



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 1, 2026 – 01:03 PM UTC

PDB ID : 6LPL / pdb_00006lpl
Title : A2AR crystallized in EROCO17+4, SS-ROX at 100 K
Authors : Ihara, K.; Hato, M.; Nakane, T.; Yamashita, K.; Kimura-Someya, T.; Hosaka, T.; Ishizuka-Katsura, Y.; Tanaka, R.; Tanaka, T.; Sugahara, M.; Hirata, K.; Yamamoto, M.; Nureki, O.; Tono, K.; Nango, E.; Iwata, S.; Shirouzu, M.
Deposited on : 2020-01-11
Resolution : 2.00 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

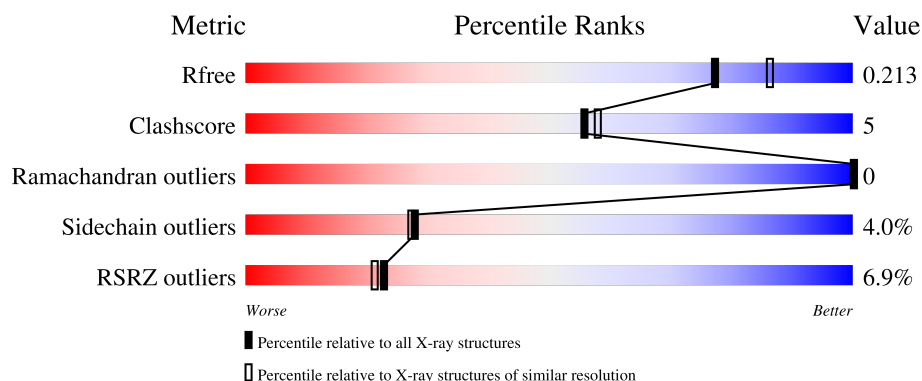
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	447	6% 77% 9% • 13%

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 3605 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 Adenosine receptor A2a,Soluble cytochrome b562,Adenosine receptor A2a.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	390	Total	C	N	O	S	0	0	0
			3036	1977	515	522	22			

There are 39 discrepancies between the modelled and reference sequences:

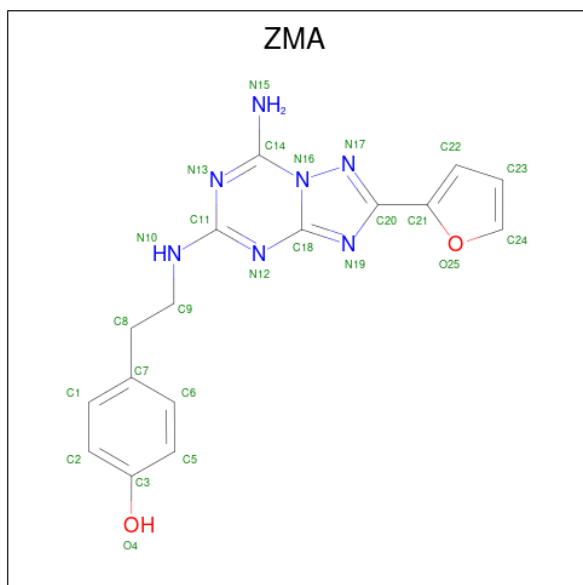
Chain	Residue	Modelled	Actual	Comment	Reference
A	-24	MET	-	initiating methionine	UNP P29274
A	-23	LYS	-	expression tag	UNP P29274
A	-22	THR	-	expression tag	UNP P29274
A	-21	ILE	-	expression tag	UNP P29274
A	-20	ILE	-	expression tag	UNP P29274
A	-19	ALA	-	expression tag	UNP P29274
A	-18	LEU	-	expression tag	UNP P29274
A	-17	SER	-	expression tag	UNP P29274
A	-16	TYR	-	expression tag	UNP P29274
A	-15	ILE	-	expression tag	UNP P29274
A	-14	PHE	-	expression tag	UNP P29274
A	-13	CYS	-	expression tag	UNP P29274
A	-12	LEU	-	expression tag	UNP P29274
A	-11	VAL	-	expression tag	UNP P29274
A	-10	PHE	-	expression tag	UNP P29274
A	-9	ALA	-	expression tag	UNP P29274
A	-8	ASP	-	expression tag	UNP P29274
A	-7	TYR	-	expression tag	UNP P29274
A	-6	LYS	-	expression tag	UNP P29274
A	-5	ASP	-	expression tag	UNP P29274
A	-4	ASP	-	expression tag	UNP P29274
A	-3	ASP	-	expression tag	UNP P29274
A	-2	ASP	-	expression tag	UNP P29274
A	-1	GLY	-	expression tag	UNP P29274
A	0	ALA	-	expression tag	UNP P29274
A	1	PRO	-	expression tag	UNP P29274

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Chain	Residue	Modelled	Actual	Comment	Reference
A	1007	TRP	MET	engineered mutation	UNP P0ABE7
A	1102	ILE	HIS	engineered mutation	UNP P0ABE7
A	1106	LEU	ARG	engineered mutation	UNP P0ABE7
A	317	HIS	-	expression tag	UNP P29274
A	318	HIS	-	expression tag	UNP P29274
A	319	HIS	-	expression tag	UNP P29274
A	320	HIS	-	expression tag	UNP P29274
A	321	HIS	-	expression tag	UNP P29274
A	322	HIS	-	expression tag	UNP P29274
A	323	HIS	-	expression tag	UNP P29274
A	324	HIS	-	expression tag	UNP P29274
A	325	HIS	-	expression tag	UNP P29274
A	326	HIS	-	expression tag	UNP P29274

- Molecule 2 is 4-{2-[(7-amino-2-furan-2-yl)[1,2,4]triazolo[1,5-a][1,3,5]triazin-5-yl)amino]ethyl} phenol (CCD ID: ZMA) (formula: C₁₆H₁₅N₇O₂).

