



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:49 PM UTC

PDB ID : 1XLS / pdb_00001xls
Title : Crystal structure of the mouse CAR/RXR LBD heterodimer bound to TCPOBOP and 9cRA and a TIF2 peptide containing the third LXXLL motifs
Authors : Suino, K.; peng, L.; Reynolds, R.; Li, Y.; Cha, J.-Y.; Repa, J.J.; Kliewer, S.A.; Xu, H.E.
Deposited on : 2004-09-30
Resolution : 2.96 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](#) 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

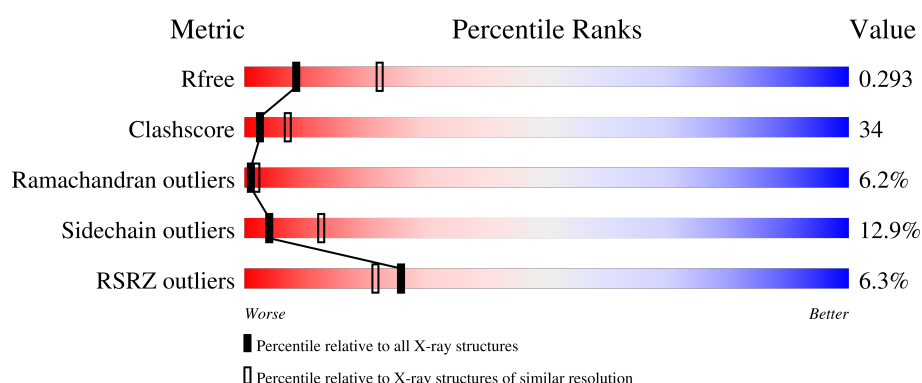
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.96 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	232	7% 54% 37% 9%
1	B	232	6% 54% 37% 9%
1	C	232	5% 55% 35% 9%
1	D	232	8% 54% 36% 10%
2	E	242	4% 41% 44% 12%

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Mol	Chain	Length	Quality of chain
2	F	242	4% 44% 40% 12%
2	G	242	5% 43% 43% 10%
2	H	242	4% 42% 44% 10%
3	I	18	6% 44% 22% 22% 11%
3	J	18	22% 39% 28% 22% 11%
3	K	18	17% 44% 22% 22% 11%
3	L	18	17% 39% 28% 22% 11%
3	M	18	22% 17% 28% 39% 17%
3	N	18	39% 17% 28% 28% 28%
3	O	18	17% 17% 33% 33% 17%
3	P	18	28% 22% 33% 28% 17%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 16288 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 Retinoic acid receptor RXR-alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1755	1117	306	322	10			
1	B	232	Total	C	N	O	S	0	0	0
			1755	1117	306	322	10			
1	C	232	Total	C	N	O	S	0	0	0
			1755	1117	306	322	10			
1	D	232	Total	C	N	O	S	0	0	0
			1755	1117	306	322	10			

- Molecule 2 is a protein called Orphan nuclear receptor NR1I3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	242	Total	C	N	O	S	0	0	0
			1969	1269	334	353	13			
2	F	242	Total	C	N	O	S	0	0	0
			1969	1269	334	353	13			
2	G	242	Total	C	N	O	S	0	0	0
			1969	1269	334	353	13			
2	H	242	Total	C	N	O	S	0	0	0
			1969	1269	334	353	13			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	146	ARG	LYS	conflict	UNP O35627
F	146	ARG	LYS	conflict	UNP O35627
G	146	ARG	LYS	conflict	UNP O35627
H	146	ARG	LYS	conflict	UNP O35627

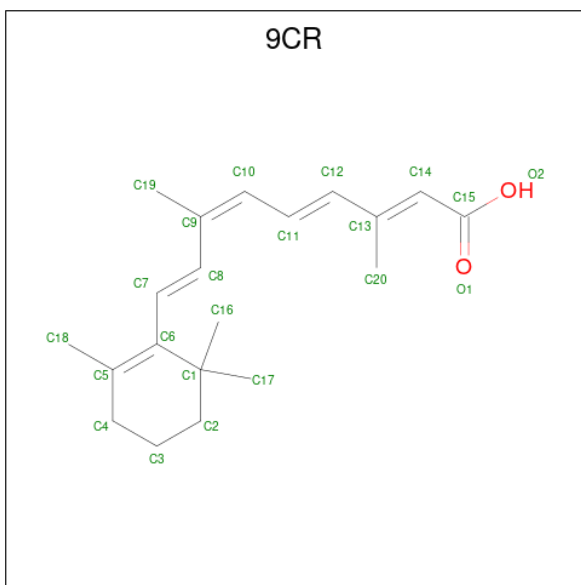
- Molecule 3 is a protein called Nuclear receptor coactivator 2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	I	16	Total 131	C 82	N 22	O 27	0	0	0
3	J	16	Total 131	C 82	N 22	O 27	0	0	0
3	K	16	Total 131	C 82	N 22	O 27	0	0	0
3	L	16	Total 131	C 82	N 22	O 27	0	0	0
3	M	18	Total 149	C 92	N 25	O 32	0	0	0
3	N	18	Total 149	C 92	N 25	O 32	0	0	0
3	O	18	Total 149	C 92	N 25	O 32	0	0	0
3	P	18	Total 149	C 92	N 25	O 32	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

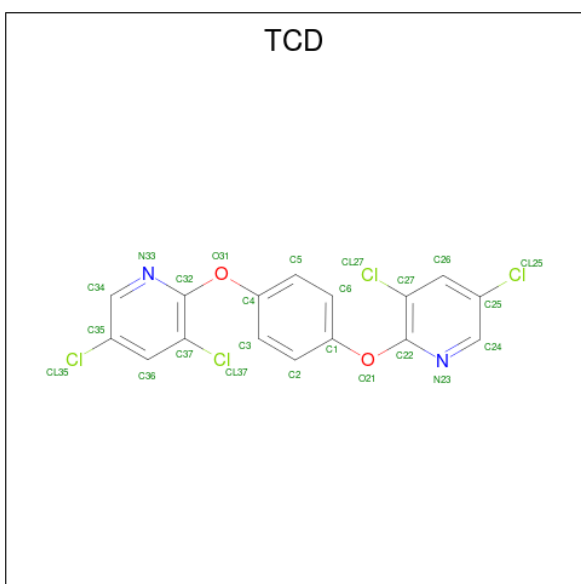
Chain	Residue	Modelled	Actual	Comment	Reference
I	739	ALA	LYS	conflict	UNP Q9WUI9
J	739	ALA	LYS	conflict	UNP Q9WUI9
K	739	ALA	LYS	conflict	UNP Q9WUI9
L	739	ALA	LYS	conflict	UNP Q9WUI9
M	739	ALA	LYS	conflict	UNP Q9WUI9
N	739	ALA	LYS	conflict	UNP Q9WUI9
O	739	ALA	LYS	conflict	UNP Q9WUI9
P	739	ALA	LYS	conflict	UNP Q9WUI9

- Molecule 4 is (9cis)-retinoic acid (CCD ID: 9CR) (formula: C₂₀H₂₈O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			22	20	2		
4	B	1	Total	C	O	0	0
			22	20	2		
4	C	1	Total	C	O	0	0
			22	20	2		
4	D	1	Total	C	O	0	0
			22	20	2		

- Molecule 5 is 3,5-DICHLORO-2-{4-[(3,5-DICHLOROPYRIDIN-2-YL)OXY]PHENOXY}PYRIDINE (CCD ID: TCD) (formula: C₁₆H₈Cl₄N₂O₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	E	1	Total	C	Cl	N	O	0	0
			24	16	4	2	2		
5	F	1	Total	C	Cl	N	O	0	0
			24	16	4	2	2		
5	G	1	Total	C	Cl	N	O	0	0
			24	16	4	2	2		
5	H	1	Total	C	Cl	N	O	0	0
			24	16	4	2	2		

