



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 6, 2022 – 02:54 PM EDT

PDB ID : 5SJS  
Title : Crystal Structure of human phosphodiesterase 10 in complex with 6-cyclopropyl-N-[4-(dimethylcarbamoyl)pyridin-3-yl]-3-(pyrimidin-5-ylamino)pyridine-2-carboxamide  
Authors : Joseph, C.; Benz, J.; Flohr, A.; Groebke-Zbinden, K.; Rudolph, M.G.  
Deposited on : 2022-02-01  
Resolution : 2.70 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](mailto: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 : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.31.2  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

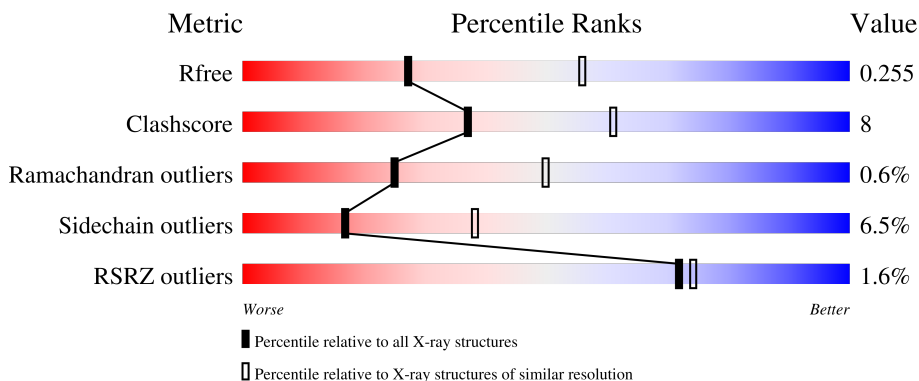
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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))
$R_{free}$	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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  $\geq 3$ , 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	343	 73% 17% • 9%
1	B	343	 71% 19% • 8%
1	C	343	 74% 15% • 9%
1	D	343	 5% 68% 22% • 9%

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 10473 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 cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	313	2541	1624	432	461	24	0	0	0
1	B	315	2551	1630	434	463	24	0	0	0
1	C	313	2541	1624	432	461	24	0	0	0
1	D	313	2537	1622	433	458	24	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	447	GLY	-	expression tag	UNP Q9Y233
A	448	SER	-	expression tag	UNP Q9Y233
B	447	GLY	-	expression tag	UNP Q9Y233
B	448	SER	-	expression tag	UNP Q9Y233
C	447	GLY	-	expression tag	UNP Q9Y233
C	448	SER	-	expression tag	UNP Q9Y233
D	447	GLY	-	expression tag	UNP Q9Y233
D	448	SER	-	expression tag	UNP Q9Y233

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Zn 1	0	0
2	B	1	Total 1	Zn 1	0	0
2	C	1	Total 1	Zn 1	0	0
2	D	1	Total 1	Zn 1	0	0

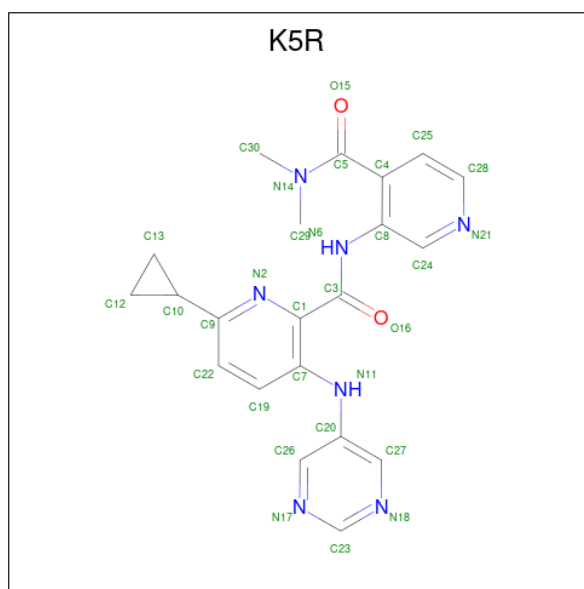
- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Mg 1 1	0	0
4	B	1	Total Mg 1 1	0	0
4	C	1	Total Mg 1 1	0	0
4	D	1	Total Mg 1 1	0	0

- Molecule 5 is 6-cyclopropyl-N-[4-(dimethylcarbamoyl)pyridin-3-yl]-3-[(pyrimidin-5-yl)amino]pyridine-2-carboxamide (three-letter code: K5R) (formula: C<sub>21</sub>H<sub>21</sub>N<sub>7</sub>O<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C N O 30 21 7 2	0	0
5	B	1	Total C N O 30 21 7 2	0	0
5	C	1	Total C N O 30 21 7 2	0	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
5	D	1	30	21	7	2	0	0

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	B	1	6	3	3	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	45	Total	O	0	0
			45	45		
7	B	51	Total	O	0	0
			51	51		
7	C	56	Total	O	0	0
			56	56		
7	D	16	Total	O	0	0
			16	16		

### 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.

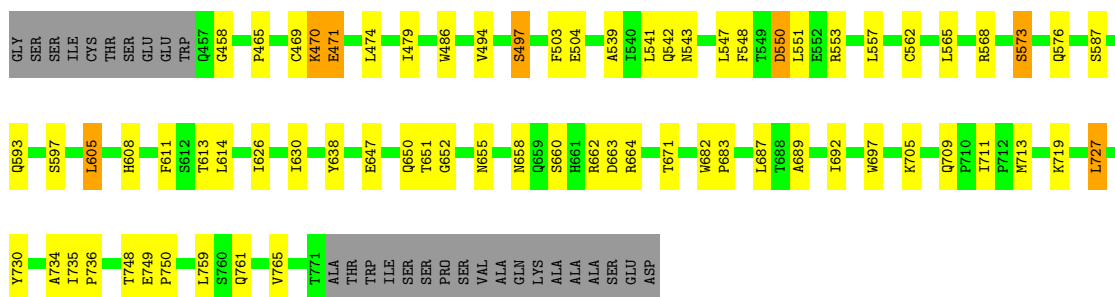
- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

Chain A: 



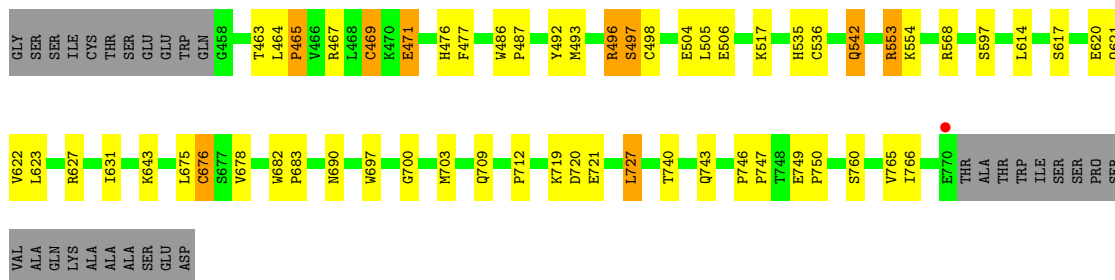
- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

Chain B: 



