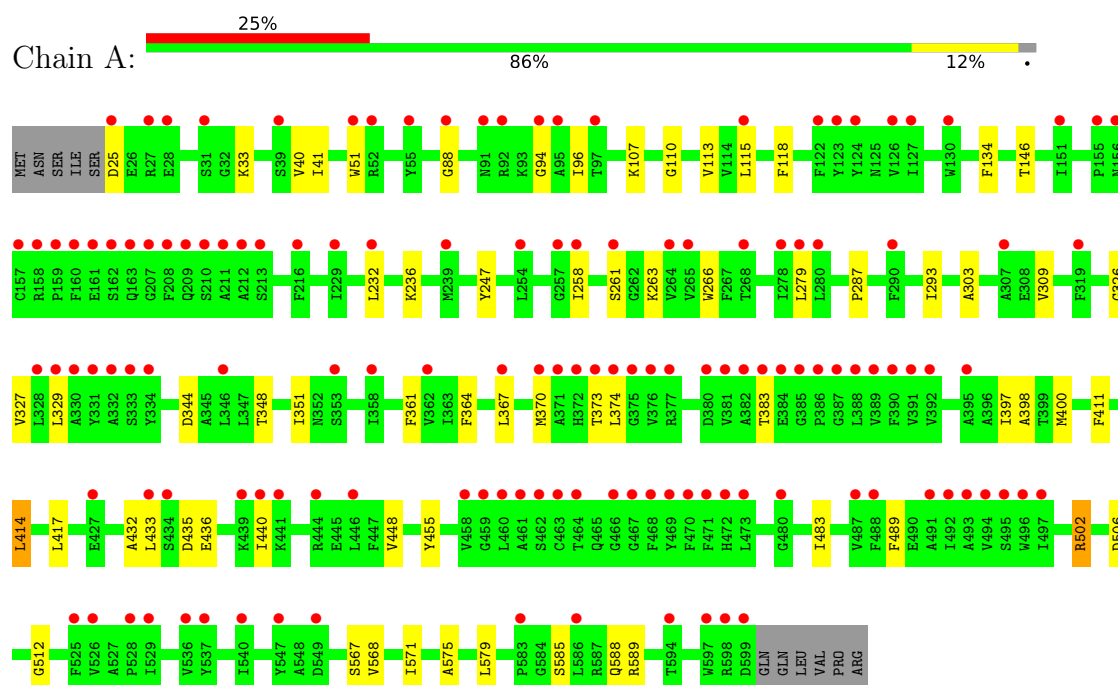
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	16	Total	O	0	0
			16	16		
8	L	9	Total	O	0	0
			9	9		
8	H	7	Total	O	0	0
			7	7		

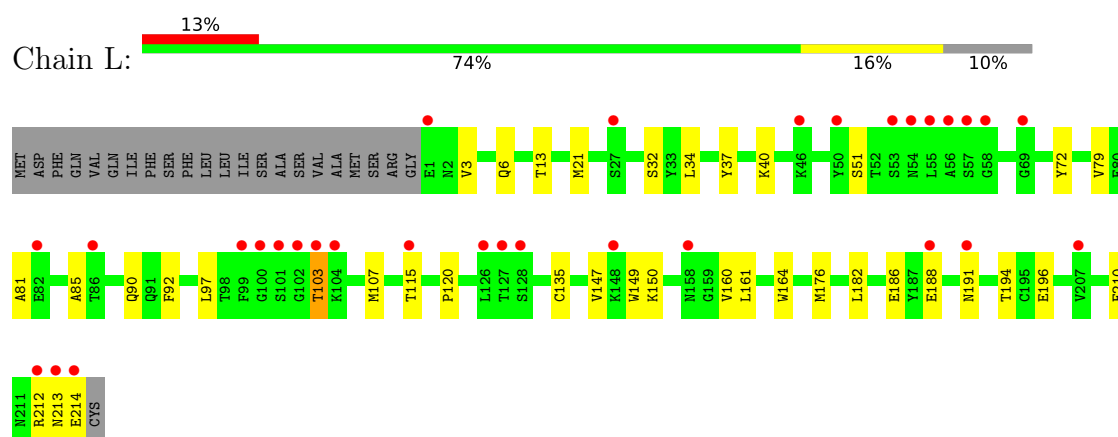
3 Residue-property plots

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.