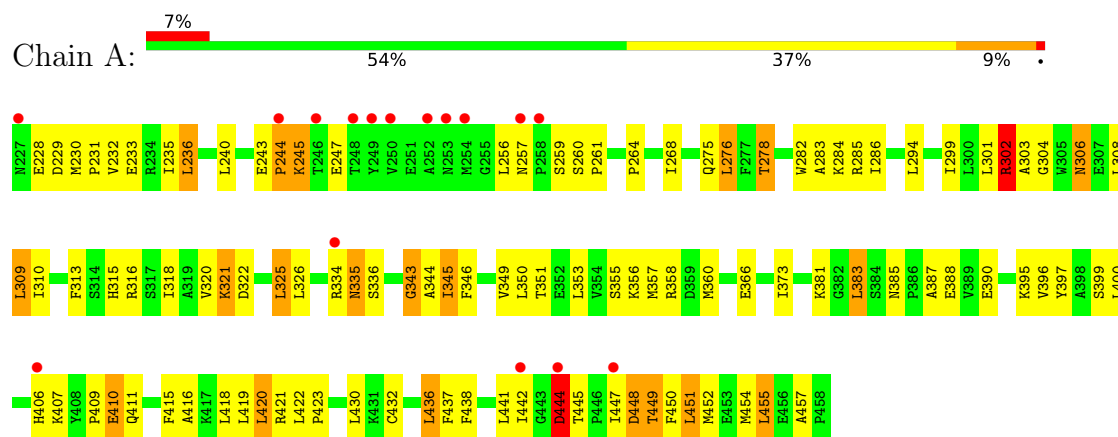
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	7	Total	O	0	0
			7	7		
6	B	8	Total	O	0	0
			8	8		
6	C	10	Total	O	0	0
			10	10		
6	D	20	Total	O	0	0
			20	20		
6	E	4	Total	O	0	0
			4	4		
6	F	17	Total	O	0	0
			17	17		
6	G	10	Total	O	0	0
			10	10		
6	H	4	Total	O	0	0
			4	4		
6	I	1	Total	O	0	0
			1	1		
6	J	1	Total	O	0	0
			1	1		
6	K	1	Total	O	0	0
			1	1		
6	L	1	Total	O	0	0
			1	1		
6	M	1	Total	O	0	0
			1	1		
6	O	1	Total	O	0	0
			1	1		
6	P	2	Total	O	0	0
			2	2		

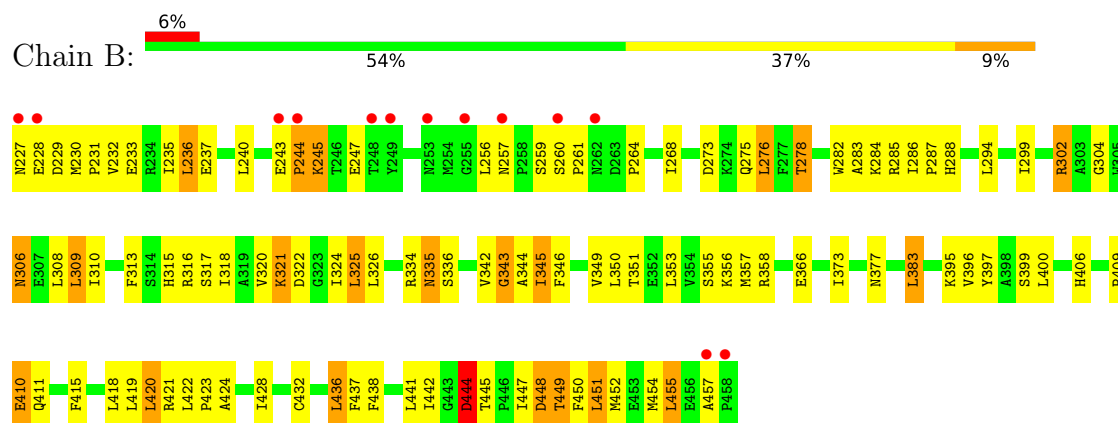
3 Residue-property plots

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.

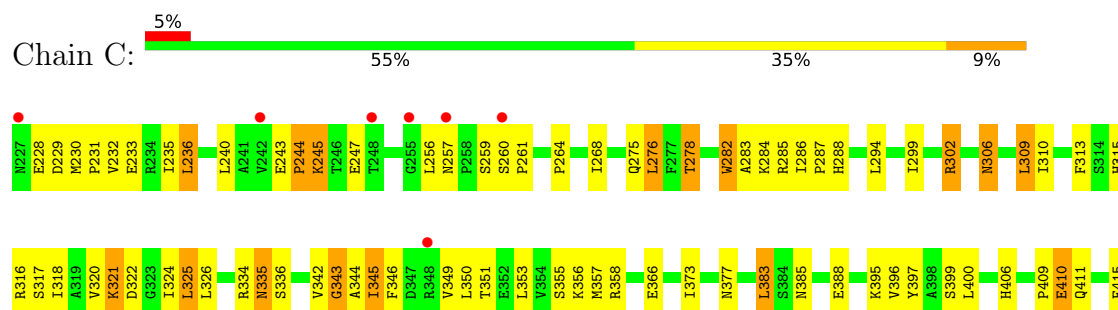
• Molecule 1: Retinoic acid receptor RXR-alpha

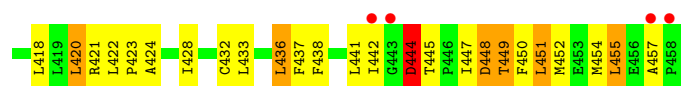


• Molecule 1: Retinoic acid receptor RXR-alpha

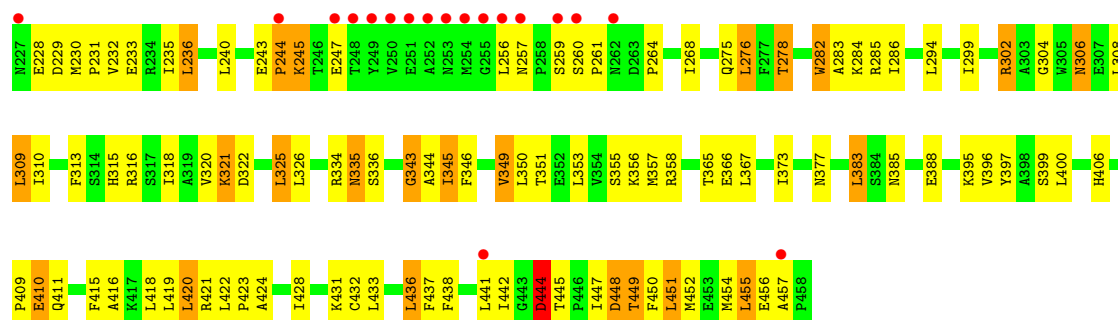


• Molecule 1: Retinoic acid receptor RXR-alpha

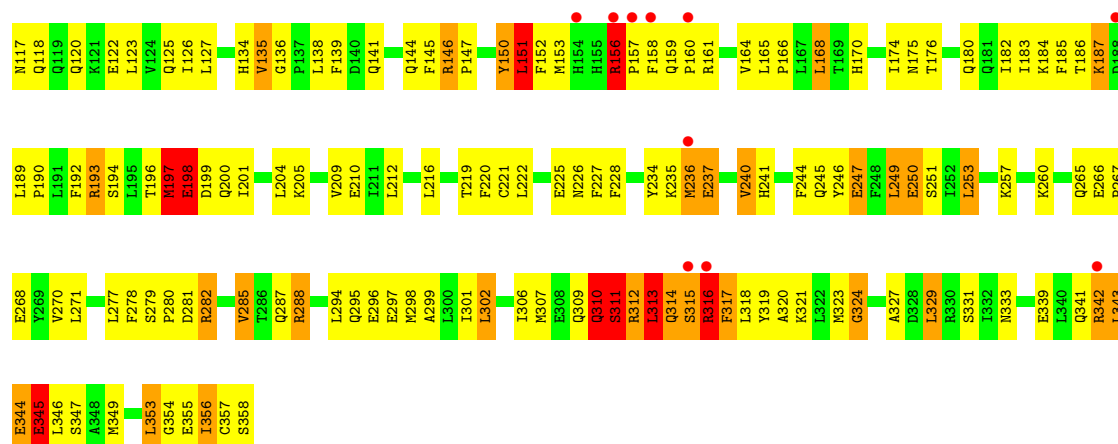




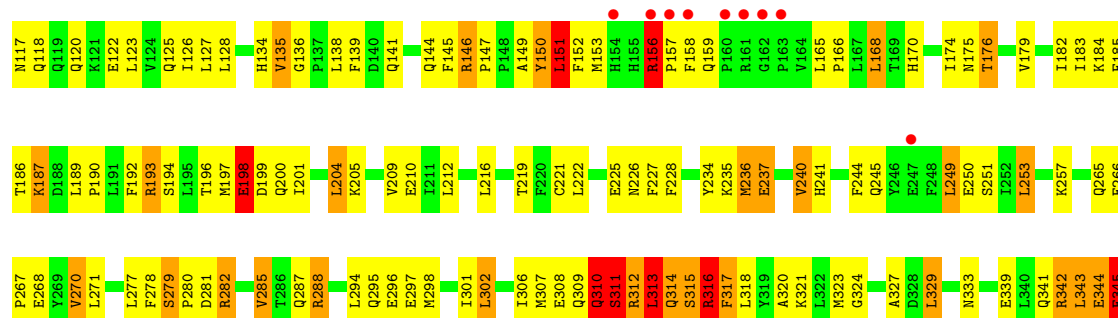
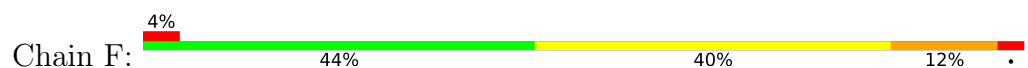
• Molecule 1: Retinoic acid receptor RXR-alpha