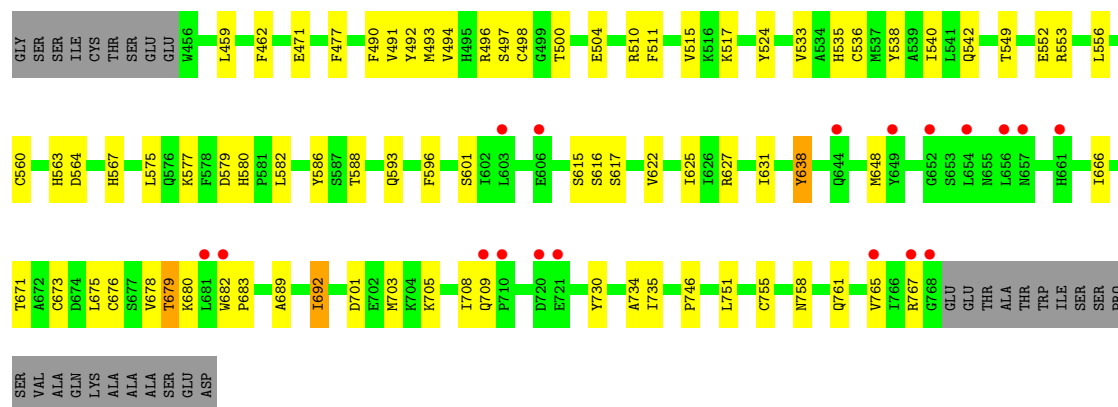
- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

Chain C: 



- Molecule 1: cAMP and cAMP-inhibited cGMP 3',5'-cyclic phosphodiesterase 10A

Chain D: 



## 4 Data and refinement statistics i

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	135.23Å 135.23Å 234.16Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.48 – 2.70 43.48 – 2.70	Depositor EDS
% Data completeness (in resolution range)	96.1 (43.48-2.70) 96.1 (43.48-2.70)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.09 (at 2.69Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.173 , 0.254 0.182 , 0.255	Depositor DCC
$R_{free}$ test set	2148 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	54.5	Xtrriage
Anisotropy	0.171	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 35.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	10473	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	64.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: MG, GOL, CL, K5R, ZN, CME

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	0.77	0/2592	0.93	0/3507
1	B	0.76	0/2602	0.97	1/3521 (0.0%)
1	C	0.75	0/2592	0.96	2/3507 (0.1%)
1	D	0.80	0/2588	0.91	0/3502
All	All	0.77	0/10374	0.94	3/14037 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	690	ASN	CB-CA-C	-5.77	98.86	110.40
1	B	664	ARG	NE-CZ-NH1	5.21	122.91	120.30
1	C	553	ARG	NE-CZ-NH1	5.17	122.89	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2541	0	2513	36	0
1	B	2551	0	2515	35	0
1	C	2541	0	2511	33	0
1	D	2537	0	2511	45	0

*Continued on next page...*

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	A	30	0	0	4	0
5	B	30	0	0	5	0
5	C	30	0	0	4	0
5	D	30	0	0	1	0
6	B	6	0	8	1	0
7	A	45	0	0	2	0
7	B	51	0	0	2	1
7	C	56	0	0	2	2
7	D	16	0	0	3	1
All	All	10473	0	10058	157	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 8.

All (157) 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)
5:A:804:K5R:C19	5:A:804:K5R:C27	2.53	0.84
1:C:493:MET:O	1:C:497:SER:HB2	1.84	0.77
1:B:683:PRO:O	1:B:687:LEU:HD12	1.85	0.76
1:D:490:PHE:O	1:D:494:VAL:HG23	1.88	0.73
5:C:803:K5R:C19	5:C:803:K5R:C27	2.69	0.70
1:B:761:GLN:O	1:B:765:VAL:HG23	1.91	0.70
1:A:469:CYS:SG	7:A:943:HOH:O	2.50	0.70
1:C:492:TYR:CZ	1:C:496:ARG:HD2	2.28	0.68
1:B:568:ARG:HD2	6:B:803:GOL:O2	1.92	0.66
1:D:493:MET:O	1:D:497:SER:HB2	1.97	0.65
1:A:722:VAL:HB	1:A:723:PRO:HD3	1.79	0.65
1:A:498:CYS:SG	1:A:554:LYS:HG2	2.38	0.63
1:C:492:TYR:CE1	1:C:496:ARG:HD2	2.33	0.63
1:B:548:PHE:O	1:B:553:ARG:NH1	2.31	0.63
1:D:735:ILE:HD13	1:D:755:CYS:SG	2.39	0.62

Continued on next page...

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:675:LEU:O	1:C:678:VAL:HG22	2.00	0.61
1:D:689:ALA:O	1:D:692:ILE:HG22	2.01	0.61
1:A:713:MET:HE2	5:A:804:K5R:C25	2.33	0.58
5:B:804:K5R:C25	5:B:804:K5R:C30	2.81	0.58
1:B:593:GLN:HG2	7:B:922:HOH:O	2.02	0.58
1:B:647:GLU:O	1:B:651:THR:HG23	2.04	0.58
1:D:761:GLN:O	1:D:765:VAL:HG23	2.03	0.57
1:D:510:ARG:HB2	7:D:907:HOH:O	2.05	0.57
5:B:804:K5R:C19	5:B:804:K5R:C27	2.83	0.56
1:D:730:TYR:HA	1:D:734:ALA:HB3	1.89	0.55
1:C:493:MET:SD	1:C:535:HIS:HA	2.46	0.55
1:D:627:ARG:O	1:D:631:ILE:HG12	2.07	0.55
1:C:720:ASP:OD1	1:C:721:GLU:HG3	2.08	0.54
1:C:505:LEU:O	1:C:506:GLU:C	2.46	0.54
1:C:727:LEU:HD12	1:C:766:ILE:CD1	2.37	0.54
1:A:627:ARG:O	1:A:631:ILE:HG12	2.08	0.53
1:C:727:LEU:HD12	1:C:766:ILE:HD13	1.89	0.53
1:C:749:GLU:N	1:C:750:PRO:CD	2.71	0.53
5:C:803:K5R:C25	5:C:803:K5R:C30	2.86	0.53
1:D:564:ASP:O	1:D:567:HIS:HB2	2.09	0.53
1:A:727:LEU:HD21	1:A:763:GLU:HG3	1.91	0.53
1:A:719:LYS:O	1:A:722:VAL:HG23	2.09	0.53
1:B:573:SER:HB2	7:B:929:HOH:O	2.09	0.52
1:D:648:MET:HE1	7:D:912:HOH:O	2.10	0.52
1:C:765:VAL:O	1:C:766:ILE:C	2.49	0.51
1:D:680:LYS:O	1:D:758:ASN:ND2	2.37	0.51
1:A:493:MET:O	1:A:497:SER:HB2	2.10	0.51
1:A:713:MET:CE	5:A:804:K5R:C25	2.89	0.51
1:C:740:THR:HA	1:C:743:GLN:HE21	1.76	0.51
1:A:493:MET:SD	1:A:535:HIS:HA	2.50	0.51
1:C:627:ARG:O	1:C:631:ILE:HG12	2.10	0.51
1:B:682:TRP:HB3	1:B:683:PRO:HD3	1.92	0.51
1:D:493:MET:SD	1:D:535:HIS:HA	2.49	0.51
1:A:735:ILE:HB	1:A:736:PRO:HD3	1.93	0.50
1:D:533:VAL:HG12	1:D:560:CYS:HB3	1.93	0.50
1:D:588:THR:O	1:D:593:GLN:NE2	2.44	0.50
1:B:539:ALA:O	1:B:543:ASN:ND2	2.36	0.50
5:D:803:K5R:C27	5:D:803:K5R:C19	2.88	0.50
1:C:542:GLN:NE2	1:C:542:GLN:HA	2.27	0.50
1:D:701:ASP:O	1:D:705:LYS:HG3	2.12	0.50
1:A:602:ILE:HA	1:A:605:LEU:HD22	1.95	0.49