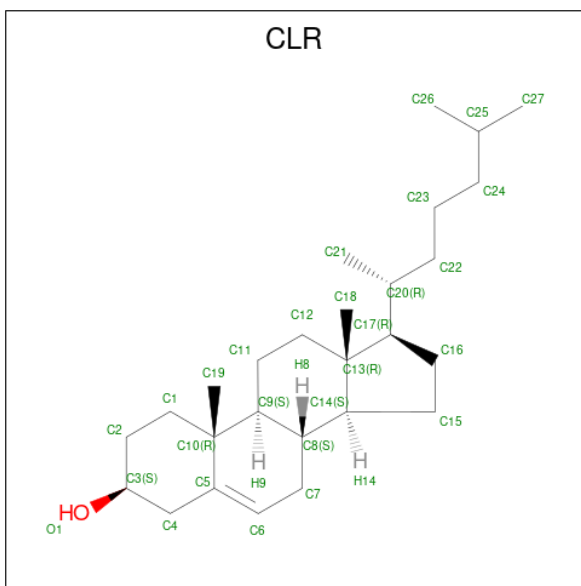


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			25	16	7	2		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

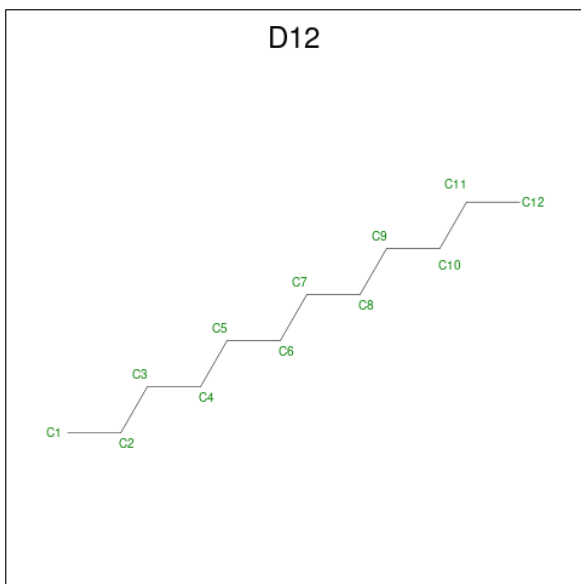
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Na	0	0
			1	1		

- Molecule 4 is CHOLESTEROL (CCD ID: CLR) (formula: $C_{27}H_{46}O$).



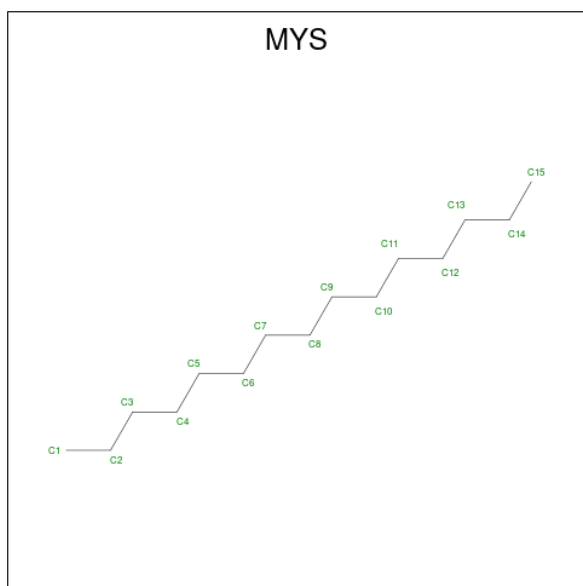
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			28	27	1		
4	A	1	Total	C	O	0	0
			28	27	1		
4	A	1	Total	C	O	0	0
			28	27	1		

- Molecule 5 is DODECANE (CCD ID: D12) (formula: $C_{12}H_{26}$).



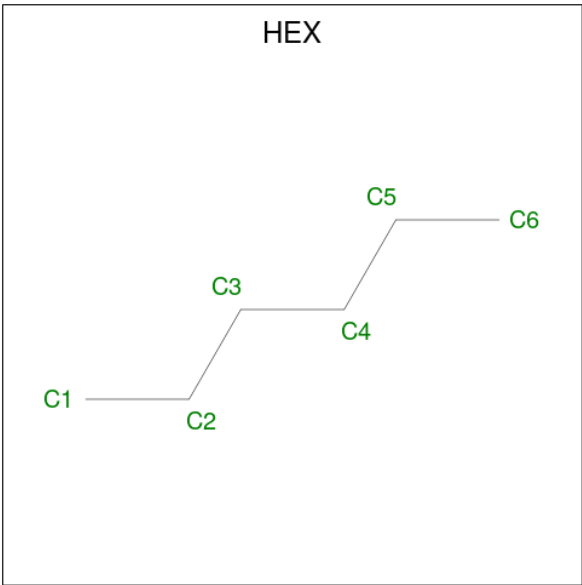
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C 12 12	0	0

- Molecule 6 is PENTADECANE (CCD ID: MYS) (formula: $C_{15}H_{32}$).



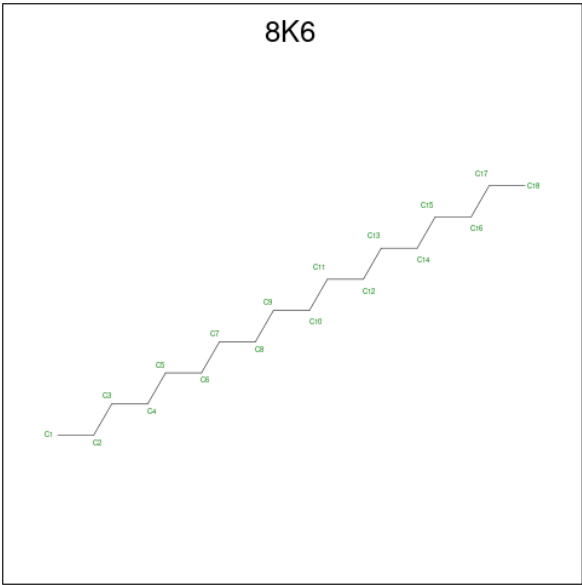
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C 15 15	0	0
6	A	1	Total C 15 15	0	0
6	A	1	Total C 15 15	0	0
6	A	1	Total C 15 15	0	0
6	A	1	Total C 15 15	0	0
6	A	1	Total C 15 15	0	0

- Molecule 7 is HEXANE (CCD ID: HEX) (formula: C_6H_{14}).