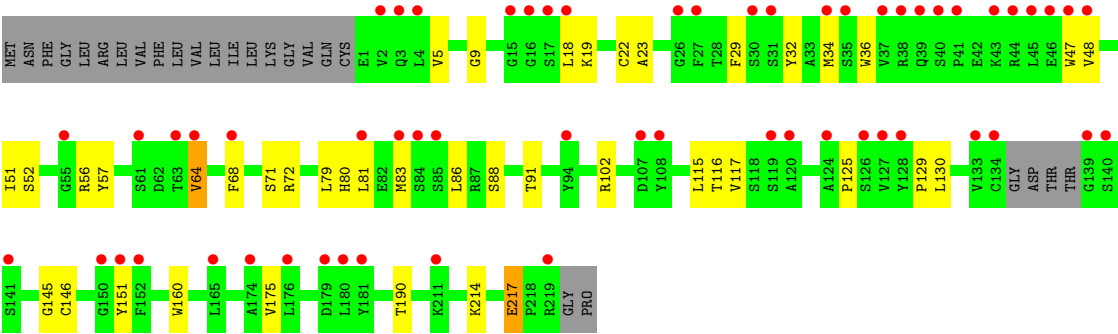
• Molecule 1: Transporter



• Molecule 2: 9D5 antibody, light chain



• Molecule 3: 9D5 antibody, heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.84Å 133.68Å 162.44Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.38 – 2.96 47.38 – 2.96	Depositor EDS
% Data completeness (in resolution range)	93.0 (47.38-2.96) 93.0 (47.38-2.96)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.18 (at 2.96Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1402)	Depositor
R, R_{free}	0.221 , 0.256 0.230 , 0.265	Depositor DCC
R_{free} test set	2086 reflections (4.60%)	wwPDB-VP
Wilson B-factor (Å ²)	89.9	Xtriage
Anisotropy	0.388	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 25.5	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	0.89	EDS
Total number of atoms	7496	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.92% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 21B, CLR, NA, CL

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	0.36	0/4329	0.73	0/5918
2	L	0.33	0/1667	0.70	0/2265
3	H	0.32	0/1638	0.72	2/2232 (0.1%)
All	All	0.34	0/7634	0.72	2/10415 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	H	217	GLU	CA-C-N	6.44	127.89	119.84
3	H	217	GLU	C-N-CA	6.44	127.89	119.84