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:497:SER:O	1:C:553:ARG:HD2	2.12	0.49
1:B:727:LEU:HD23	1:B:759:LEU:CD1	2.43	0.48
1:A:682:TRP:N	1:A:683:PRO:CD	2.76	0.48
1:D:622:VAL:HA	1:D:625:ILE:HD12	1.95	0.48
1:A:498:CYS:CB	1:A:502:CYS:HG	2.26	0.48
1:D:497:SER:HA	1:D:542:GLN:NE2	2.28	0.48
1:A:503:PHE:CD1	1:A:610:ILE:HB	2.49	0.47
1:C:620:GLU:OE1	7:C:901:HOH:O	2.20	0.47
1:B:730:TYR:HA	1:B:734:ALA:HB3	1.96	0.47
5:C:803:K5R:O16	5:C:803:K5R:N11	2.47	0.47
1:B:611:PHE:HB3	1:B:614:LEU:HD22	1.95	0.47
1:C:740:THR:HA	1:C:743:GLN:NE2	2.30	0.47
1:D:497:SER:O	1:D:553:ARG:HD2	2.14	0.47
1:D:586:TYR:HB3	1:D:593:GLN:NE2	2.29	0.47
1:C:697:TRP:CZ2	1:C:719:LYS:HG3	2.49	0.47
1:A:658:ASN:HB3	1:A:661:HIS:HB2	1.97	0.47
1:B:735:ILE:N	1:B:736:PRO:HD2	2.30	0.47
1:C:469:CYS:HB3	7:C:949:HOH:O	2.15	0.47
1:A:524:TYR:CD2	1:A:692:ILE:HD13	2.50	0.46
1:C:464:LEU:O	1:C:465:PRO:C	2.52	0.46
1:A:749:GLU:N	1:A:750:PRO:CD	2.78	0.46
1:C:746:PRO:N	1:C:747:PRO:CD	2.78	0.46
1:C:467:ARG:O	1:C:471:GLU:HB2	2.16	0.46
5:C:803:K5R:O16	5:C:803:K5R:C24	2.63	0.46
1:B:550:ASP:OD1	1:B:550:ASP:N	2.48	0.46
1:A:498:CYS:SG	1:A:554:LYS:CG	3.04	0.46
1:D:638:TYR:CD1	1:D:671:THR:HG21	2.50	0.46
1:C:498:CYS:SG	1:C:554:LYS:HG3	2.55	0.45
1:A:585:LEU:O	1:A:585:LEU:HD12	2.16	0.45
1:D:493:MET:HA	1:D:538:TYR:CE1	2.51	0.45
1:D:498:CYS:HB3	1:D:553:ARG:HB3	1.97	0.45
1:D:524:TYR:CD2	1:D:692:ILE:HD13	2.51	0.45
1:D:492:TYR:CZ	1:D:496:ARG:HD2	2.51	0.45
1:D:596:PHE:CE2	1:D:627:ARG:HG3	2.51	0.45
1:D:675:LEU:O	1:D:678:VAL:HG22	2.16	0.45
1:D:556:LEU:HD21	1:D:666:ILE:HG23	1.97	0.45
1:A:739:THR:HA	1:A:752:LEU:HD22	1.98	0.45
1:C:498:CYS:SG	1:C:554:LYS:CG	3.04	0.45
1:C:700:GLY:O	1:C:703:MET:HB2	2.17	0.45
1:D:556:LEU:HD21	1:D:666:ILE:CG2	2.47	0.45
1:B:638:TYR:CD1	1:B:671:THR:HG21	2.51	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:536:CYS:HB2	1:C:676:CYS:SG	2.57	0.45
1:C:749:GLU:HB3	1:C:750:PRO:HD3	1.98	0.44
1:A:461:GLN:NE2	1:A:461:GLN:HA	2.32	0.44
1:B:662:ARG:O	1:B:663:ASP:C	2.56	0.44
1:D:536:CYS:SG	1:D:673:CYS:HA	2.57	0.44
1:B:749:GLU:N	1:B:750:PRO:CD	2.80	0.44
1:B:497:SER:HA	1:B:542:GLN:NE2	2.33	0.44
1:C:749:GLU:N	1:C:750:PRO:HD2	2.33	0.44
1:D:679:THR:OG1	1:D:751:LEU:HD22	2.18	0.44
1:B:541:LEU:HD23	1:B:541:LEU:HA	1.89	0.44
1:B:713:MET:SD	5:B:804:K5R:C4	3.06	0.44
1:B:697:TRP:CZ2	1:B:719:LYS:HG3	2.53	0.43
1:D:730:TYR:O	1:D:735:ILE:HG12	2.17	0.43
1:B:470:LYS:HE2	1:D:746:PRO:HG3	2.00	0.43
1:A:724:GLN:NE2	1:A:727:LEU:HD12	2.34	0.43
1:B:562:CYS:HB3	1:B:565:LEU:HD12	2.01	0.43
1:D:580:HIS:CE1	1:D:582:LEU:HD12	2.53	0.43
1:D:540:ILE:HD12	1:D:673:CYS:SG	2.58	0.43
1:A:735:ILE:N	1:A:736:PRO:CD	2.81	0.43
1:A:611:PHE:O	1:A:612:SER:C	2.57	0.43
1:B:479:ILE:HD12	1:B:486:TRP:CD1	2.54	0.42
1:A:763:GLU:O	1:A:767:ARG:HG3	2.19	0.42
1:B:605:LEU:HB3	1:B:608:HIS:ND1	2.34	0.42
5:B:804:K5R:O16	5:B:804:K5R:C24	2.68	0.42
1:A:523:PRO:HD2	1:A:695:GLU:HG2	2.02	0.42
1:B:689:ALA:O	1:B:692:ILE:HG22	2.19	0.42
1:A:611:PHE:HB3	1:A:614:LEU:HD22	2.01	0.42
1:D:462:PHE:CD1	1:D:491:VAL:HG11	2.55	0.42
1:D:511:PHE:O	1:D:515:VAL:HG23	2.19	0.42
1:A:766:ILE:C	1:A:768:GLY:H	2.23	0.42
1:D:471:GLU:O	1:D:477:PHE:HB2	2.20	0.42
1:D:549:THR:HG23	1:D:552:GLU:OE1	2.20	0.42
1:B:626:ILE:O	1:B:630:ILE:HG13	2.20	0.42
1:B:655:ASN:HD22	1:B:658:ASN:HB2	1.84	0.42
1:A:671:THR:O	1:A:675:LEU:HG	2.20	0.42
1:D:533:VAL:HG21	1:D:563:HIS:CE1	2.55	0.41
1:A:677:SER:HB2	5:A:804:K5R:N18	2.36	0.41
1:C:471:GLU:HB3	1:C:477:PHE:CD1	2.56	0.41
1:A:683:PRO:O	1:A:687:LEU:HD12	2.20	0.41
1:C:476:HIS:O	1:C:477:PHE:C	2.58	0.41
1:A:469:CYS:HB2	7:A:937:HOH:O	2.19	0.41