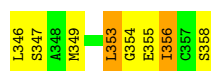


• Molecule 2: Orphan nuclear receptor NR1I3

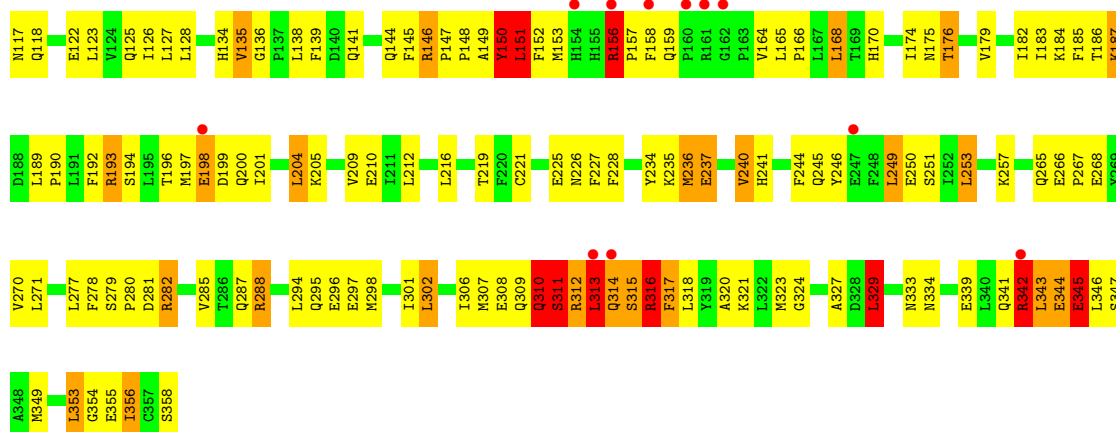
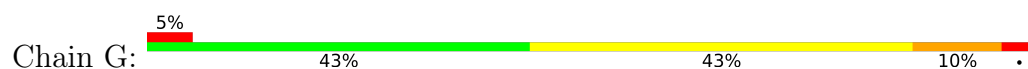


• Molecule 2: Orphan nuclear receptor NR1I3

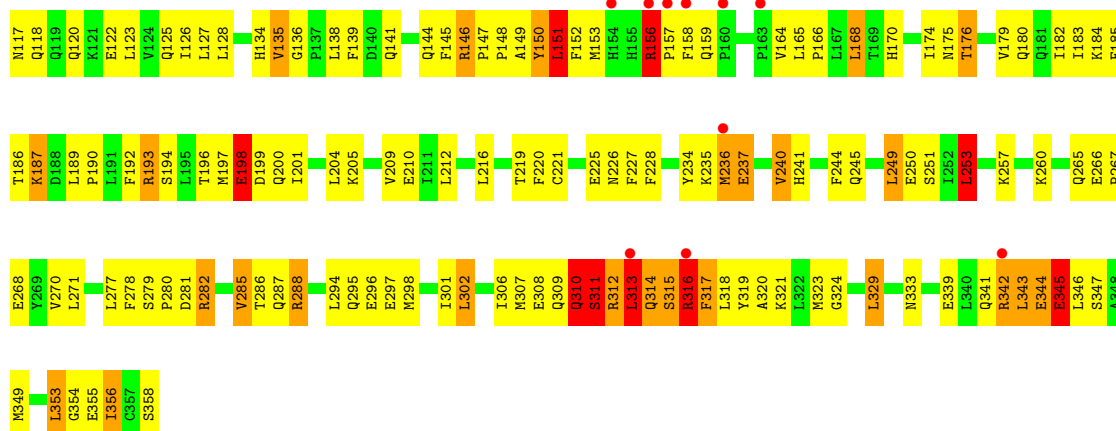




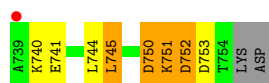
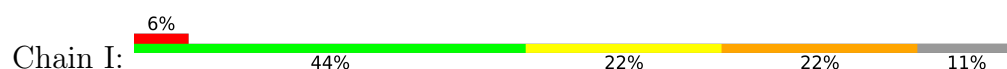
• Molecule 2: Orphan nuclear receptor NR1I3



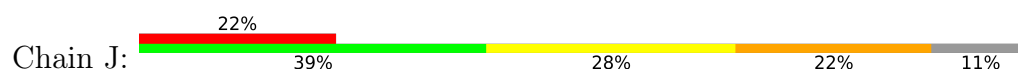
• Molecule 2: Orphan nuclear receptor NR1I3

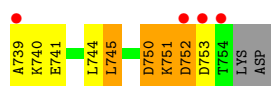


• Molecule 3: Nuclear receptor coactivator 2

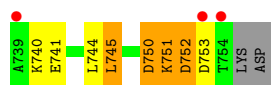
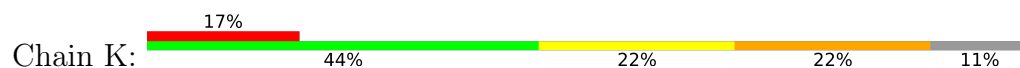


• Molecule 3: Nuclear receptor coactivator 2





- Molecule 3: Nuclear receptor coactivator 2



- Molecule 3: Nuclear receptor coactivator 2



- Molecule 3: Nuclear receptor coactivator 2



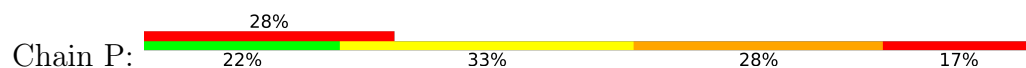
- Molecule 3: Nuclear receptor coactivator 2



- Molecule 3: Nuclear receptor coactivator 2



- Molecule 3: Nuclear receptor coactivator 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	68.27Å 88.38Å 105.49Å 79.02° 85.81° 67.22°	Depositor
Resolution (Å)	19.99 – 2.96 19.99 – 2.97	Depositor EDS
% Data completeness (in resolution range)	92.5 (19.99-2.96) 92.3 (19.99-2.97)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	0.12	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.98Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.255 , 0.303 0.250 , 0.293	Depositor DCC
R_{free} test set	3463 reflections (8.12%)	wwPDB-VP
Wilson B-factor (Å ²)	56.2	Xtriage
Anisotropy	0.008	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	16288	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.53% 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: TCD, 9CR

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	0.53	0/1790	0.95	7/2414 (0.3%)
1	B	0.50	0/1790	0.97	7/2414 (0.3%)
1	C	0.48	0/1790	0.96	7/2414 (0.3%)
1	D	0.50	0/1790	0.97	7/2414 (0.3%)
2	E	0.58	0/2016	1.12	26/2727 (1.0%)
2	F	0.59	0/2016	1.07	18/2727 (0.7%)
2	G	0.59	1/2016 (0.0%)	1.06	15/2727 (0.6%)
2	H	0.62	2/2016 (0.1%)	1.20	23/2727 (0.8%)
3	I	0.47	0/131	0.89	1/175 (0.6%)
3	J	0.42	0/131	0.92	1/175 (0.6%)
3	K	0.39	0/131	0.89	1/175 (0.6%)
3	L	0.46	0/131	0.88	1/175 (0.6%)
3	M	1.24	2/149 (1.3%)	2.25	11/197 (5.6%)
3	N	1.15	1/149 (0.7%)	1.94	10/197 (5.1%)
3	O	1.10	1/149 (0.7%)	2.61	14/197 (7.1%)
3	P	1.23	2/149 (1.3%)	1.95	11/197 (5.6%)
All	All	0.58	9/16344 (0.1%)	1.10	160/22052 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	G	0	1
3	M	0	1
3	N	0	1
3	P	0	1
All	All	0	4