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	4184	0	4074	38	0
2	L	1629	0	1545	20	0
3	H	1600	0	1536	29	0
4	A	2	0	0	0	0
5	A	1	0	0	0	0
6	A	20	0	21	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	28	0	46	1	0
8	A	16	0	0	0	0
8	H	7	0	0	0	0
8	L	9	0	0	0	0
All	All	7496	0	7222	80	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 (80) 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:94:GLY:N	1:A:435:ASP:OD2	2.27	0.67
3:H:29:PHE:O	3:H:72:ARG:NH2	2.26	0.66
1:A:33:LYS:NZ	1:A:344:ASP:OD2	2.28	0.65
1:A:107:LYS:NZ	1:A:436:GLU:OE2	2.24	0.65
1:A:40:VAL:HG12	1:A:348:THR:HG21	1.80	0.64
3:H:83:MET:HE2	3:H:86:LEU:HD21	1.85	0.59
2:L:40:LYS:HD2	2:L:85:ALA:HB2	1.84	0.59
3:H:83:MET:HE1	3:H:115:LEU:HD22	1.85	0.57
1:A:41:ILE:HD13	1:A:348:THR:HG23	1.87	0.57
1:A:303:ALA:HB1	1:A:309:VAL:HG21	1.87	0.56
3:H:32:TYR:O	3:H:72:ARG:NH2	2.37	0.55
1:A:585:SER:O	1:A:589:ARG:HG2	2.06	0.55
3:H:52:SER:HB3	3:H:57:TYR:HB2	1.89	0.55
1:A:433:LEU:HB3	1:A:440:ILE:HD11	1.88	0.55
2:L:191:ASN:OD1	2:L:212:ARG:N	2.38	0.55
2:L:13:THR:HG21	2:L:79:VAL:HG21	1.89	0.55
2:L:150:LYS:HB2	2:L:194:THR:HB	1.89	0.55
1:A:94:GLY:HA3	1:A:432:ALA:HA	1.89	0.55
1:A:414:LEU:HA	1:A:417:LEU:HB2	1.88	0.55
2:L:191:ASN:HA	2:L:212:ARG:HD3	1.89	0.55
1:A:364:PHE:HA	1:A:367:LEU:HB2	1.89	0.55
1:A:512:GLY:HA2	3:H:102:ARG:HD2	1.89	0.54
2:L:188:GLU:HG2	2:L:212:ARG:HH12	1.72	0.54
3:H:91:THR:HG23	3:H:116:THR:HA	1.89	0.54
3:H:71:SER:HB3	3:H:80:HIS:HB2	1.92	0.51
3:H:129:PRO:HD3	3:H:214:LYS:HE2	1.92	0.51
3:H:51:ILE:HD13	3:H:72:ARG:HB2	1.93	0.50
2:L:147:VAL:HB	2:L:176:MET:HE1	1.93	0.50
1:A:567:SER:OG	1:A:568:VAL:N	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:81:ALA:HA	2:L:107:MET:HE3	1.94	0.50
1:A:575:ALA:O	1:A:579:LEU:HB2	2.13	0.49
1:A:397:ILE:O	1:A:400:MET:HG2	2.12	0.49
1:A:351:ILE:HD13	7:A:705:CLR:H71	1.94	0.49
3:H:34:MET:HB3	3:H:79:LEU:HD22	1.93	0.49
2:L:6:GLN:NE2	2:L:103:THR:HG22	2.27	0.49
1:A:115:LEU:HA	1:A:118:PHE:HB3	1.95	0.48
1:A:585:SER:H	1:A:588:GLN:HB2	1.77	0.48
2:L:135:CYS:HB2	2:L:149:TRP:CH2	2.48	0.47
2:L:164:TRP:CE2	2:L:176:MET:HG3	2.50	0.47
1:A:489:PHE:CD2	1:A:571:ILE:HG21	2.50	0.47
3:H:48:VAL:HG13	3:H:64:VAL:HG21	1.96	0.47
2:L:37:TYR:HE2	2:L:90:GLN:HB3	1.80	0.47
3:H:9:GLY:H	3:H:18:LEU:HD21	1.81	0.46
1:A:146:THR:HG22	1:A:398:ALA:HB1	1.98	0.46
1:A:506:ASP:OD1	3:H:57:TYR:OH	2.26	0.46
1:A:287:PRO:HG2	1:A:373:THR:HG21	1.98	0.45
2:L:32:SER:HA	2:L:51:SER:OG	2.17	0.45
3:H:64:VAL:HG13	3:H:68:PHE:HB2	1.98	0.45
3:H:68:PHE:CE1	3:H:83:MET:HB3	2.52	0.45
1:A:433:LEU:HB3	1:A:440:ILE:CD1	2.47	0.44
3:H:36:TRP:NE1	3:H:81:LEU:HB2	2.31	0.44
3:H:146:CYS:HB2	3:H:160:TRP:CH2	2.52	0.44
2:L:161:LEU:HD11	3:H:175:VAL:HB	1.99	0.44
2:L:34:LEU:HD22	2:L:72:TYR:CD2	2.53	0.44
1:A:506:ASP:OD1	3:H:56:ARG:NH2	2.50	0.44
3:H:125:PRO:HB3	3:H:151:TYR:HB3	2.00	0.44
1:A:263:LYS:O	1:A:266:TRP:HB2	2.18	0.43
3:H:88:SER:HA	3:H:117:VAL:HB	2.00	0.43
1:A:33:LYS:HZ1	1:A:344:ASP:CG	2.22	0.43
1:A:483:ILE:HD12	1:A:483:ILE:HA	1.86	0.43
1:A:96:ILE:HA	1:A:110:GLY:HA3	1.99	0.42
1:A:247:TYR:CZ	1:A:455:TYR:HB3	2.54	0.42
1:A:258:ILE:HA	1:A:261:SER:OG	2.19	0.42
2:L:92:PHE:CE1	2:L:97:LEU:HD21	2.54	0.42
3:H:19:LYS:HE3	3:H:80:HIS:ND1	2.34	0.42
1:A:51:TRP:C	1:A:51:TRP:CD1	2.98	0.42
2:L:120:PRO:HB3	2:L:210:PHE:CE1	2.55	0.42
1:A:113:VAL:HG11	1:A:326:GLY:HA3	2.02	0.42
1:A:88:GLY:CA	1:A:329:LEU:HD12	2.50	0.42
1:A:134:PHE:HB3	1:A:411:PHE:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:22:CYS:HB3	3:H:79:LEU:HB3	2.02	0.41
1:A:502:ARG:HG2	3:H:56:ARG:NE	2.35	0.41
1:A:370:MET:HG2	1:A:374:LEU:HD12	2.02	0.41
2:L:21:MET:H	2:L:21:MET:HG2	1.75	0.41
3:H:130:LEU:HB2	3:H:145:GLY:C	2.46	0.41
1:A:502:ARG:HG2	3:H:56:ARG:CZ	2.51	0.41
3:H:5:VAL:HG23	3:H:23:ALA:HB3	2.03	0.41
1:A:293:ILE:HD12	1:A:361:PHE:HD1	1.86	0.41
2:L:182:LEU:HD22	2:L:186:GLU:HG3	2.03	0.40
2:L:97:LEU:HB2	3:H:47:TRP:CD2	2.56	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	531/543 (98%)	505 (95%)	26 (5%)	0	100	100
2	L	212/237 (90%)	204 (96%)	8 (4%)	0	100	100
3	H	211/240 (88%)	202 (96%)	9 (4%)	0	100	100
All	All	954/1020 (94%)	911 (96%)	43 (4%)	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	424/448 (95%)	415 (98%)	9 (2%)	47	69
2	L	184/207 (89%)	177 (96%)	7 (4%)	29	55
3	H	174/205 (85%)	171 (98%)	3 (2%)	53	73
All	All	782/860 (91%)	763 (98%)	19 (2%)	43	67