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:727:LEU:CD2	1:B:759:LEU:HD11	2.49	0.41
1:C:682:TRP:N	1:C:683:PRO:HD2	2.34	0.41
1:D:493:MET:O	1:D:497:SER:CB	2.68	0.41
1:B:557:LEU:HD23	1:B:557:LEU:HA	1.90	0.41
1:C:486:TRP:N	1:C:487:PRO:CD	2.84	0.41
1:B:497:SER:HA	1:B:542:GLN:HE22	1.85	0.41
1:D:510:ARG:HA	7:D:907:HOH:O	2.21	0.41
1:A:484:ASN:HD22	1:A:484:ASN:HA	1.72	0.41
1:D:462:PHE:CE1	1:D:491:VAL:HG11	2.56	0.41
1:D:703:MET:HB3	1:D:708:ILE:HG22	2.01	0.41
1:D:493:MET:HB3	1:D:538:TYR:CD1	2.56	0.41
1:A:611:PHE:O	1:A:613:THR:N	2.54	0.40
5:B:804:K5R:O16	5:B:804:K5R:N11	2.52	0.40
1:D:682:TRP:N	1:D:683:PRO:CD	2.84	0.40
1:A:684:VAL:HG22	1:B:705:LYS:HG2	2.02	0.40
1:C:498:CYS:SG	1:C:554:LYS:HG2	2.61	0.40
1:B:748:THR:C	1:B:750:PRO:HD2	2.42	0.40
1:B:471:GLU:HG3	1:B:474:LEU:HD12	2.04	0.40
1:B:494:VAL:HG11	1:B:503:PHE:CD2	2.56	0.40

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)
7:C:941:HOH:O	7:C:941:HOH:O[2_655]	1.78	0.42
7:B:907:HOH:O	7:D:910:HOH:O[8_544]	1.84	0.36
7:C:905:HOH:O	7:C:905:HOH:O[2_655]	2.19	0.01

## 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	310/343 (90%)	283 (91%)	25 (8%)	2 (1%)	25	50
1	B	312/343 (91%)	286 (92%)	23 (7%)	3 (1%)	15	37
1	C	310/343 (90%)	285 (92%)	25 (8%)	0	100	100
1	D	310/343 (90%)	291 (94%)	17 (6%)	2 (1%)	25	50
All	All	1242/1372 (90%)	1145 (92%)	90 (7%)	7 (1%)	25	50

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	612	SER
1	B	652	GLY
1	D	615	SER
1	A	483	GLU
1	D	579	ASP
1	B	465	PRO
1	B	458	GLY

### 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	281/305 (92%)	264 (94%)	17 (6%)	19	42
1	B	281/305 (92%)	262 (93%)	19 (7%)	16	36
1	C	281/305 (92%)	259 (92%)	22 (8%)	12	29
1	D	280/305 (92%)	265 (95%)	15 (5%)	22	47
All	All	1123/1220 (92%)	1050 (94%)	73 (6%)	17	38

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	471	GLU
1	A	496	ARG
1	A	497	SER
1	A	500	THR

*Continued on next page...*

*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	504	GLU
1	A	517	LYS
1	A	573	SER
1	A	575	LEU
1	A	587	SER
1	A	605	LEU
1	A	606	GLU
1	A	613	THR
1	A	622	VAL
1	A	638	TYR
1	A	653	SER
1	A	719	LYS
1	A	720	ASP
1	B	469	CYS
1	B	470	LYS
1	B	471	GLU
1	B	497	SER
1	B	504	GLU
1	B	547	LEU
1	B	550	ASP
1	B	551	LEU
1	B	573	SER
1	B	576	GLN
1	B	587	SER
1	B	597	SER
1	B	605	LEU
1	B	613	THR
1	B	650	GLN
1	B	660	SER
1	B	709	GLN
1	B	711	ILE
1	B	727	LEU
1	C	463	THR
1	C	465	PRO
1	C	469	CYS
1	C	471	GLU
1	C	496	ARG
1	C	497	SER
1	C	504	GLU
1	C	517	LYS
1	C	542	GLN
1	C	568	ARG

*Continued on next page...*



*Continued from previous page...*

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	C	597	SER
1	C	614	LEU
1	C	617	SER
1	C	621	GLN
1	C	622	VAL
1	C	623	LEU
1	C	643	LYS
1	C	676	CYS
1	C	709	GLN
1	C	712	PRO
1	C	727	LEU
1	C	760	SER
1	D	459	LEU
1	D	500	THR
1	D	504	GLU
1	D	517	LYS
1	D	575	LEU
1	D	577	LYS
1	D	601	SER
1	D	616	SER
1	D	617	SER
1	D	638	TYR
1	D	676	CYS
1	D	679	THR
1	D	692	ILE
1	D	709	GLN
1	D	767	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	461	GLN
1	A	604	GLN
1	A	761	GLN
1	B	484	ASN
1	B	542	GLN
1	B	576	GLN
1	B	604	GLN
1	B	655	ASN
1	B	743	GLN
1	C	542	GLN
1	C	543	ASN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	C	604	GLN
1	C	644	GLN
1	C	743	GLN
1	D	476	HIS
1	D	484	ASN
1	D	542	GLN
1	D	621	GLN
1	D	650	GLN
1	D	743	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	CME	C	509	1	8,9,10	0.41	0	5,9,11	0.36	0
1	CME	A	509	1	8,9,10	0.56	0	5,9,11	0.56	0
1	CME	B	509	1	8,9,10	0.46	0	5,9,11	0.86	0
1	CME	D	509	1	8,9,10	0.41	0	5,9,11	0.81	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CME	C	509	1	-	3/5/8/10	-
1	CME	A	509	1	-	2/5/8/10	-

*Continued on next page...*

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	CME	B	509	1	-	1/5/8/10	-
1	CME	D	509	1	-	2/5/8/10	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	509	CME	SD-CE-CZ-OH
1	C	509	CME	CE-SD-SG-CB
1	A	509	CME	SD-CE-CZ-OH
1	C	509	CME	SD-CE-CZ-OH
1	A	509	CME	CZ-CE-SD-SG
1	D	509	CME	CZ-CE-SD-SG
1	D	509	CME	N-CA-CB-SG
1	C	509	CME	CZ-CE-SD-SG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 9 are monoatomic - leaving 5 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	$\# Z  > 2$
5	K5R	B	804	-	33,33,33	2.41	8 (24%)	40,46,46	2.40	14 (35%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	K5R	D	803	-	33,33,33	1.66	11 (33%)	40,46,46	2.11	9 (22%)
5	K5R	A	804	-	33,33,33	2.17	8 (24%)	40,46,46	2.50	17 (42%)
6	GOL	B	803	-	5,5,5	0.25	0	5,5,5	0.61	0
5	K5R	C	803	-	33,33,33	1.67	7 (21%)	40,46,46	2.04	15 (37%)

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
5	K5R	B	804	-	-	3/24/26/26	0/4/4/4
5	K5R	D	803	-	-	0/24/26/26	0/4/4/4
5	K5R	A	804	-	-	2/24/26/26	0/4/4/4
6	GOL	B	803	-	-	3/4/4/4	-
5	K5R	C	803	-	-	2/24/26/26	0/4/4/4

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	804	K5R	C5-N14	8.76	1.46	1.34
5	A	804	K5R	C5-N14	7.56	1.44	1.34
5	A	804	K5R	C4-C8	5.31	1.49	1.41
5	C	803	K5R	C5-N14	4.79	1.40	1.34
5	B	804	K5R	C4-C8	4.13	1.47	1.41
5	B	804	K5R	C1-C3	-3.91	1.44	1.50
5	B	804	K5R	C4-C5	3.77	1.56	1.50
5	B	804	K5R	C26-C20	3.76	1.46	1.39
5	B	804	K5R	O15-C5	3.62	1.29	1.22
5	A	804	K5R	C24-C8	3.31	1.44	1.39
5	C	803	K5R	C4-C8	3.28	1.46	1.41
5	D	803	K5R	C5-N14	3.25	1.38	1.34
5	D	803	K5R	C4-C8	3.00	1.45	1.41
5	D	803	K5R	C7-C1	3.00	1.45	1.41
5	B	804	K5R	C19-C22	2.99	1.44	1.38
5	A	804	K5R	C25-C4	2.94	1.44	1.39
5	A	804	K5R	C4-C5	2.91	1.55	1.50
5	C	803	K5R	C1-C3	-2.69	1.46	1.50
5	D	803	K5R	C26-C20	2.67	1.44	1.39
5	D	803	K5R	C19-C22	2.49	1.43	1.38
5	D	803	K5R	C22-C9	2.47	1.43	1.38