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	193	ARG	CZ-NH1	-11.19	1.17	1.32
3	M	750	ASP	CA-C	-8.86	1.41	1.52
3	P	750	ASP	CA-C	-8.78	1.42	1.52
3	N	750	ASP	CA-C	-7.42	1.43	1.52
3	M	750	ASP	CB-CG	-6.43	1.35	1.52

The worst 5 of 160 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	H	193	ARG	NE-CZ-NH2	19.75	136.98	119.20
3	O	746	ARG	NE-CZ-NH1	-16.57	104.93	121.50
3	O	746	ARG	NE-CZ-NH2	16.53	134.08	119.20
3	M	746	ARG	NE-CZ-NH1	-14.43	107.07	121.50
3	M	746	ARG	NE-CZ-NH2	14.09	131.88	119.20

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	G	150	TYR	Sidechain
3	M	746	ARG	Sidechain
3	N	746	ARG	Sidechain
3	P	746	ARG	Sidechain

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	1755	0	1733	123	0
1	B	1755	0	1733	118	1
1	C	1755	0	1733	95	0
1	D	1755	0	1733	99	0
2	E	1969	0	1964	170	1
2	F	1969	0	1964	146	2
2	G	1969	0	1964	169	0
2	H	1969	0	1964	161	2
3	I	131	0	132	10	0
3	J	131	0	132	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	K	131	0	132	10	0
3	L	131	0	132	12	0
3	M	149	0	149	29	0
3	N	149	0	149	27	0
3	O	149	0	149	28	0
3	P	149	0	149	33	0
4	A	22	0	27	3	0
4	B	22	0	27	3	0
4	C	22	0	27	4	0
4	D	22	0	27	4	0
5	E	24	0	8	1	0
5	F	24	0	8	1	0
5	G	24	0	8	1	0
5	H	24	0	8	1	0
6	A	7	0	0	1	0
6	B	8	0	0	1	0
6	C	10	0	0	1	0
6	D	20	0	0	2	0
6	E	4	0	0	2	0
6	F	17	0	0	2	0
6	G	10	0	0	1	0
6	H	4	0	0	0	0
6	I	1	0	0	0	0
6	J	1	0	0	3	0
6	K	1	0	0	0	0
6	L	1	0	0	1	0
6	M	1	0	0	0	0
6	O	1	0	0	0	0
6	P	2	0	0	1	0
All	All	16288	0	16052	1109	3

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 34.

The worst 5 of 1109 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)
2:E:157:PRO:CD	2:G:342:ARG:HH12	1.16	1.54
2:E:157:PRO:CD	2:G:342:ARG:NH1	1.74	1.39
2:E:157:PRO:HD3	2:G:342:ARG:NH1	1.09	1.37
1:A:406:HIS:CD2	1:B:233:GLU:HA	1.64	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:406:HIS:CE1	1:B:236:LEU:HB3	1.72	1.25

All (3) 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)
2:F:342:ARG:NH1	2:H:156:ARG:O[1_655]	1.81	0.39
2:F:342:ARG:NH1	2:H:157:PRO:CD[1_655]	1.88	0.32
1:B:442:ILE:O	2:E:161:ARG:NH1[1_554]	2.17	0.03

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	230/232 (99%)	191 (83%)	26 (11%)	13 (6%)	1	2
1	B	230/232 (99%)	190 (83%)	27 (12%)	13 (6%)	1	2
1	C	230/232 (99%)	191 (83%)	25 (11%)	14 (6%)	1	2
1	D	230/232 (99%)	189 (82%)	27 (12%)	14 (6%)	1	2
2	E	240/242 (99%)	206 (86%)	22 (9%)	12 (5%)	1	3
2	F	240/242 (99%)	207 (86%)	20 (8%)	13 (5%)	1	3
2	G	240/242 (99%)	206 (86%)	21 (9%)	13 (5%)	1	3
2	H	240/242 (99%)	209 (87%)	18 (8%)	13 (5%)	1	3
3	I	14/18 (78%)	10 (71%)	3 (21%)	1 (7%)	1	1
3	J	14/18 (78%)	10 (71%)	3 (21%)	1 (7%)	1	1
3	K	14/18 (78%)	10 (71%)	3 (21%)	1 (7%)	1	1
3	L	14/18 (78%)	10 (71%)	3 (21%)	1 (7%)	1	1
3	M	16/18 (89%)	9 (56%)	3 (19%)	4 (25%)	0	0

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	N	16/18 (89%)	10 (62%)	1 (6%)	5 (31%)	0	0
3	O	16/18 (89%)	10 (62%)	3 (19%)	3 (19%)	0	0
3	P	16/18 (89%)	9 (56%)	4 (25%)	3 (19%)	0	0
All	All	2000/2040 (98%)	1667 (83%)	209 (10%)	124 (6%)	1	2

5 of 124 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	244	PRO
1	A	245	LYS
1	A	256	LEU
1	A	260	SER
1	A	261	PRO

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	182/200 (91%)	166 (91%)	16 (9%)	9	24
1	B	182/200 (91%)	166 (91%)	16 (9%)	9	24
1	C	182/200 (91%)	166 (91%)	16 (9%)	9	24
1	D	182/200 (91%)	165 (91%)	17 (9%)	8	23
2	E	217/217 (100%)	188 (87%)	29 (13%)	4	11
2	F	217/217 (100%)	188 (87%)	29 (13%)	4	11
2	G	217/217 (100%)	188 (87%)	29 (13%)	4	11
2	H	217/217 (100%)	188 (87%)	29 (13%)	4	11
3	I	14/16 (88%)	10 (71%)	4 (29%)	0	0
3	J	14/16 (88%)	10 (71%)	4 (29%)	0	0
3	K	14/16 (88%)	10 (71%)	4 (29%)	0	0
3	L	14/16 (88%)	10 (71%)	4 (29%)	0	0
3	M	16/16 (100%)	10 (62%)	6 (38%)	0	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	N	16/16 (100%)	9 (56%)	7 (44%)	0	0
3	O	16/16 (100%)	10 (62%)	6 (38%)	0	0
3	P	16/16 (100%)	11 (69%)	5 (31%)	0	0
All	All	1716/1796 (96%)	1495 (87%)	221 (13%)	4	13

5 of 221 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	F	296	GLU
2	G	296	GLU
3	P	754	THR
3	M	746	ARG
2	F	343	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 85 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	125	GLN
2	H	120	GLN
2	G	144	GLN
2	G	245	GLN
2	H	159	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

8 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	9CR	C	803	-	22,22,22	4.10	14 (63%)	30,30,30	2.75	15 (50%)
5	TCD	H	808	-	26,26,26	2.08	4 (15%)	36,36,36	2.14	13 (36%)
5	TCD	F	806	-	26,26,26	2.15	4 (15%)	36,36,36	2.01	9 (25%)
5	TCD	G	807	-	26,26,26	2.44	8 (30%)	36,36,36	2.19	13 (36%)
4	9CR	B	802	-	22,22,22	4.03	12 (54%)	30,30,30	2.74	15 (50%)
5	TCD	E	805	-	26,26,26	2.41	7 (26%)	36,36,36	2.23	13 (36%)
4	9CR	D	804	-	22,22,22	4.09	13 (59%)	30,30,30	2.72	14 (46%)
4	9CR	A	801	-	22,22,22	4.01	12 (54%)	30,30,30	2.72	13 (43%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	9CR	C	803	-	-	4/15/32/32	0/1/1/1
5	TCD	H	808	-	-	0/8/8/8	0/3/3/3
5	TCD	F	806	-	-	0/8/8/8	0/3/3/3
5	TCD	G	807	-	-	0/8/8/8	0/3/3/3
4	9CR	B	802	-	-	4/15/32/32	0/1/1/1
5	TCD	E	805	-	-	0/8/8/8	0/3/3/3
4	9CR	D	804	-	-	4/15/32/32	0/1/1/1
4	9CR	A	801	-	-	4/15/32/32	0/1/1/1

The worst 5 of 74 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	803	9CR	C1-C6	11.09	1.68	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	804	9CR	C1-C6	11.05	1.67	1.53
4	B	802	9CR	C1-C6	10.78	1.67	1.53
4	A	801	9CR	C1-C6	10.56	1.67	1.53
4	C	803	9CR	C5-C6	10.03	1.51	1.34

The worst 5 of 105 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	807	TCD	C26-C27-C22	-5.84	114.53	118.28
5	E	805	TCD	C26-C27-C22	-5.72	114.61	118.28
4	B	802	9CR	C1-C6-C5	-5.55	115.06	122.64
4	C	803	9CR	C1-C6-C5	-5.51	115.10	122.64
4	D	804	9CR	C1-C6-C5	-5.49	115.13	122.64

There are no chirality outliers.