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	ASP
1	A	232	LEU
1	A	236	LYS
1	A	279	LEU
1	A	327	VAL
1	A	383	THR
1	A	414	LEU
1	A	448	VAL
1	A	502	ARG
2	L	3	VAL
2	L	103	THR
2	L	115	THR
2	L	160	VAL
2	L	196	GLU
2	L	213	ASN
2	L	214	GLU
3	H	64	VAL
3	H	190	THR
3	H	217	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	90	HIS
1	A	91	ASN
1	A	150	ASN
1	A	338	HIS
1	A	443	ASN
1	A	588	GLN
2	L	38	GLN
2	L	138	ASN
3	H	197	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 5 ligands modelled in this entry, 3 are monoatomic - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	21B	A	704	-	22,22,22	0.66	1 (4%)	27,29,29	1.28	3 (11%)
7	CLR	A	705	-	31,31,31	0.64	0	48,48,48	1.16	5 (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
6	21B	A	704	-	-	3/5/18/18	0/3/3/3
7	CLR	A	705	-	-	0/10/68/68	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	704	21B	C3-C2	-2.02	1.37	1.40

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	705	CLR	C4-C5-C10	3.04	120.32	116.42
6	A	704	21B	C16-N-C15	2.84	119.93	112.01
7	A	705	CLR	C7-C8-C9	2.65	112.78	109.72
6	A	704	21B	C3-C4-C13	-2.46	115.34	121.21
7	A	705	CLR	C7-C6-C5	-2.40	120.97	125.02
6	A	704	21B	C5-C4-C13	2.33	126.76	121.21
7	A	705	CLR	C10-C5-C6	-2.28	119.61	122.93
7	A	705	CLR	C14-C8-C9	-2.26	106.14	109.09

There are no chirality outliers.

All (3) torsion outliers are listed below:

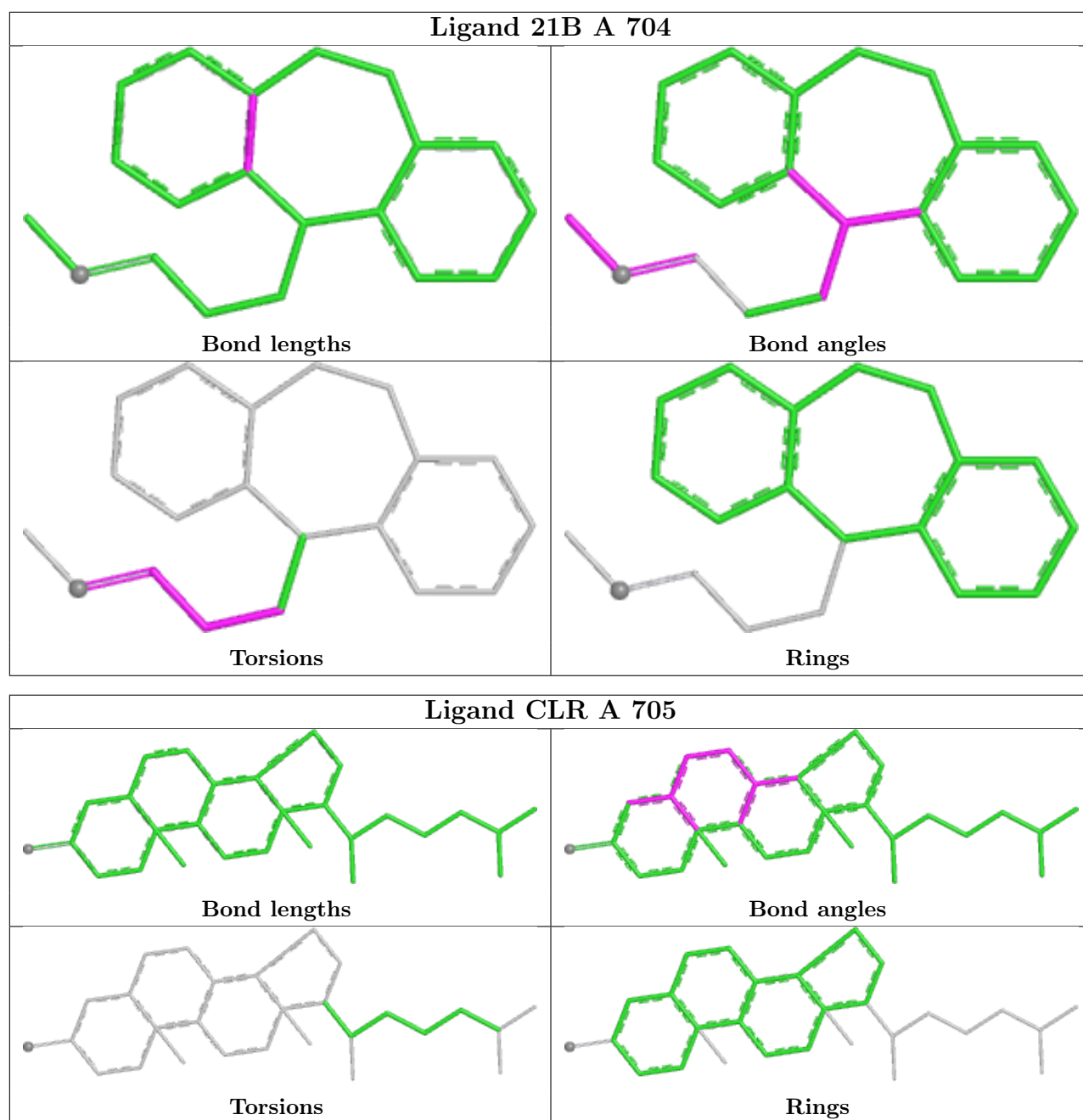
Mol	Chain	Res	Type	Atoms
6	A	704	21B	C14-C15-N-C16
6	A	704	21B	C13-C14-C15-N
6	A	704	21B	C4-C13-C14-C15

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	705	CLR	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [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	532/543 (97%)	1.48	137 (25%)	1 1	48, 84, 102, 136	1 (0%)
2	L	214/237 (90%)	0.79	31 (14%)	6 5	62, 76, 103, 133	0
3	H	215/240 (89%)	1.21	58 (26%)	1 1	63, 81, 101, 117	0
All	All	961/1020 (94%)	1.27	226 (23%)	2 2	48, 82, 102, 136	1 (0%)

All (226) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	GLU	14.0
1	A	375	GLY	12.4
1	A	380	ASP	10.9
1	A	384	GLU	10.5
1	A	462	SER	9.5
2	L	57	SER	9.5
1	A	209	GLN	8.8
1	A	207	GLY	8.8
1	A	208	PHE	8.0
1	A	385	GLY	7.9
1	A	160	PHE	7.9
1	A	461	ALA	7.9
1	A	158	ARG	7.8
1	A	387	GLY	7.5
3	H	44	ARG	7.4
1	A	376	VAL	7.3
1	A	163	GLN	7.2
1	A	374	LEU	7.2
1	A	468	PHE	7.2
2	L	213	ASN	7.1
1	A	386	PRO	7.0
1	A	130	TRP	6.8
1	A	470	PHE	6.4