*Continued on next page...*

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	D	803	K5R	C19-C7	2.32	1.43	1.39
5	C	803	K5R	C26-C20	2.29	1.43	1.39
5	B	804	K5R	C12-C10	2.29	1.57	1.50
5	A	804	K5R	C12-C10	2.24	1.57	1.50
5	D	803	K5R	C9-C10	2.21	1.56	1.50
5	C	803	K5R	C9-N2	-2.20	1.32	1.34
5	A	804	K5R	C19-C22	2.20	1.42	1.38
5	A	804	K5R	C19-C7	2.16	1.43	1.39
5	C	803	K5R	C24-C8	2.12	1.42	1.39
5	D	803	K5R	C25-C4	2.12	1.43	1.39
5	D	803	K5R	C12-C10	2.04	1.56	1.50
5	D	803	K5R	C9-N2	-2.02	1.32	1.34
5	C	803	K5R	C22-C9	2.01	1.42	1.38

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	804	K5R	C4-C5-N14	7.80	126.63	118.37
5	B	804	K5R	C27-N18-C23	6.61	124.26	115.80
5	D	803	K5R	C27-N18-C23	5.87	123.32	115.80
5	D	803	K5R	C22-C9-N2	-5.77	116.48	122.45
5	B	804	K5R	C8-C4-C5	5.71	128.76	120.69
5	B	804	K5R	C22-C9-N2	-5.66	116.59	122.45
5	C	803	K5R	C27-N18-C23	5.55	122.91	115.80
5	D	803	K5R	C4-C5-N14	5.53	124.22	118.37
5	A	804	K5R	C26-N17-C23	4.82	121.97	115.80
5	B	804	K5R	C25-C4-C8	-4.81	113.35	118.81
5	A	804	K5R	C22-C9-N2	-4.80	117.49	122.45
5	A	804	K5R	C27-N18-C23	4.56	121.64	115.80
5	C	803	K5R	C4-C5-N14	4.23	122.85	118.37
5	A	804	K5R	C3-C1-N2	4.11	119.83	115.99
5	B	804	K5R	C20-C27-N18	-3.56	116.08	123.13
5	C	803	K5R	C26-N17-C23	3.51	120.29	115.80
5	B	804	K5R	C19-C7-C1	-3.50	114.28	117.94
5	A	804	K5R	C28-N21-C24	3.38	122.69	116.85
5	B	804	K5R	C4-C8-N6	3.32	124.69	118.69
5	D	803	K5R	C20-C27-N18	-3.26	116.67	123.13
5	A	804	K5R	C25-C4-C8	-3.25	115.12	118.81
5	C	803	K5R	C8-C4-C5	3.16	125.16	120.69
5	D	803	K5R	C22-C9-C10	3.16	128.44	121.03
5	D	803	K5R	C28-N21-C24	3.15	122.30	116.85
5	A	804	K5R	C8-C4-C5	3.15	125.14	120.69

Continued on next page...

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	804	K5R	N18-C23-N17	-3.09	120.56	126.61
5	C	803	K5R	C28-N21-C24	3.09	122.19	116.85
5	C	803	K5R	C25-C4-C8	-3.03	115.37	118.81
5	C	803	K5R	C19-C7-N11	3.01	127.59	121.39
5	C	803	K5R	N18-C23-N17	-2.96	120.81	126.61
5	A	804	K5R	C20-N11-C7	-2.89	119.10	126.66
5	B	804	K5R	C28-N21-C24	2.79	121.68	116.85
5	A	804	K5R	O15-C5-C4	-2.79	114.43	120.06
5	B	804	K5R	C7-C1-N2	2.73	124.20	120.97
5	B	804	K5R	C4-C5-N14	2.70	121.23	118.37
5	B	804	K5R	O15-C5-C4	-2.67	114.67	120.06
5	C	803	K5R	C22-C9-N2	-2.67	119.69	122.45
5	C	803	K5R	C12-C10-C9	-2.50	117.39	120.33
5	B	804	K5R	C19-C7-N11	2.49	126.52	121.39
5	A	804	K5R	C25-C28-N21	-2.45	119.35	123.62
5	A	804	K5R	C4-C8-N6	2.44	123.11	118.69
5	D	803	K5R	C8-C4-C5	2.42	124.11	120.69
5	A	804	K5R	C13-C10-C9	2.40	123.16	120.33
5	A	804	K5R	C28-C25-C4	2.36	123.19	118.92
5	D	803	K5R	O15-C5-N14	-2.32	117.61	122.36
5	C	803	K5R	C20-C27-N18	-2.17	118.83	123.13
5	C	803	K5R	C22-C9-C10	2.17	126.12	121.03
5	C	803	K5R	O15-C5-C4	-2.13	115.77	120.06
5	C	803	K5R	C7-C1-N2	2.12	123.48	120.97
5	B	804	K5R	O16-C3-N6	2.09	128.48	123.71
5	A	804	K5R	C20-C27-N18	-2.07	119.03	123.13
5	D	803	K5R	C3-C1-N2	-2.07	114.06	115.99
5	A	804	K5R	C20-C26-N17	-2.03	119.11	123.13
5	C	803	K5R	O16-C3-C1	2.02	123.61	120.59
5	B	804	K5R	C22-C9-C10	2.02	125.76	121.03

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	803	K5R	C13-C10-C9-N2
6	B	803	GOL	O1-C1-C2-C3
5	B	804	K5R	C12-C10-C9-C22
5	C	803	K5R	C12-C10-C9-C22
6	B	803	GOL	O2-C2-C3-O3
5	A	804	K5R	C12-C10-C9-C22
5	B	804	K5R	C13-C10-C9-C22