5 of 16 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	801	9CR	C13-C14-C15-O1
4	A	801	9CR	C13-C14-C15-O2
4	B	802	9CR	C13-C14-C15-O1
4	B	802	9CR	C13-C14-C15-O2
4	C	803	9CR	C13-C14-C15-O1

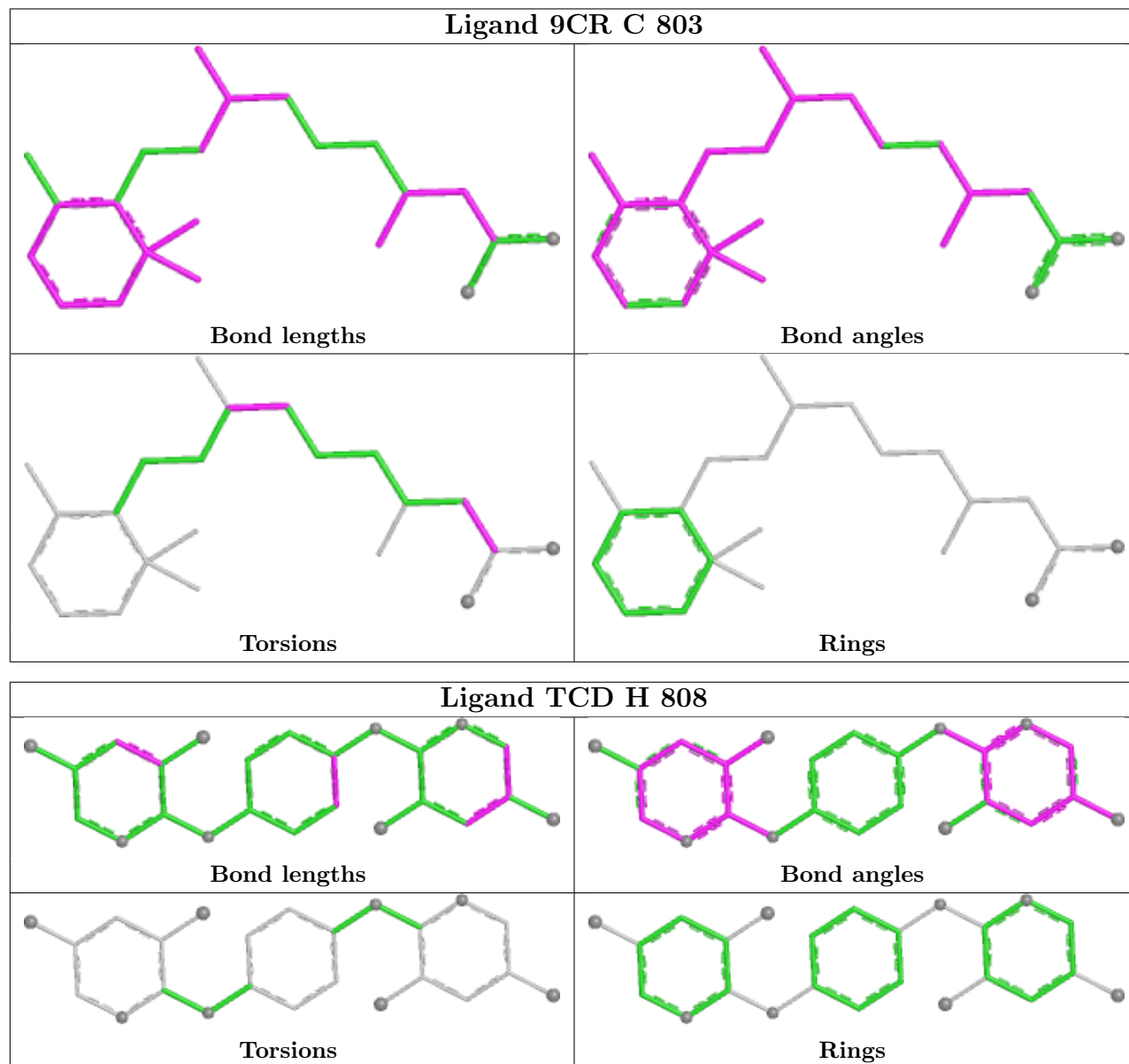
There are no ring outliers.

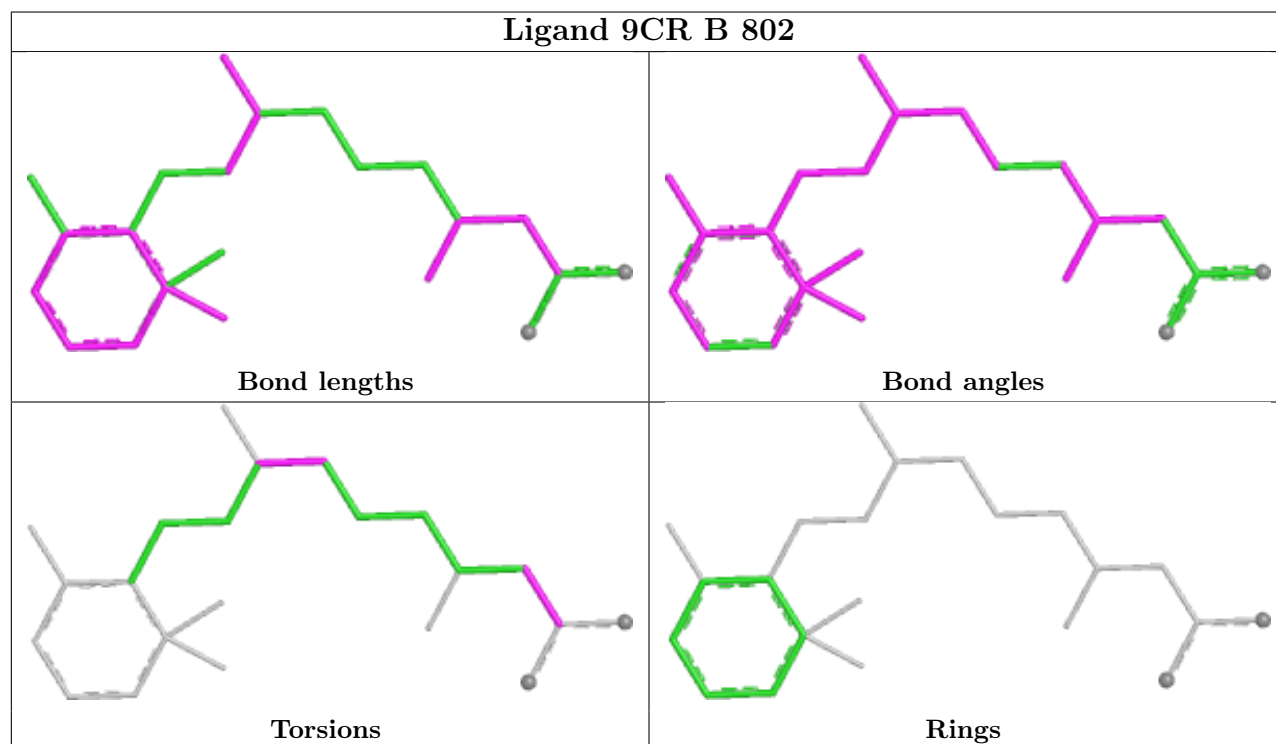
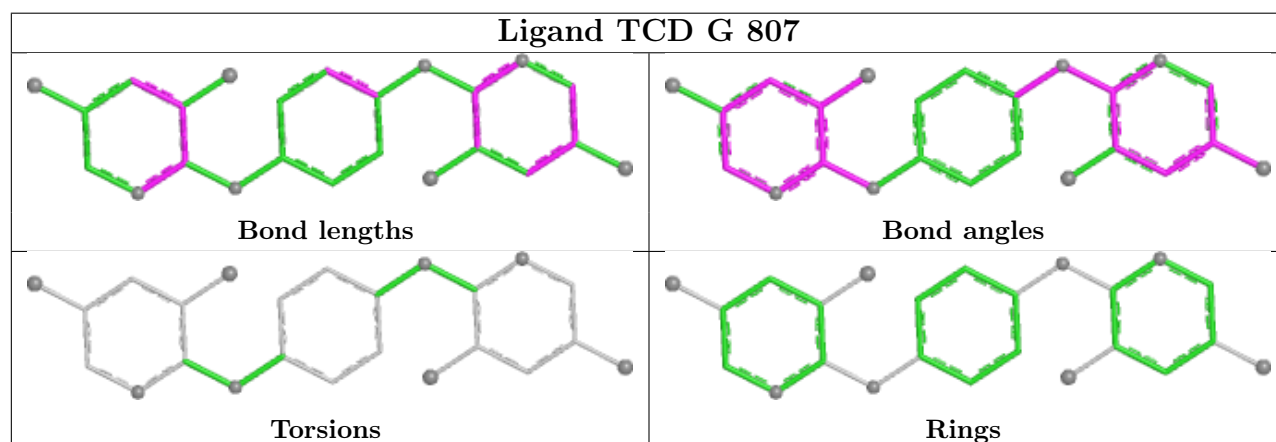
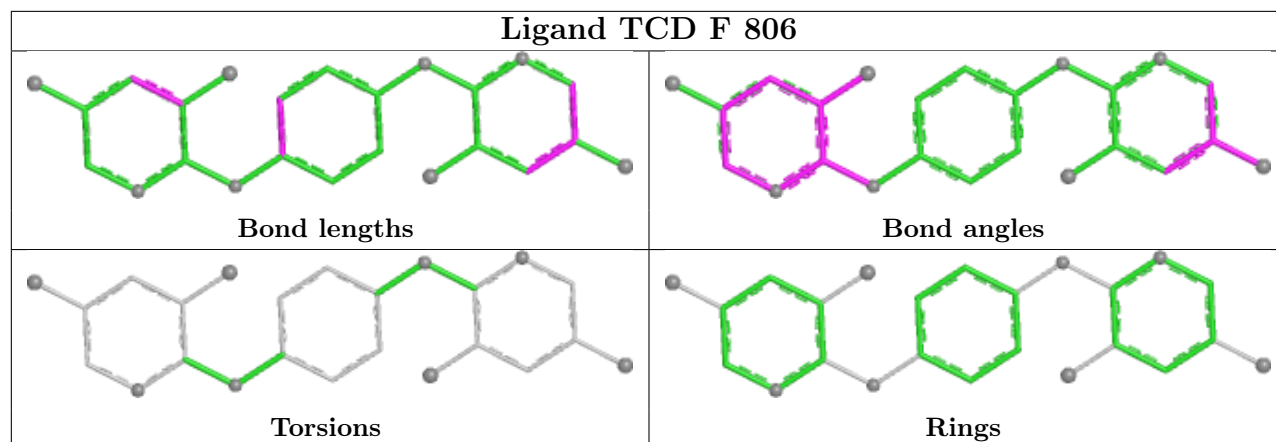
8 monomers are involved in 18 short contacts:

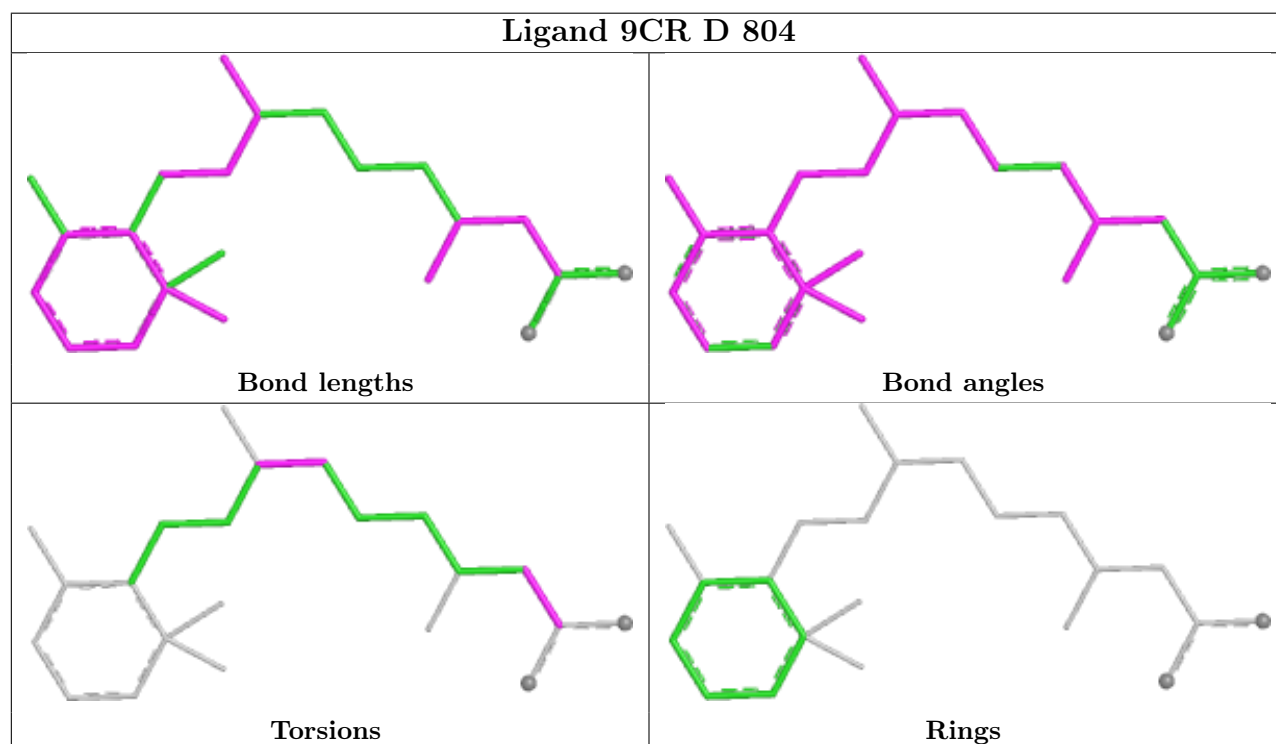
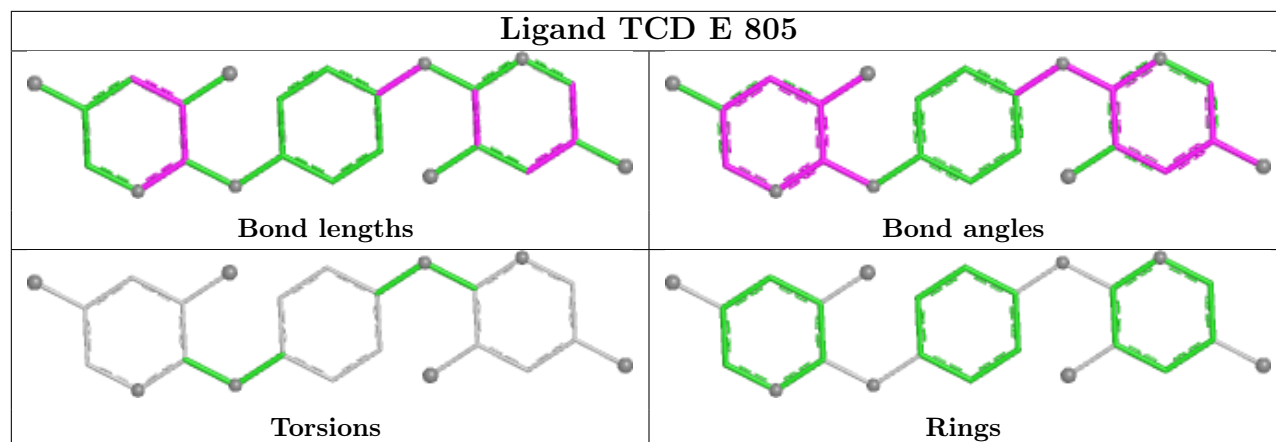
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	803	9CR	4	0
5	H	808	TCD	1	0
5	F	806	TCD	1	0
5	G	807	TCD	1	0
4	B	802	9CR	3	0
5	E	805	TCD	1	0
4	D	804	9CR	4	0
4	A	801	9CR	3	0