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Mol	Chain	Res	Type	RSRZ
1	A	210	SER	6.4
1	A	162	SER	6.3
1	A	330	ALA	6.1
1	A	216	PHE	6.0
1	A	371	ALA	6.0
1	A	471	PHE	5.7
3	H	61	SER	5.7
3	H	48	VAL	5.7
1	A	383	THR	5.7
1	A	391	VAL	5.6
1	A	495	SER	5.3
1	A	258	ILE	5.3
1	A	381	VAL	5.2
2	L	214	GLU	5.1
1	A	492	ILE	5.0
1	A	390	PHE	4.9
1	A	467	GLY	4.9
1	A	469	TYR	4.9
3	H	108	TYR	4.9
1	A	392	VAL	4.8
2	L	56	ALA	4.8
3	H	46	GLU	4.8
3	H	134	CYS	4.7
1	A	382	ALA	4.7
1	A	213	SER	4.6
1	A	159	PRO	4.6
1	A	388	LEU	4.6
1	A	51	TRP	4.6
1	A	472	HIS	4.6
1	A	496	TRP	4.5
3	H	45	LEU	4.5
1	A	491	ALA	4.5
1	A	290[A]	PHE	4.5
2	L	54	ASN	4.5
2	L	58	GLY	4.5
1	A	307	ALA	4.5
1	A	497	ILE	4.4
1	A	332	ALA	4.4
1	A	460	LEU	4.4
1	A	126	VAL	4.3
3	H	133	VAL	4.3
1	A	28	GLU	4.3