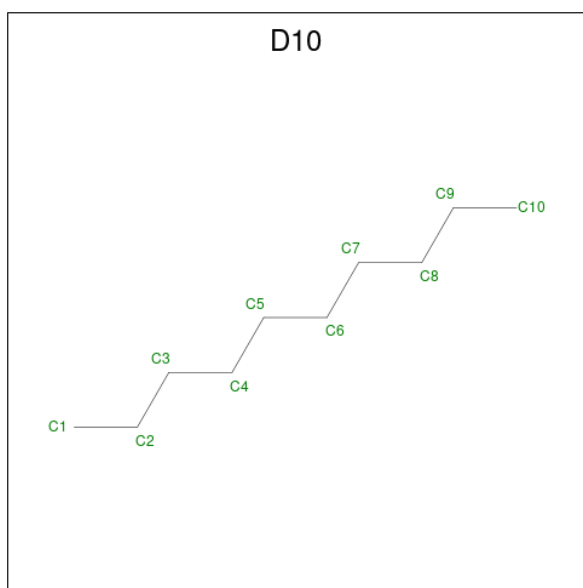
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	C	0	0
			6	6		

- Molecule 8 is Octadecane (CCD ID: 8K6) (formula: C₁₈H₃₈).



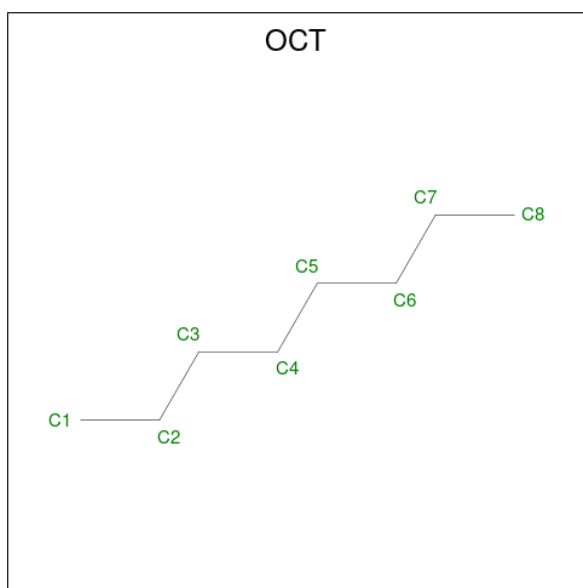
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	C	0	0
			18	18		
8	A	1	Total	C	0	0
			18	18		
8	A	1	Total	C	0	0
			18	18		

- Molecule 9 is DECANE (CCD ID: D10) (formula: $C_{10}H_{22}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total C 10 10	0	0

- Molecule 10 is N-OCTANE (CCD ID: OCT) (formula: C_8H_{18}).



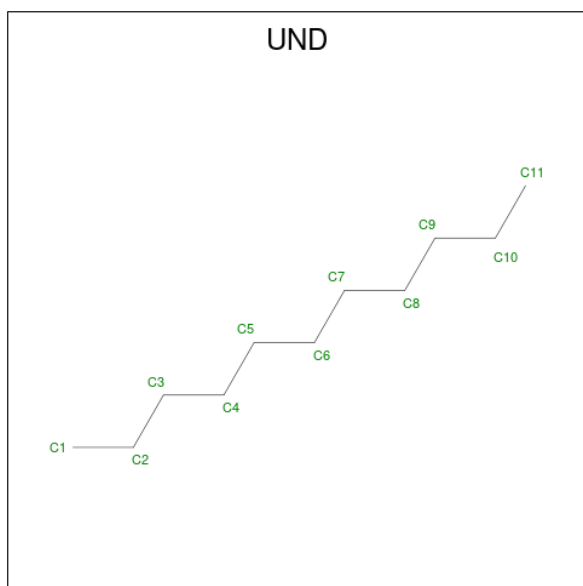
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total C 8 8	0	0
10	A	1	Total C 8 8	0	0

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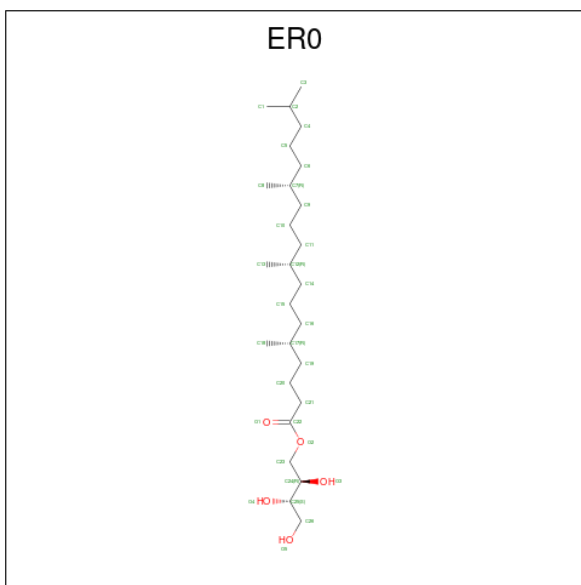
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	1	Total C 8 8	0	0

- Molecule 11 is UNDECANE (CCD ID: UND) (formula: $C_{11}H_{24}$).