*Continued on next page...*

*Continued from previous page...*

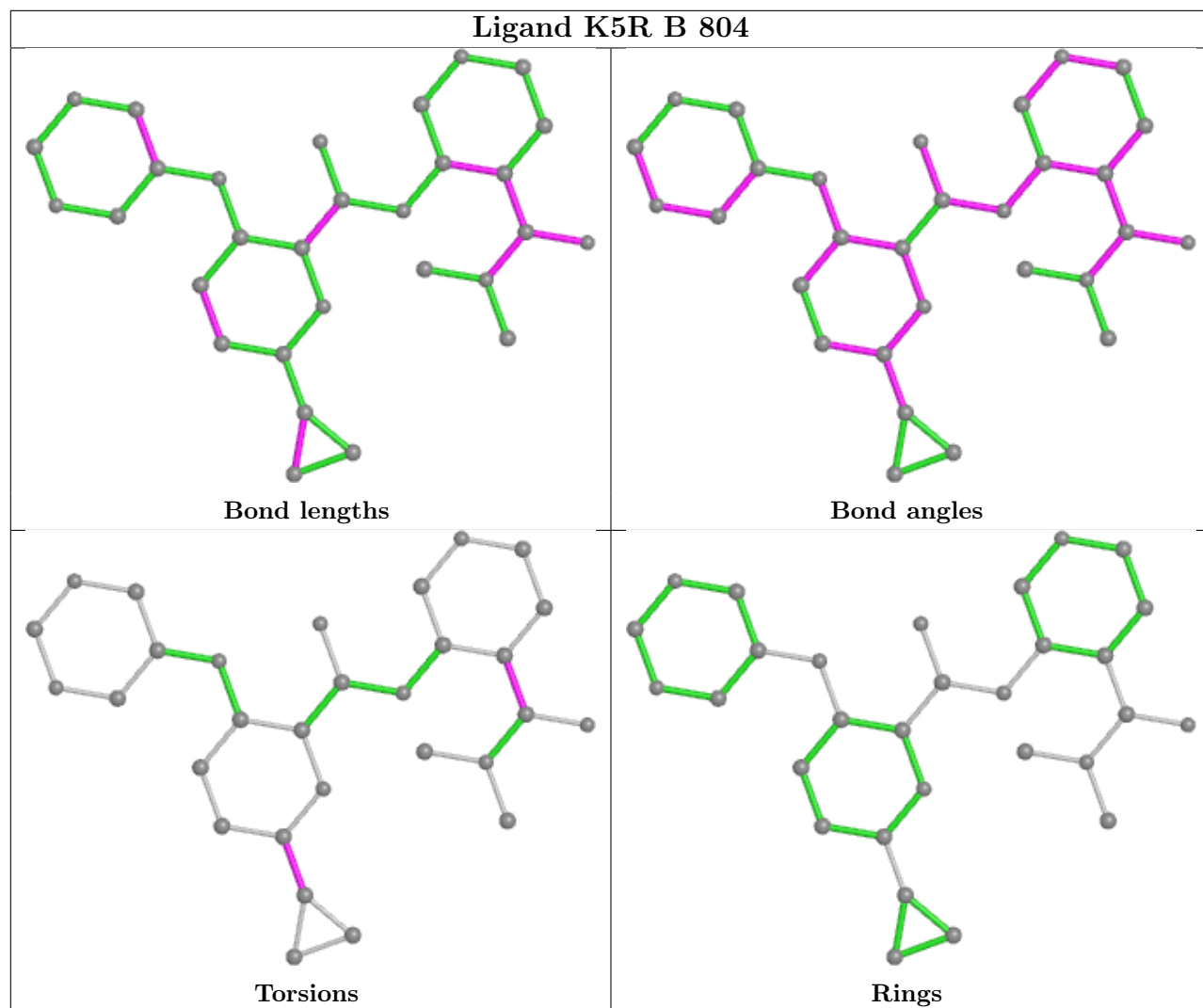
Mol	Chain	Res	Type	Atoms
6	B	803	GOL	C1-C2-C3-O3
5	B	804	K5R	C25-C4-C5-N14
5	A	804	K5R	C13-C10-C9-C22

There are no ring outliers.

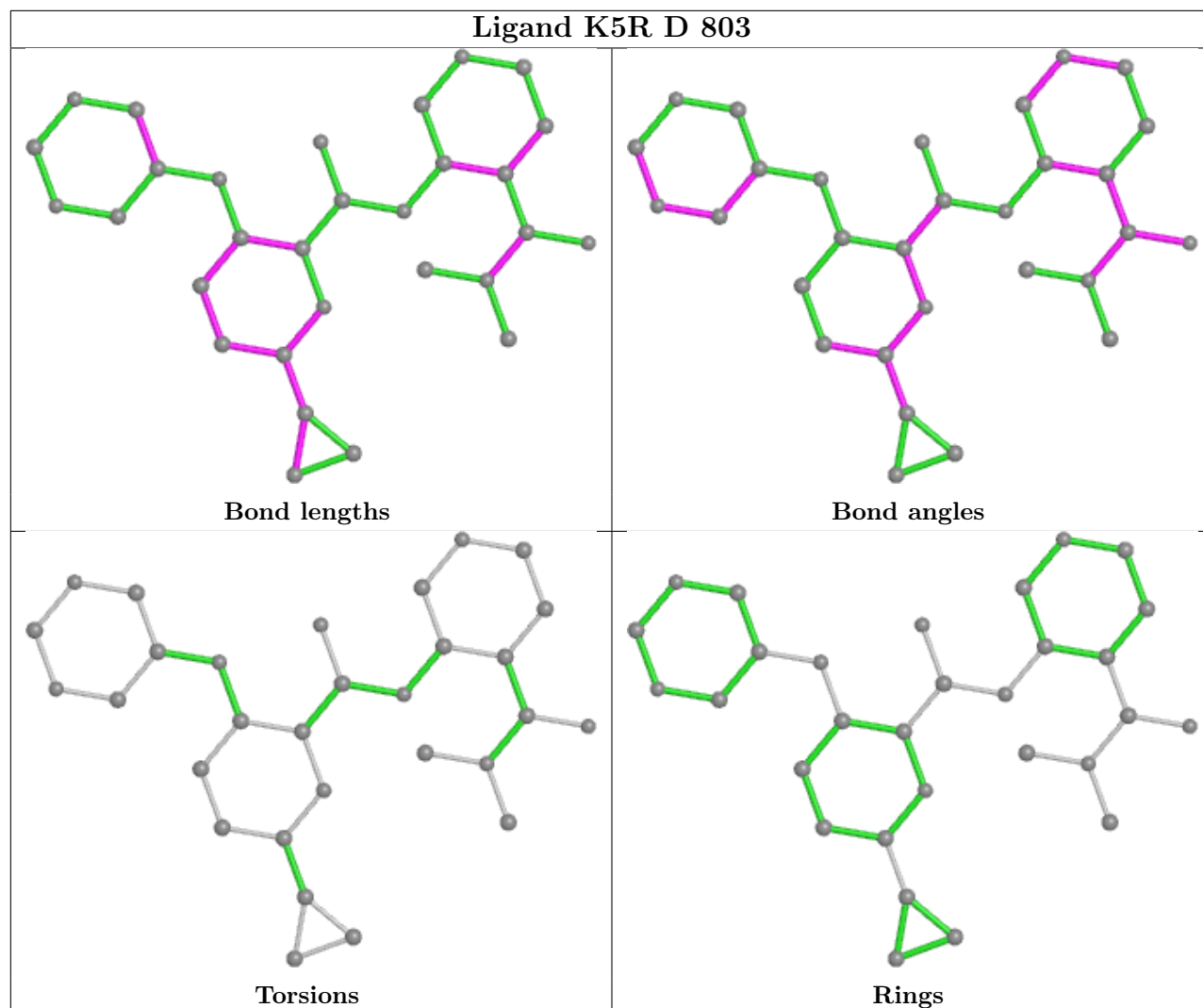
5 monomers are involved in 15 short contacts:

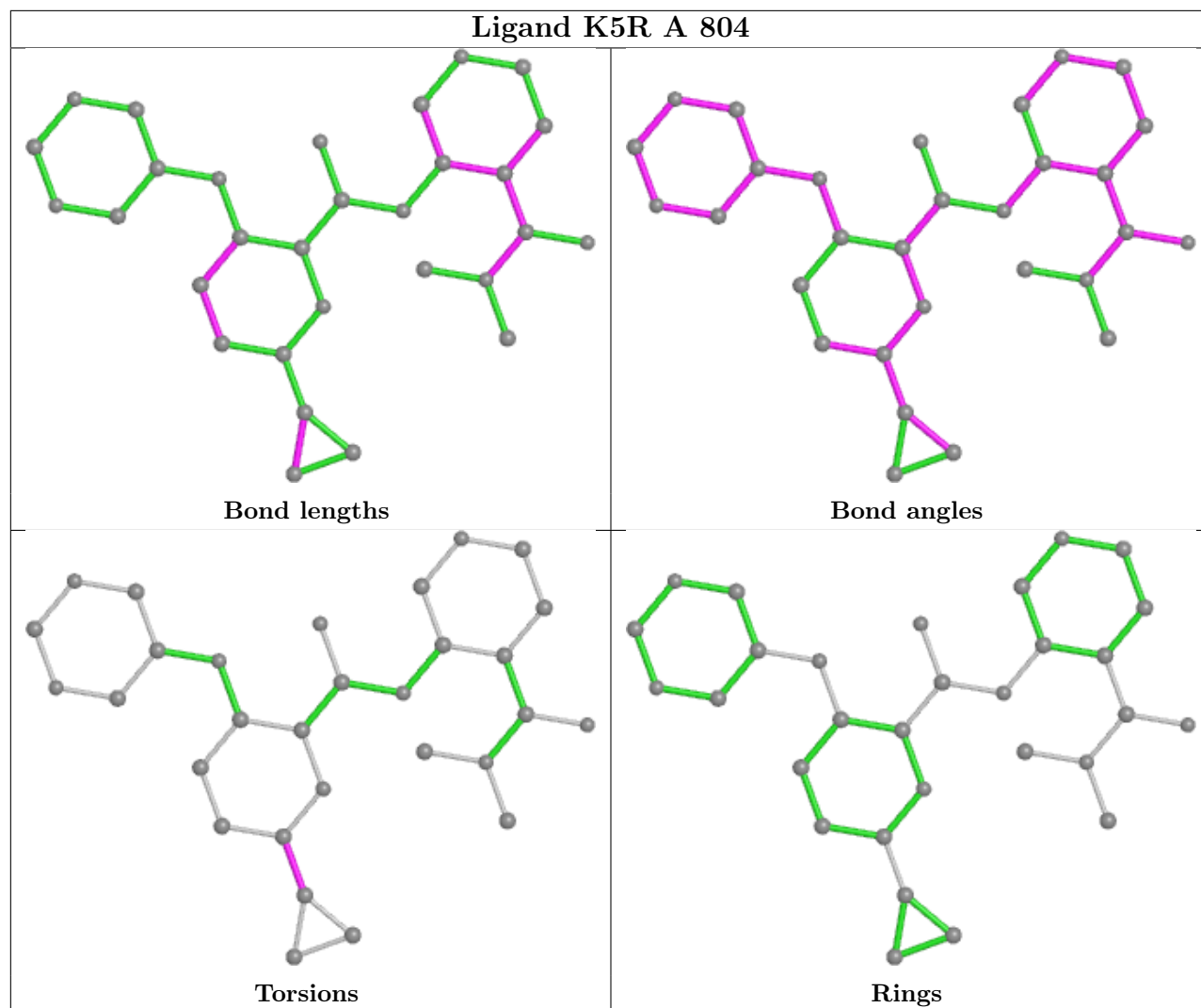
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	804	K5R	5	0
5	D	803	K5R	1	0
5	A	804	K5R	4	0
6	B	803	GOL	1	0
5	C	803	K5R	4	0

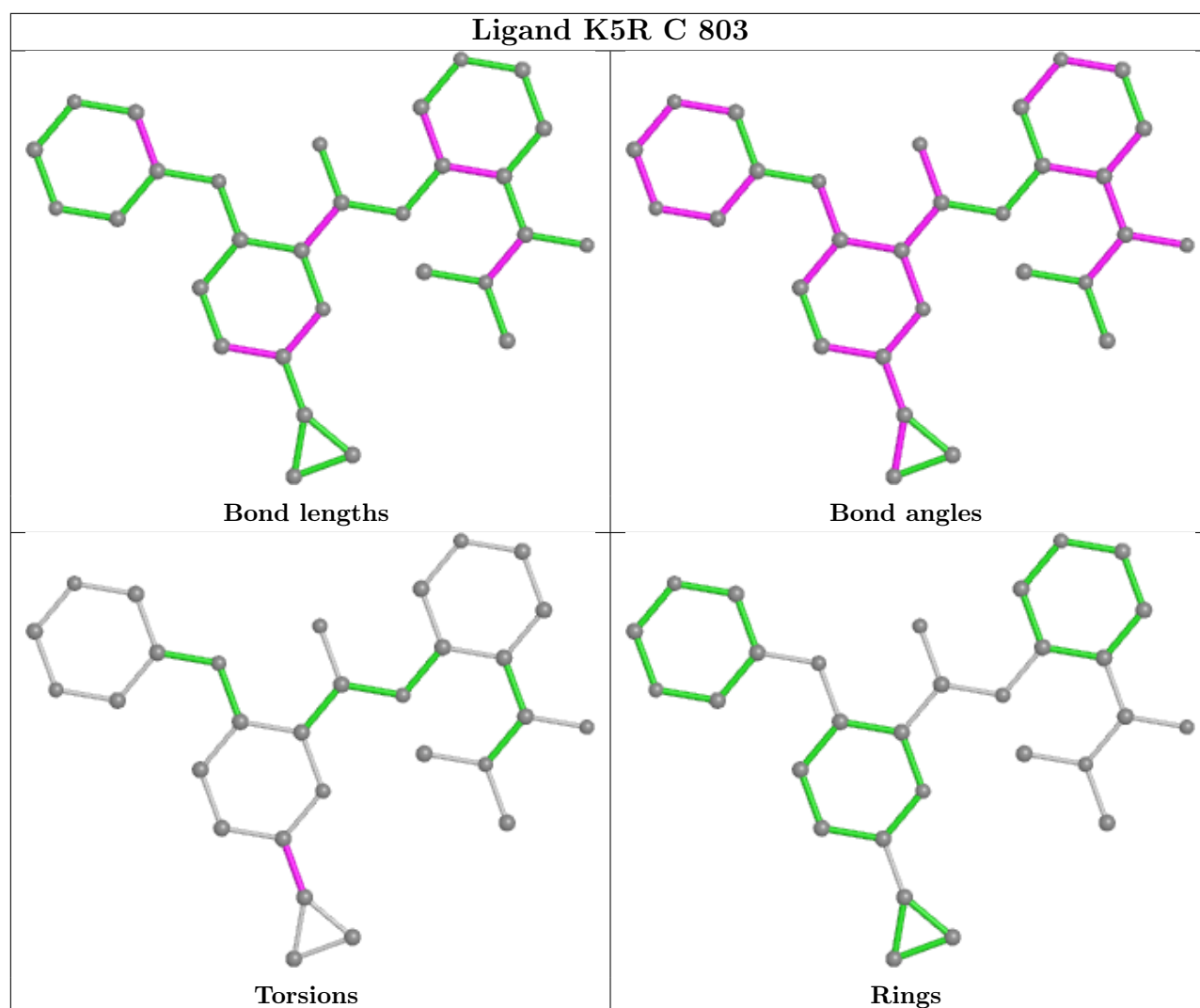
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	312/343 (90%)	-0.38	1 (0%) 94 95	37, 52, 84, 119	0
1	B	314/343 (91%)	-0.38	0 100 100	35, 55, 91, 112	0
1	C	312/343 (90%)	-0.41	1 (0%) 94 95	37, 52, 83, 111	0
1	D	312/343 (90%)	0.20	18 (5%) 23 22	63, 88, 109, 126	0
All	All	1250/1372 (91%)	-0.24	20 (1%) 72 74	35, 60, 102, 126	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	649	TYR	3.3
1	D	720	ASP	3.3
1	D	768	GLY	3.1
1	D	765	VAL	3.1
1	D	681	LEU	2.8
1	D	682	TRP	2.8
1	D	603	LEU	2.8
1	D	656	LEU	2.8
1	D	654	LEU	2.6
1	D	657	ASN	2.5
1	A	460	MET	2.4
1	D	606	GLU	2.4
1	D	710	PRO	2.3
1	C	770	GLU	2.3
1	D	644	GLN	2.2
1	D	767	ARG	2.1
1	D	709	GLN	2.1
1	D	652	GLY	2.1
1	D	661	HIS	2.0
1	D	721	GLU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	CME	B	509	10/11	0.90	0.20	58,71,100,105	0
1	CME	D	509	10/11	0.90	0.22	77,100,124,124	0
1	CME	C	509	10/11	0.94	0.14	52,67,108,116	0
1	CME	A	509	10/11	0.94	0.11	59,66,91,97	0