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Mol	Chain	Res	Type	RSRZ
1	A	329	LEU	4.2
1	A	395	ALA	4.2
1	A	459	GLY	4.2
2	L	50	TYR	4.1
3	H	85	SER	4.1
3	H	2	VAL	4.1
1	A	261	SER	4.1
1	A	537	TYR	4.0
2	L	188	GLU	4.0
3	H	64	VAL	4.0
1	A	331	TYR	3.9
1	A	333	SER	3.9
3	H	179	ASP	3.9
2	L	46	LYS	3.8
1	A	346	LEU	3.8
1	A	536	VAL	3.8
1	A	599	ASP	3.8
1	A	547	TYR	3.8
2	L	104	LYS	3.8
1	A	373	THR	3.7
3	H	63	THR	3.7
1	A	458	VAL	3.7
1	A	446	LEU	3.7
1	A	157	CYS	3.6
3	H	176	LEU	3.6
1	A	427	GLU	3.6
1	A	372	HIS	3.5
1	A	494	VAL	3.5
1	A	92	ARG	3.5
3	H	38	ARG	3.5
1	A	493	ALA	3.5
3	H	81	LEU	3.4
1	A	155	PRO	3.4
3	H	181	TYR	3.4
1	A	151	ILE	3.4
3	H	47	TRP	3.3
1	A	123	TYR	3.3
3	H	174	ALA	3.3
1	A	358	ILE	3.3
3	H	43	LYS	3.2
3	H	107	ASP	3.2
1	A	480	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	25	ASP	3.2
1	A	88	GLY	3.1
1	A	583	PRO	3.1
3	H	219	ARG	3.1
1	A	487	VAL	3.1
3	H	18	LEU	3.1
1	A	122	PHE	3.1
2	L	207	VAL	3.1
1	A	463	CYS	3.1
2	L	53	SER	3.1
1	A	257	GLY	3.1
1	A	334	TYR	3.0
1	A	156	ASN	3.0
1	A	127	ILE	3.0
1	A	464	THR	3.0
3	H	68	PHE	3.0
3	H	31	SER	3.0
1	A	488	PHE	3.0
1	A	212	ALA	3.0
1	A	540	ILE	2.9
3	H	4	LEU	2.9
3	H	55	GLY	2.9
3	H	41	PRO	2.9
3	H	83	MET	2.9
2	L	212	ARG	2.9
1	A	124	TYR	2.8
1	A	389	VAL	2.8
3	H	127	VAL	2.8
1	A	279	LEU	2.8
1	A	434	SER	2.8
2	L	103	THR	2.8
1	A	229	ILE	2.8
2	L	158	ASN	2.8
1	A	353	SER	2.8
2	L	127	THR	2.8
1	A	254	LEU	2.8
1	A	441	LYS	2.7
2	L	126	LEU	2.7
3	H	151	TYR	2.7
2	L	115	THR	2.7
3	H	17	SER	2.7
3	H	180	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
3	H	34	MET	2.7
1	A	91	ASN	2.7
2	L	191	ASN	2.7
1	A	549	ASP	2.7
3	H	84	SER	2.7
1	A	278	ILE	2.6
2	L	128	SER	2.7
3	H	120	ALA	2.6
1	A	39	SER	2.6
1	A	319	PHE	2.6
1	A	370	MET	2.6
1	A	52	ARG	2.6
1	A	268	THR	2.6
3	H	211	LYS	2.6
1	A	115	LEU	2.6
3	H	140	SER	2.5
3	H	16	GLY	2.5
1	A	440	ILE	2.5
1	A	594	THR	2.5
3	H	119	SER	2.5
3	H	139	GLY	2.5
3	H	165	LEU	2.5
3	H	30	SER	2.5
1	A	439	LYS	2.5
1	A	526	VAL	2.4
1	A	97	THR	2.4
3	H	150	GLY	2.4
1	A	27	ARG	2.4
1	A	377	ARG	2.4
3	H	27	PHE	2.4
2	L	86	THR	2.4
1	A	362	VAL	2.4
1	A	598	ARG	2.4
2	L	99	PHE	2.4
2	L	148	LYS	2.4
1	A	211	ALA	2.3
3	H	26	GLY	2.3
2	L	69	GLY	2.3
3	H	15	GLY	2.3
2	L	1	GLU	2.3
1	A	31	SER	2.3
3	H	40	SER	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	265	VAL	2.3
1	A	55	TYR	2.3
1	A	367	LEU	2.2
1	A	466	GLY	2.2
1	A	433	LEU	2.2
3	H	94	TYR	2.2
1	A	264	VAL	2.2
1	A	597	TRP	2.2
2	L	27	SER	2.2
1	A	528	PRO	2.2
1	A	280	LEU	2.2
1	A	328	LEU	2.2
1	A	586	LEU	2.2
3	H	35	SER	2.2
1	A	473	LEU	2.1
1	A	95	ALA	2.1
2	L	82	GLU	2.1
1	A	94	GLY	2.1
2	L	102	GLY	2.1
1	A	529	ILE	2.1
3	H	3	GLN	2.1
3	H	37	VAL	2.1
2	L	55	LEU	2.1
1	A	444	ARG	2.1
2	L	101	SER	2.1
3	H	126	SER	2.1
1	A	239	MET	2.1
2	L	100	GLY	2.1
3	H	141	SER	2.0
1	A	232	LEU	2.0
3	H	152	PHE	2.0
3	H	124	ALA	2.0
3	H	39	GLN	2.0
1	A	525	PHE	2.0
3	H	128	TYR	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