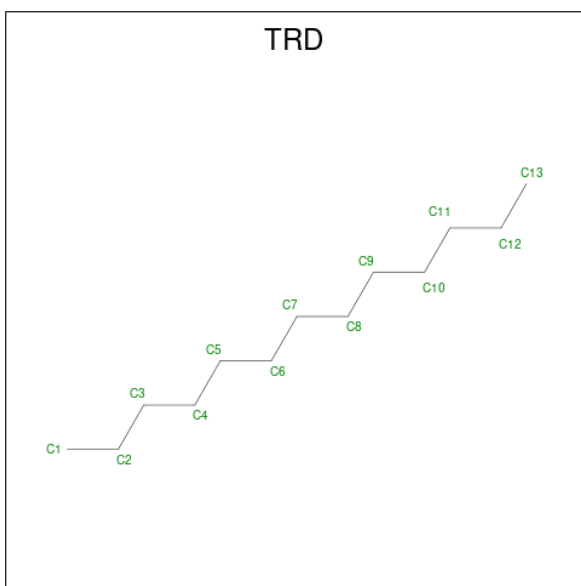
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	1	Total C 11 11	0	0

- Molecule 12 is [(2 {R},3 {S})-2,3,4-tris(oxidanyl)butyl] (5 {R},9 {R},13 {R})-5,9,13,17-tetramethyloctadecanoate (CCD ID: ER0) (formula: $C_{26}H_{52}O_5$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	A	1	Total	C	O	0	0
			31	26	5		
12	A	1	Total	C	O	0	0
			31	26	5		

- Molecule 13 is TRIDECANE (CCD ID: TRD) (formula: $\text{C}_{13}\text{H}_{28}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	1	Total C 13 13	0	0
13	A	1	Total C 13 13	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
13	A	1	Total C 13 13	0	0
13	A	1	Total C 13 13	0	0

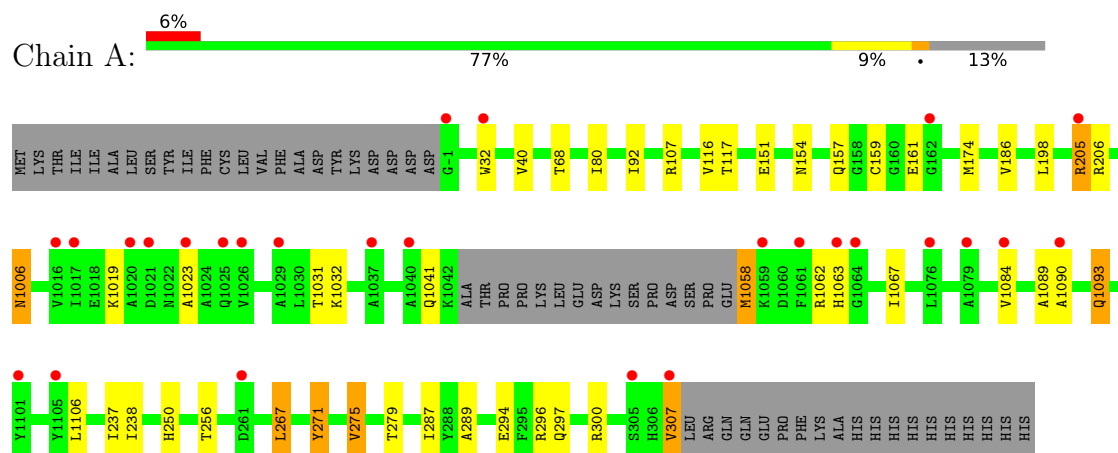
- Molecule 14 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	A	138	Total O 138 138	0	0

3 Residue-property plots [i](#)

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

- Molecule 1: Adenosine receptor A2a,Soluble cytochrome b562,Adenosine receptor A2a



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	39.89Å 179.28Å 140.96Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.75 – 2.00 42.75 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (42.75-2.00) 99.9 (42.75-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.77 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.173 , 0.208 0.185 , 0.213	Depositor DCC
R_{free} test set	1756 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	35.0	Xtriage
Anisotropy	0.189	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 75.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3605	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.98% 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: TRD, ER0, OCT, UND, D12, CLR, ZMA, MYS, 8K6, D10, NA, HEX

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	1.10	1/3101 (0.0%)	1.47	6/4215 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	294	GLU	C-O	5.09	1.30	1.24

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	117	THR	CA-C-N	6.59	127.43	119.99
1	A	117	THR	C-N-CA	6.59	127.43	119.99
1	A	271	TYR	CB-CA-C	5.50	120.20	110.85
1	A	1006	ASN	CA-C-N	5.30	127.33	120.44
1	A	1006	ASN	C-N-CA	5.30	127.33	120.44

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	3036	0	3112	30	1
2	A	25	0	14	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	1	0	0	0	0
4	A	84	0	138	2	0
5	A	12	0	26	0	0
6	A	90	0	192	3	0
7	A	6	0	14	0	0
8	A	54	0	114	4	0
9	A	10	0	22	1	0
10	A	24	0	54	0	0
11	A	11	0	24	0	0
12	A	62	0	0	0	0
13	A	52	0	112	0	0
14	A	138	0	0	1	1
All	All	3605	0	3822	34	2

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.

The worst 5 of 34 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:1031:THR:O	14:A:2501:HOH:O	1.95	0.84
1:A:80:ILE:HD11	4:A:2403:CLR:H182	1.77	0.66
1:A:154:ASN:OD1	1:A:159:CYS:HB2	1.97	0.64
1:A:1032:LYS:N	1:A:1032:LYS:HE2	2.13	0.62
1:A:1090:ALA:O	1:A:1093:GLN:HB2	2.06	0.56

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:TRP:O	1:A:205:ARG:NH2[1_455]	1.70	0.50
14:A:2638:HOH:O	14:A:2638:HOH:O[3_455]	2.07	0.13

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	386/447 (86%)	379 (98%)	7 (2%)	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	321/374 (86%)	308 (96%)	13 (4%)	28	27

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1058	MET
1	A	1093	GLN
1	A	307	VAL
1	A	267	LEU
1	A	275	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1071	GLN
1	A	297	GLN
1	A	1006	ASN
1	A	1022	ASN
1	A	1041	GLN