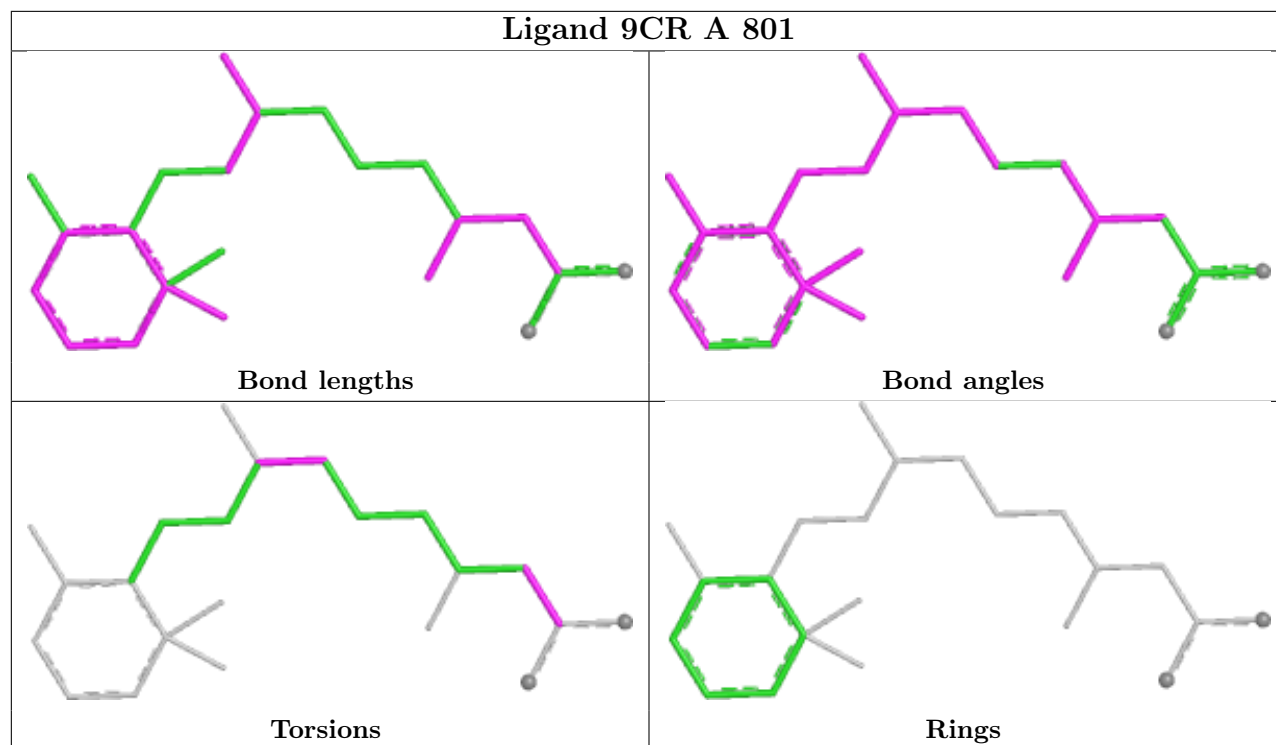
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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	232/232 (100%)	0.28	16 (6%)	23 19	22, 47, 126, 134	0
1	B	232/232 (100%)	0.27	13 (5%)	30 25	22, 50, 128, 137	0
1	C	232/232 (100%)	0.26	11 (4%)	36 30	21, 53, 127, 136	0
1	D	232/232 (100%)	0.32	18 (7%)	19 17	21, 50, 125, 135	0
2	E	242/242 (100%)	0.22	10 (4%)	41 34	21, 44, 89, 122	0
2	F	242/242 (100%)	0.18	9 (3%)	45 37	16, 42, 89, 127	0
2	G	242/242 (100%)	0.18	11 (4%)	38 31	17, 44, 88, 126	0
2	H	242/242 (100%)	0.14	10 (4%)	41 34	18, 44, 89, 121	0
3	I	16/18 (88%)	1.09	1 (6%)	26 22	43, 79, 130, 135	0
3	J	16/18 (88%)	1.32	4 (25%)	2 1	51, 82, 132, 134	0
3	K	16/18 (88%)	1.20	3 (18%)	3 3	53, 85, 134, 136	0
3	L	16/18 (88%)	0.94	3 (18%)	3 3	43, 77, 131, 137	0
3	M	18/18 (100%)	1.10	4 (22%)	2 2	37, 77, 121, 125	0
3	N	18/18 (100%)	1.07	7 (38%)	1 0	39, 76, 121, 129	0
3	O	18/18 (100%)	1.09	3 (16%)	4 4	39, 75, 120, 129	0
3	P	18/18 (100%)	1.07	5 (27%)	1 1	37, 80, 120, 124	0
All	All	2032/2040 (99%)	0.29	128 (6%)	26 22	16, 48, 120, 137	0

The worst 5 of 128 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	249	TYR	5.9
1	D	249	TYR	5.3
1	B	227	ASN	4.9
2	G	162	GLY	4.8
2	F	162	GLY	4.7

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](#)

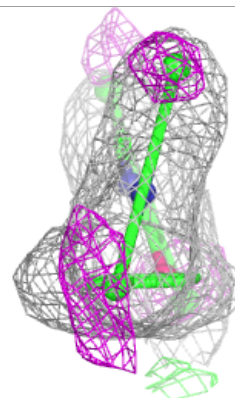
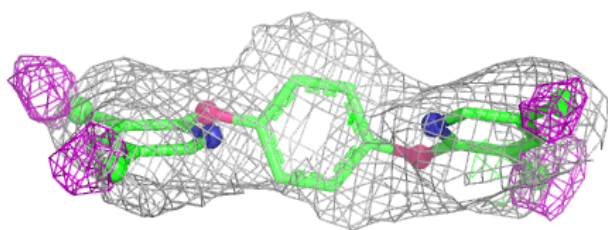
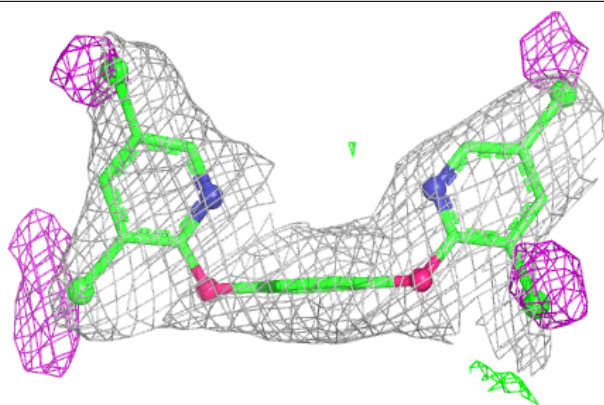
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	TCD	E	805	24/24	0.79	0.13	27,42,54,54	0
5	TCD	H	808	24/24	0.81	0.12	27,37,54,54	0
5	TCD	G	807	24/24	0.87	0.10	12,38,54,54	0
4	9CR	C	803	22/22	0.87	0.15	32,41,48,48	0
5	TCD	F	806	24/24	0.89	0.09	14,35,54,54	0
4	9CR	D	804	22/22	0.90	0.13	31,39,44,49	0
4	9CR	A	801	22/22	0.91	0.13	31,43,48,53	0
4	9CR	B	802	22/22	0.91	0.14	26,36,41,47	0

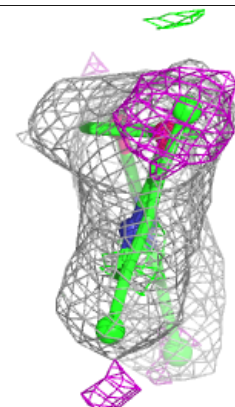
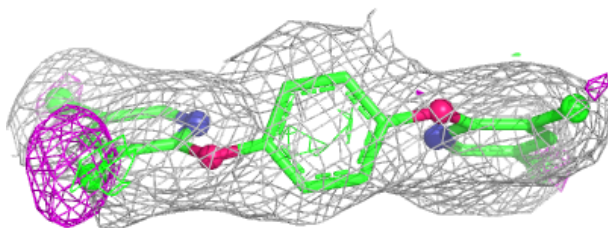
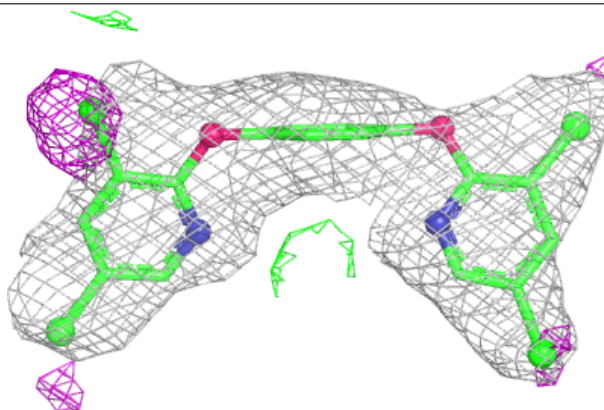
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around TCD E 805:

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

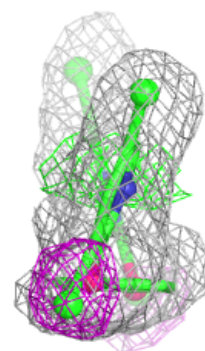
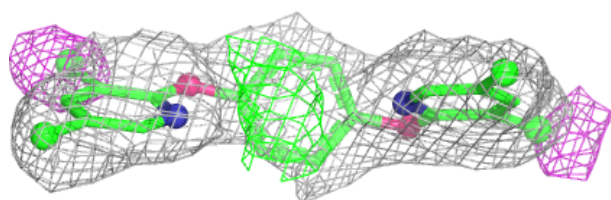
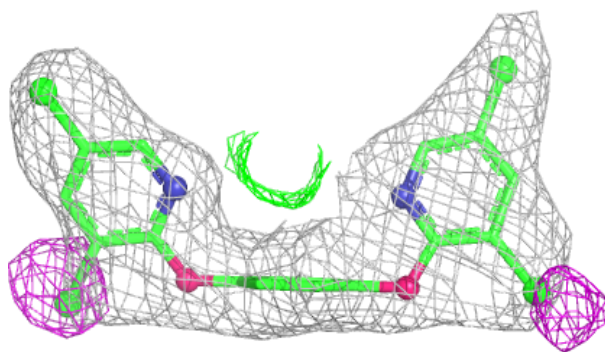
**Electron density around TCD H 808:**

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

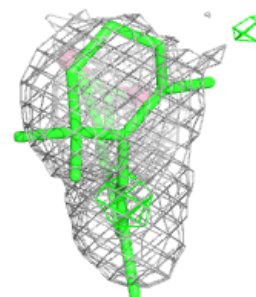
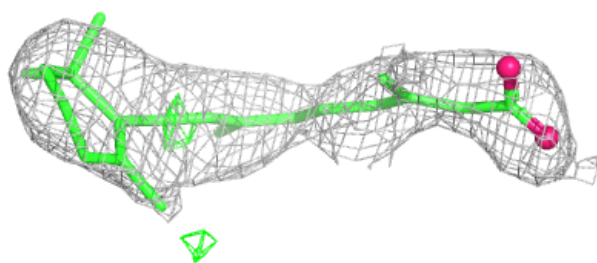


Electron density around TCD G 807:

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

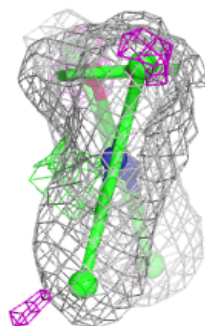
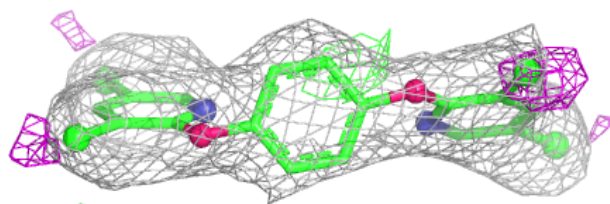
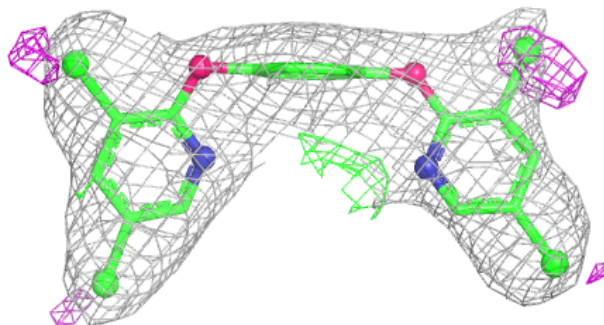
**Electron density around 9CR C 803:**

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

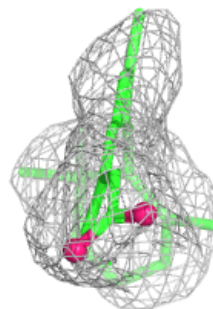
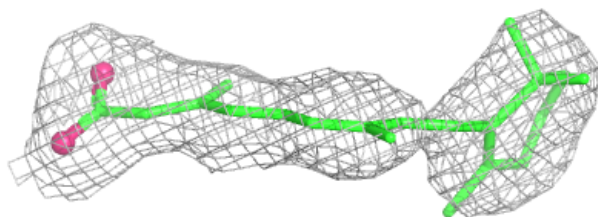
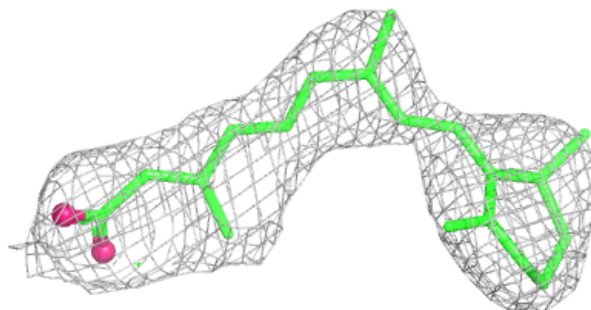


Electron density around TCD F 806:

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

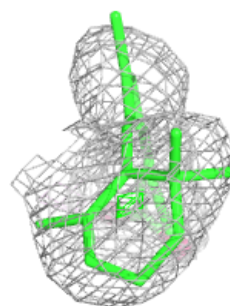
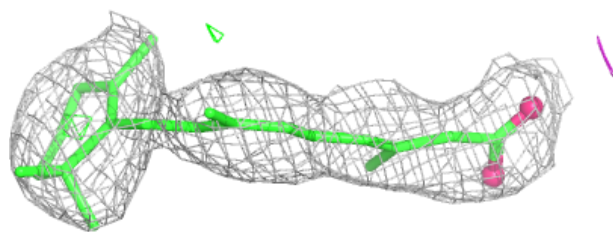
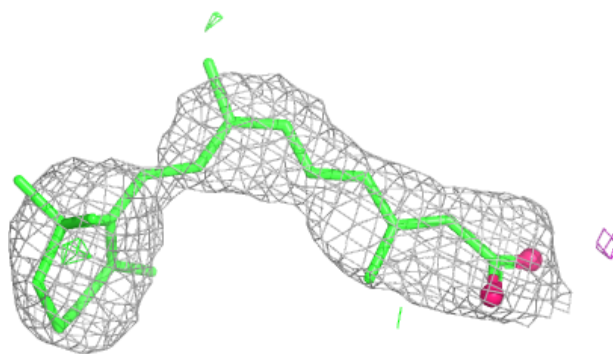
**Electron density around 9CR D 804:**

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

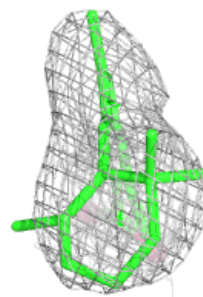
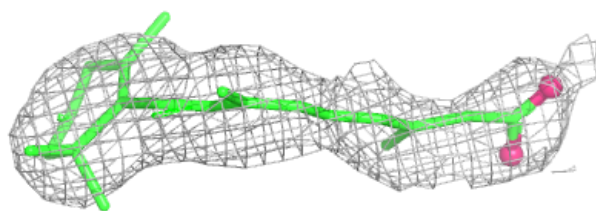
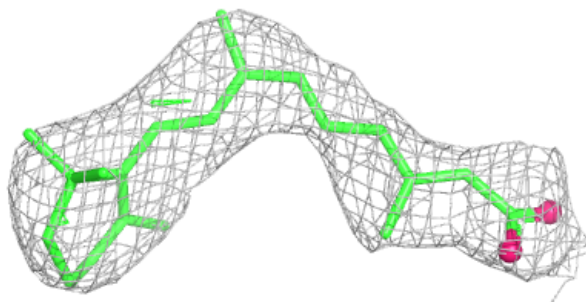


Electron density around 9CR A 801:

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

**Electron density around 9CR B 802:**

$2mF_o-DF_c$ (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.