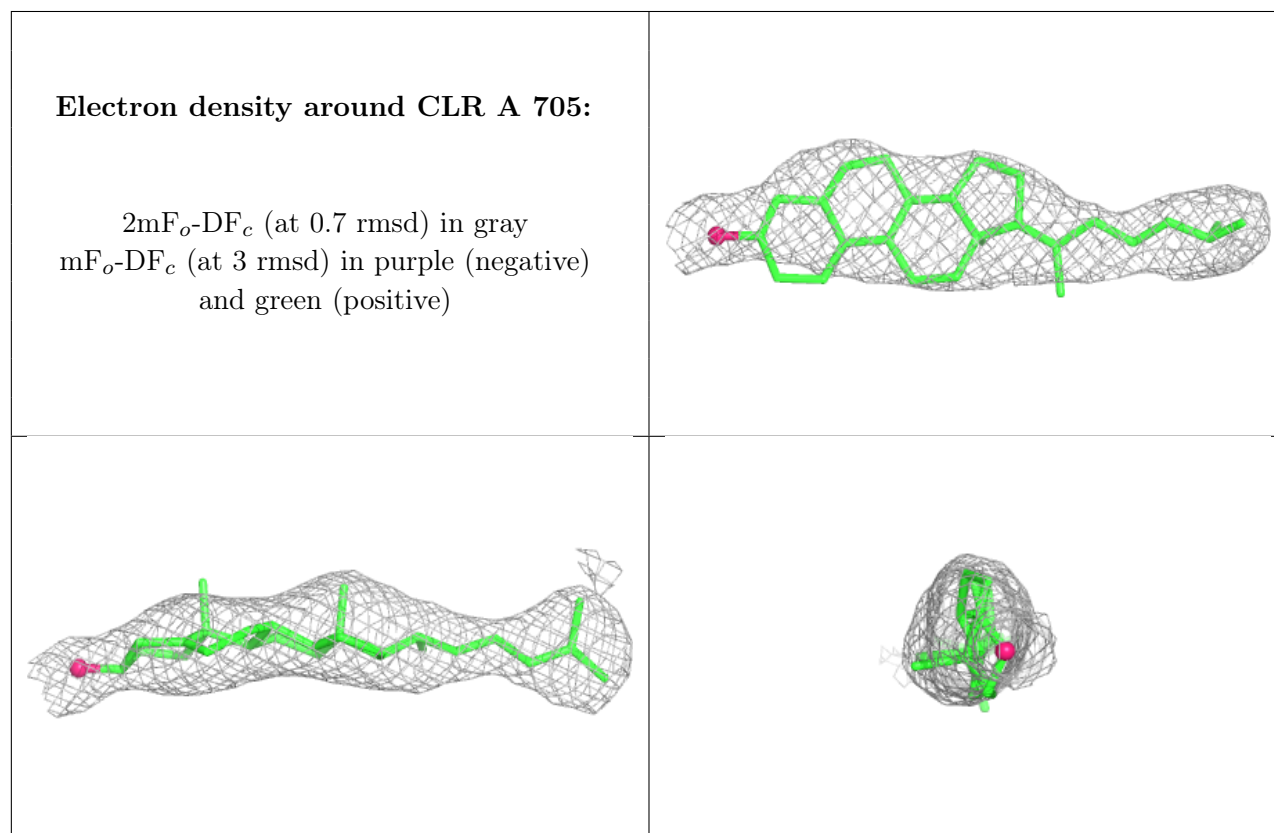
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

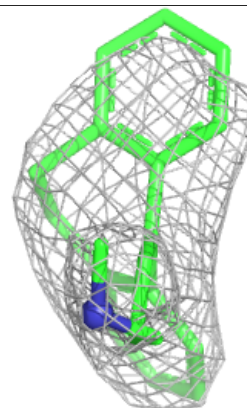
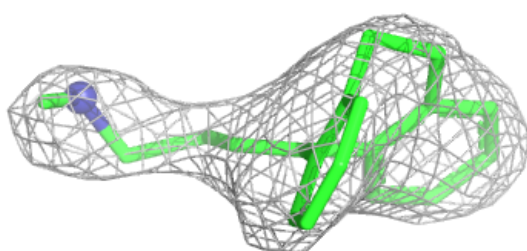
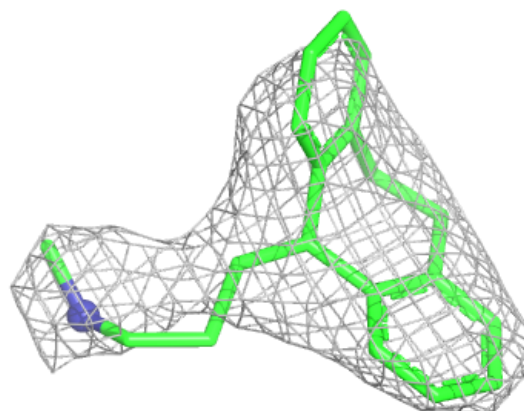
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
7	CLR	A	705	28/28	0.86	0.20	84,92,101,103	0
6	21B	A	704	20/20	0.93	0.18	71,76,83,87	0
4	NA	A	702	1/1	0.97	0.06	67,67,67,67	0
4	NA	A	701	1/1	0.99	0.04	71,71,71,71	0
5	CL	A	703	1/1	0.99	0.11	76,76,76,76	0

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 21B A 704:

$2mF_o - DF_c$ (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.