5.3.3 RNA ⓘ

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 27 ligands modelled in this entry, 1 is monoatomic - leaving 26 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	$\# Z > 2$
12	ER0	A	2416	-	30,30,30	0.41	0	35,36,36	0.48	0
8	8K6	A	2418	-	17,17,17	0.24	0	16,16,16	0.06	0
11	UND	A	2415	-	10,10,10	0.20	0	9,9,9	0.20	0
7	HEX	A	2408	-	5,5,5	0.14	0	4,4,4	0.22	0
13	TRD	A	2420	-	12,12,12	0.19	0	11,11,11	0.13	0
4	CLR	A	2404	-	31,31,31	0.35	0	48,48,48	0.74	0
9	D10	A	2411	-	9,9,9	0.31	0	8,8,8	0.38	0
6	MYS	A	2426	-	14,14,14	0.20	0	13,13,13	0.70	0
13	TRD	A	2422	-	12,12,12	0.20	0	11,11,11	0.22	0
10	OCT	A	2412	-	7,7,7	0.23	0	6,6,6	0.19	0
6	MYS	A	2417	-	14,14,14	0.41	0	13,13,13	0.57	0
6	MYS	A	2409	-	14,14,14	0.29	0	13,13,13	0.66	0
4	CLR	A	2403	-	31,31,31	0.42	0	48,48,48	0.64	0
8	8K6	A	2419	-	17,17,17	0.32	0	16,16,16	0.07	0
10	OCT	A	2413	-	7,7,7	0.17	0	6,6,6	0.15	0
13	TRD	A	2427	-	12,12,12	0.16	0	11,11,11	0.21	0
6	MYS	A	2424	-	14,14,14	0.46	0	13,13,13	0.42	0
8	8K6	A	2410	-	17,17,17	0.19	0	16,16,16	0.07	0
12	ER0	A	2423	-	30,30,30	0.37	0	35,36,36	0.46	0
5	D12	A	2406	-	11,11,11	0.32	0	10,10,10	0.70	0
2	ZMA	A	2401	-	26,28,28	0.66	0	30,39,39	1.15	3 (10%)
6	MYS	A	2414	-	14,14,14	0.45	0	13,13,13	0.30	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	CLR	A	2405	-	31,31,31	0.49	0	48,48,48	0.61	0
13	TRD	A	2425	-	12,12,12	0.17	0	11,11,11	0.14	0
10	OCT	A	2421	-	7,7,7	0.16	0	6,6,6	0.20	0
6	MYS	A	2407	-	14,14,14	0.26	0	13,13,13	0.55	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
12	ER0	A	2416	-	-	14/35/35/35	-
8	8K6	A	2418	-	-	8/15/15/15	-
11	UND	A	2415	-	-	6/8/8/8	-
7	HEX	A	2408	-	-	1/3/3/3	-
13	TRD	A	2420	-	-	4/10/10/10	-
4	CLR	A	2404	-	-	2/10/68/68	0/4/4/4
9	D10	A	2411	-	-	4/7/7/7	-
6	MYS	A	2426	-	-	3/12/12/12	-
13	TRD	A	2422	-	-	7/10/10/10	-
10	OCT	A	2412	-	-	2/5/5/5	-
6	MYS	A	2417	-	-	8/12/12/12	-
6	MYS	A	2409	-	-	4/12/12/12	-
4	CLR	A	2403	-	-	0/10/68/68	0/4/4/4
8	8K6	A	2419	-	-	9/15/15/15	-
10	OCT	A	2413	-	-	4/5/5/5	-
13	TRD	A	2427	-	-	6/10/10/10	-
6	MYS	A	2424	-	-	6/12/12/12	-
8	8K6	A	2410	-	-	10/15/15/15	-
12	ER0	A	2423	-	-	9/35/35/35	-
5	D12	A	2406	-	-	4/9/9/9	-
2	ZMA	A	2401	-	-	0/10/10/10	0/4/4/4
6	MYS	A	2414	-	-	3/12/12/12	-
4	CLR	A	2405	-	-	1/10/68/68	0/4/4/4
13	TRD	A	2425	-	-	3/10/10/10	-
10	OCT	A	2421	-	-	2/5/5/5	-
6	MYS	A	2407	-	-	6/12/12/12	-

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2401	ZMA	C9-C8-C7	-3.51	104.91	112.83
2	A	2401	ZMA	N15-C14-N16	2.72	121.73	118.32
2	A	2401	ZMA	N10-C11-N12	-2.53	114.38	116.95

There are no chirality outliers.

5 of 126 torsion outliers are listed below:

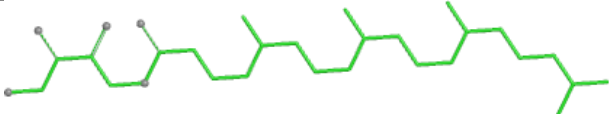
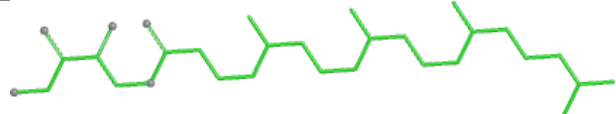
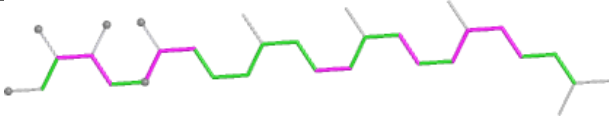
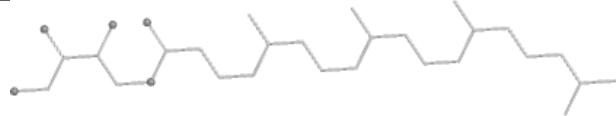
Mol	Chain	Res	Type	Atoms
12	A	2416	ER0	O2-C23-C24-O3
12	A	2416	ER0	O2-C23-C24-C25
12	A	2416	ER0	C23-C24-C25-C26
12	A	2423	ER0	O2-C23-C24-O3
12	A	2423	ER0	O2-C23-C24-C25

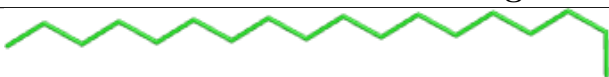
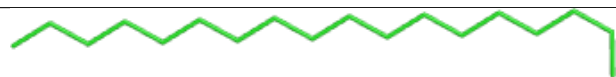
There are no ring outliers.

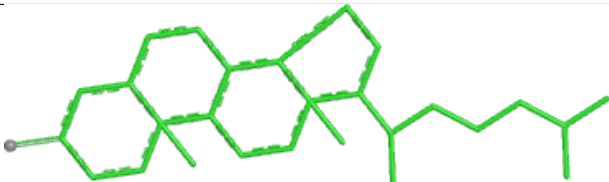
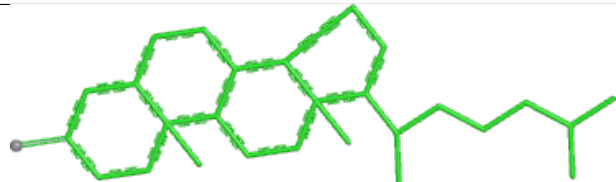
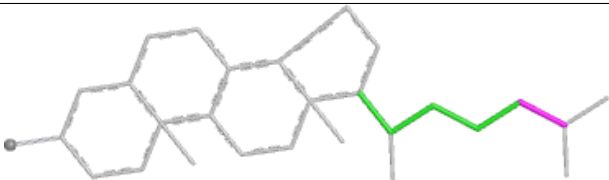
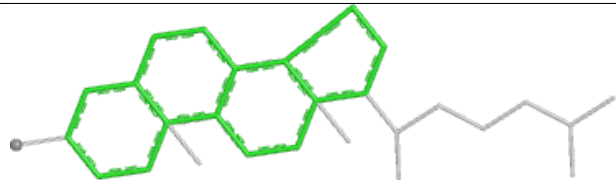
9 monomers are involved in 9 short contacts:

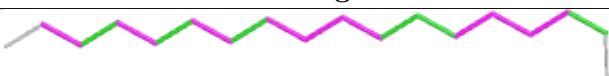
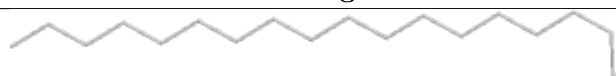
Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	2418	8K6	1	0
9	A	2411	D10	1	0
6	A	2417	MYS	1	0
4	A	2403	CLR	2	0
8	A	2419	8K6	2	0
6	A	2424	MYS	1	0
8	A	2410	8K6	1	0
2	A	2401	ZMA	1	0
6	A	2414	MYS	1	0

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.

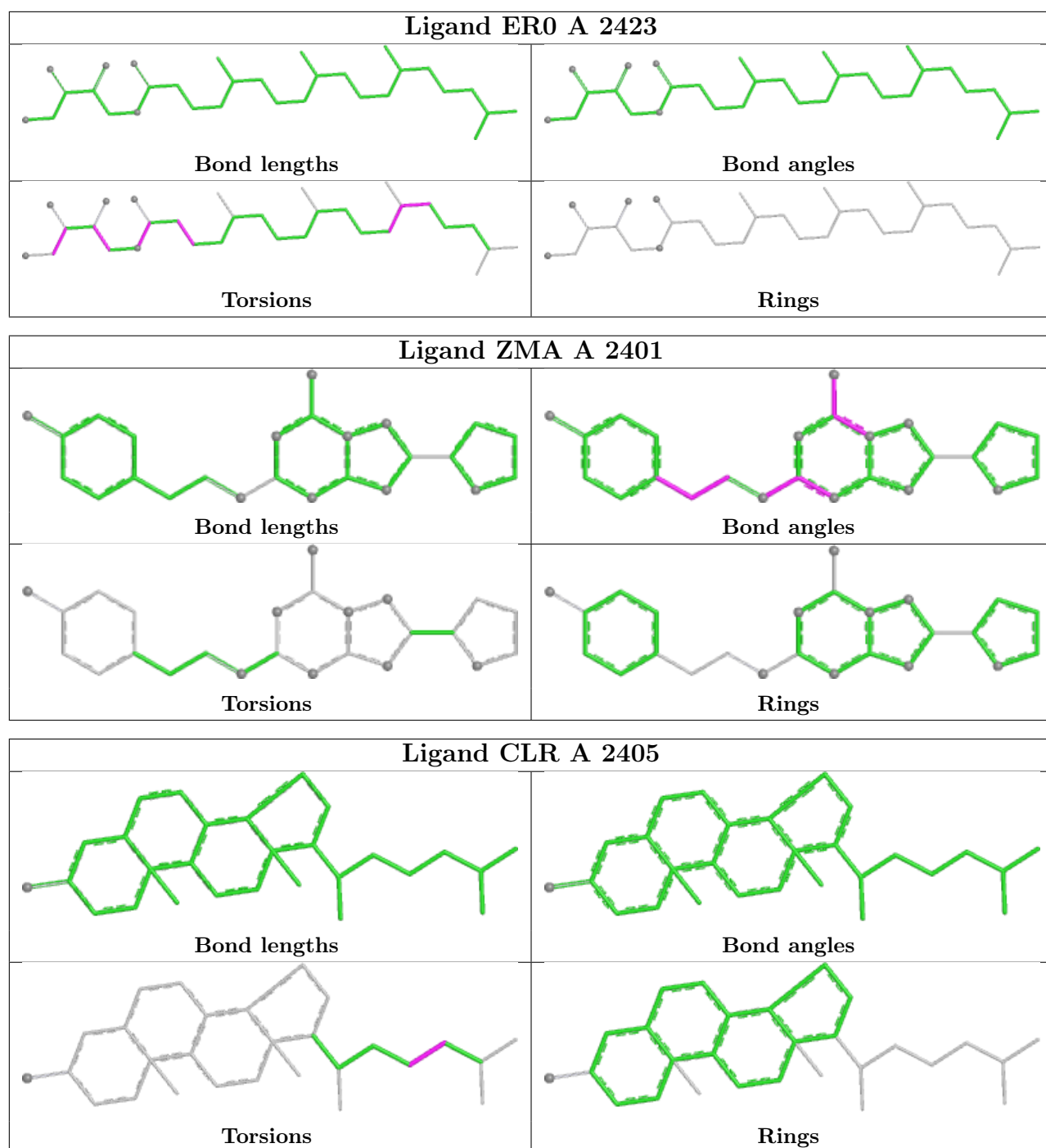
Ligand ER0 A 2416	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand 8K6 A 2418	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand CLR A 2404	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand 8K6 A 2419	
	
Bond lengths	Bond angles
	
Torsions	Rings

Ligand 8K6 A 2410	
	
Bond lengths	Bond angles
	
Torsions	Rings



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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	390/447 (87%)	0.30	27 (6%) 23 21	24, 37, 83, 122	0

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	162	GLY	3.9
1	A	1063	HIS	3.7
1	A	1059	LYS	3.7
1	A	1040	ALA	3.6
1	A	-1	GLY	3.2

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no 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(Å ²)	Q<0.9
8	8K6	A	2418	18/18	0.75	0.24	64,82,90,90	0
8	8K6	A	2419	18/18	0.78	0.24	75,82,96,97	0

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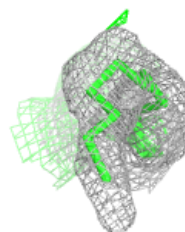
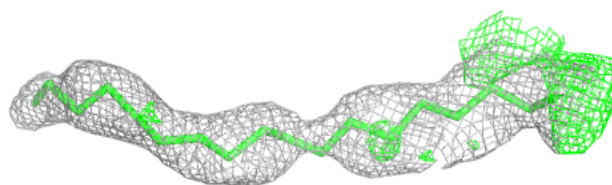
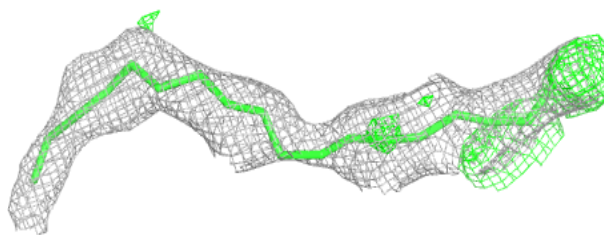
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	MYS	A	2414	15/15	0.80	0.19	60,72,77,79	0
13	TRD	A	2425	13/13	0.80	0.21	73,81,87,91	0
10	OCT	A	2412	8/8	0.82	0.23	63,76,80,81	0
6	MYS	A	2424	15/15	0.82	0.23	53,59,73,73	0
13	TRD	A	2422	13/13	0.83	0.25	66,79,90,92	0
7	HEX	A	2408	6/6	0.83	0.19	77,78,82,86	0
10	OCT	A	2421	8/8	0.84	0.22	70,72,74,74	0
12	ER0	A	2416	31/31	0.84	0.19	55,77,96,104	0
6	MYS	A	2407	15/15	0.85	0.21	58,73,88,94	0
10	OCT	A	2413	8/8	0.85	0.22	65,67,71,75	0
9	D10	A	2411	10/10	0.85	0.25	56,60,71,72	0
13	TRD	A	2420	13/13	0.86	0.17	63,72,89,90	0
6	MYS	A	2417	15/15	0.87	0.17	57,66,74,76	0
8	8K6	A	2410	18/18	0.87	0.19	61,73,87,89	0
6	MYS	A	2409	15/15	0.87	0.14	53,57,73,75	0
4	CLR	A	2403	28/28	0.88	0.13	34,41,64,74	0
13	TRD	A	2427	13/13	0.88	0.21	60,68,76,79	0
5	D12	A	2406	12/12	0.89	0.16	58,68,75,77	0
4	CLR	A	2404	28/28	0.89	0.14	45,52,61,71	0
6	MYS	A	2426	15/15	0.89	0.14	45,49,66,69	0
12	ER0	A	2423	31/31	0.89	0.14	40,71,98,99	0
11	UND	A	2415	11/11	0.91	0.17	47,63,83,84	0
4	CLR	A	2405	28/28	0.96	0.09	34,37,72,78	0
3	NA	A	2402	1/1	0.97	0.06	35,35,35,35	0
2	ZMA	A	2401	25/25	0.97	0.06	21,25,43,50	0

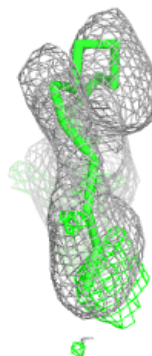
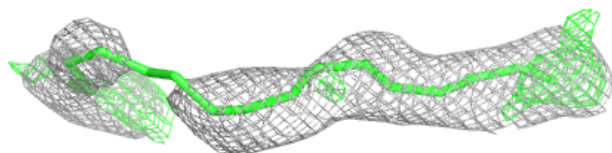
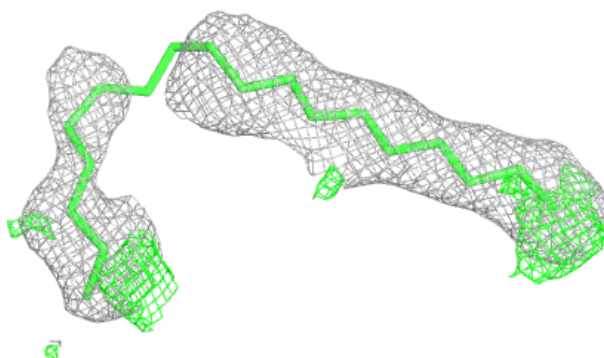
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 8K6 A 2418:

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

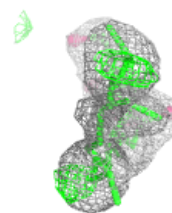
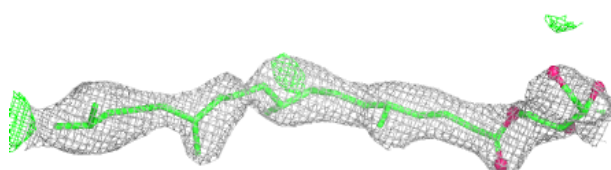
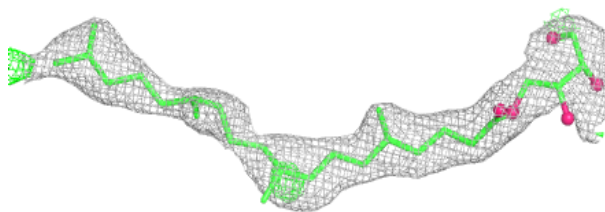
**Electron density around 8K6 A 2419:**

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

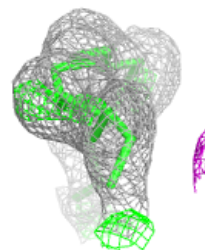
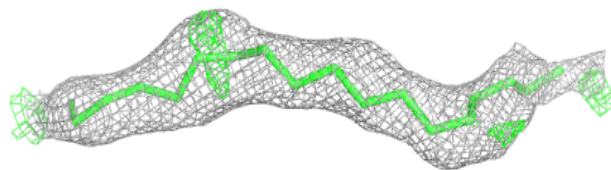
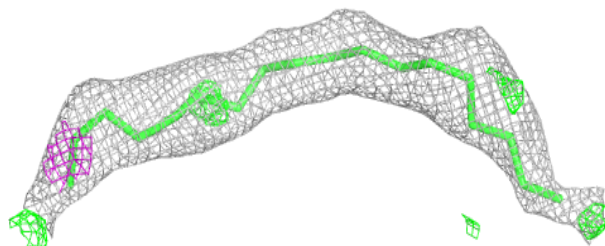


Electron density around ER0 A 2416:

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

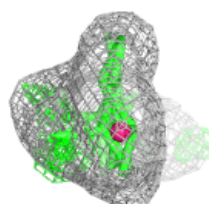
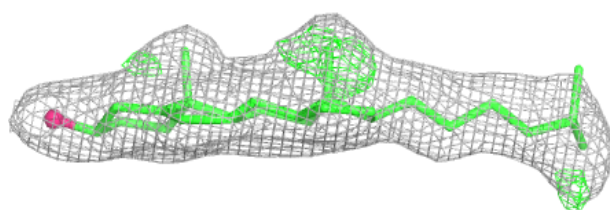
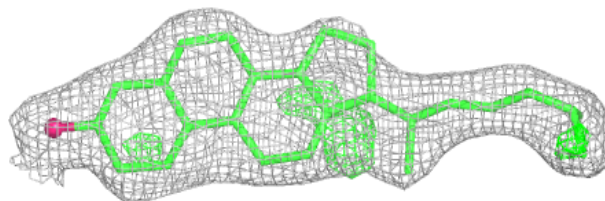
**Electron density around 8K6 A 2410:**

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

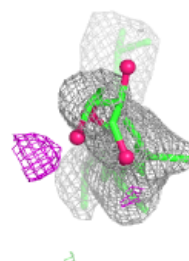
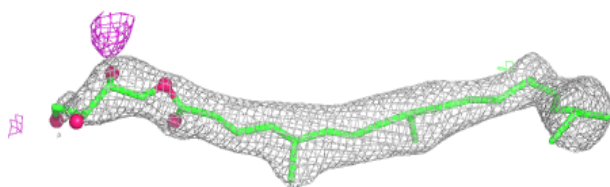
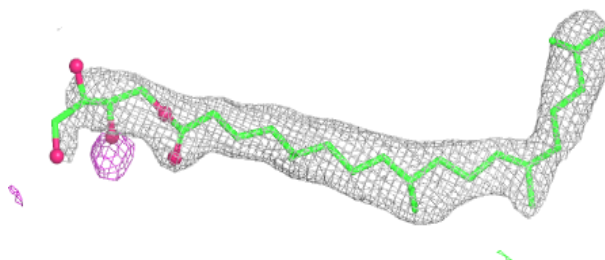


Electron density around CLR A 2404:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

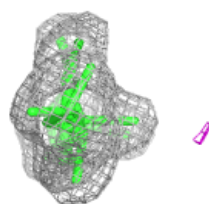
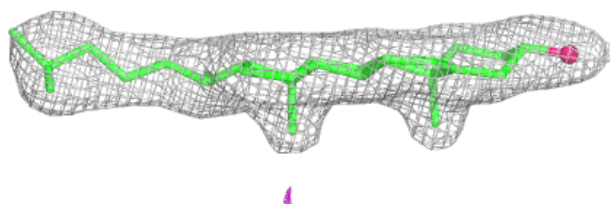
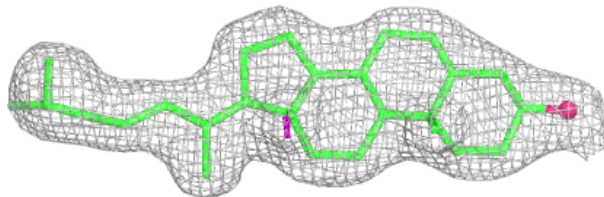
**Electron density around ER0 A 2423:**

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

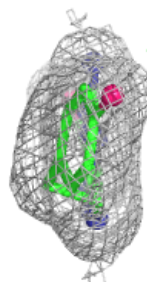
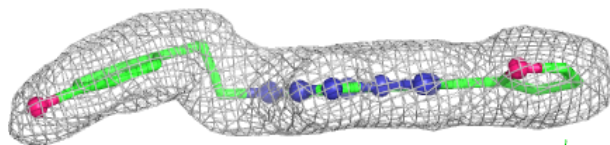
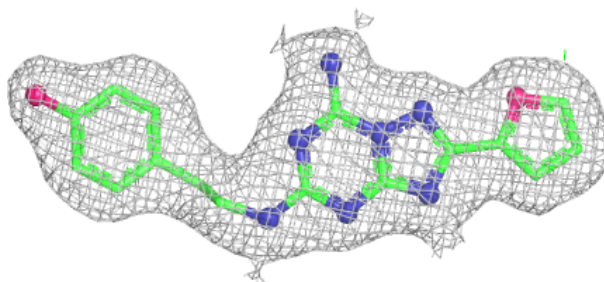


Electron density around CLR A 2405:

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

**Electron density around ZMA A 2401:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.