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

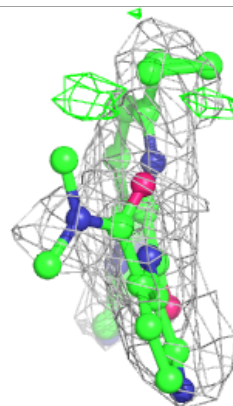
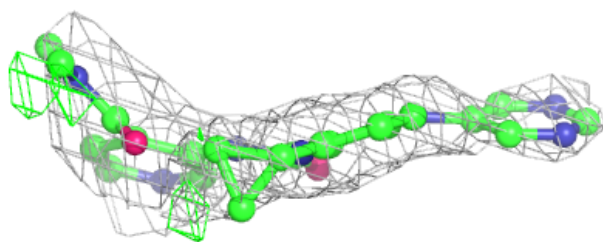
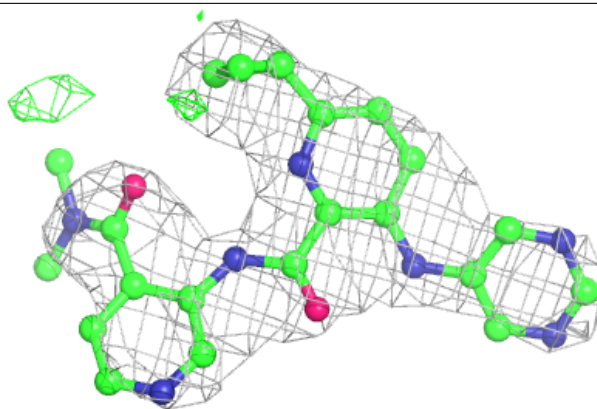
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	MG	D	802	1/1	0.49	0.15	72,72,72,72	0
3	CL	A	802	1/1	0.67	0.35	101,101,101,101	0
6	GOL	B	803	6/6	0.87	0.33	74,88,91,92	0
5	K5R	D	803	30/30	0.88	0.26	63,94,120,122	0
5	K5R	B	804	30/30	0.90	0.25	49,69,83,90	0
5	K5R	C	803	30/30	0.91	0.23	53,68,91,105	0
4	MG	A	803	1/1	0.92	0.17	34,34,34,34	0
4	MG	C	802	1/1	0.94	0.26	38,38,38,38	0
5	K5R	A	804	30/30	0.95	0.20	52,65,81,88	0
2	ZN	D	801	1/1	0.98	0.10	73,73,73,73	0
4	MG	B	802	1/1	0.99	0.09	36,36,36,36	0
2	ZN	A	801	1/1	0.99	0.14	49,49,49,49	0
2	ZN	C	801	1/1	1.00	0.12	48,48,48,48	0
2	ZN	B	801	1/1	1.00	0.13	45,45,45,45	0

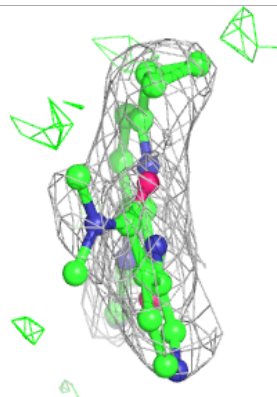
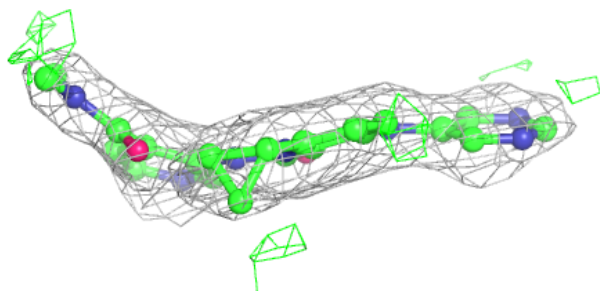
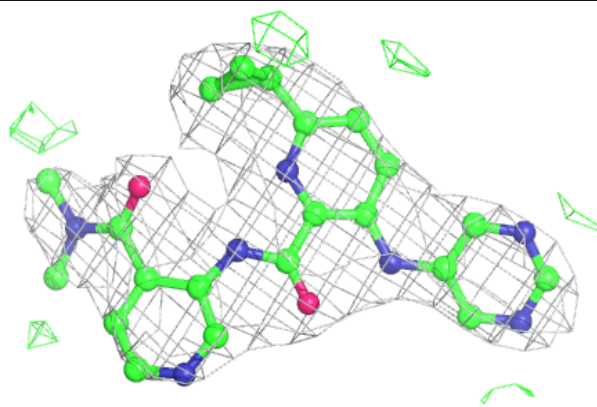
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

**Electron density around K5R D 803:**

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

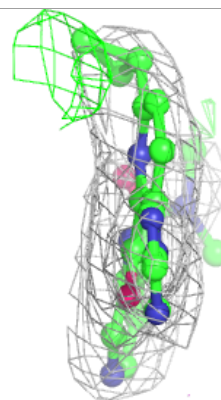
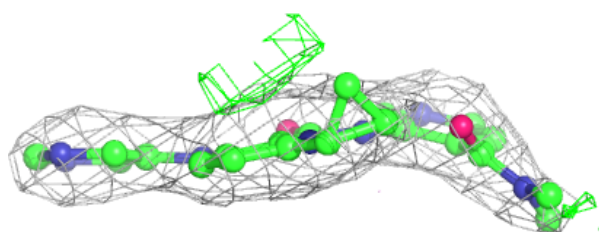
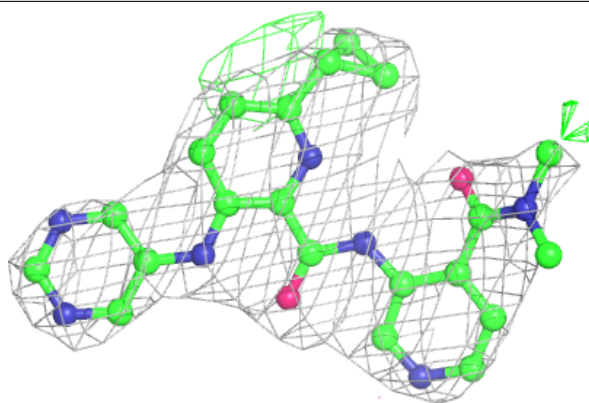
**Electron density around K5R B 804:**

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

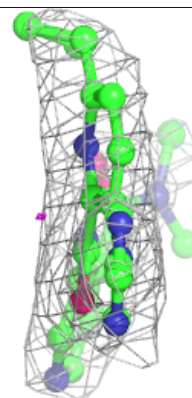
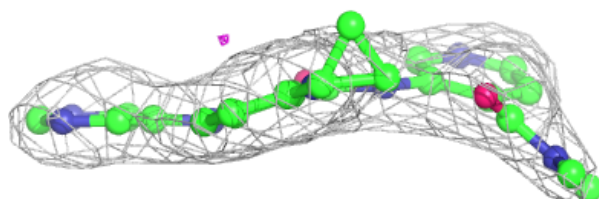
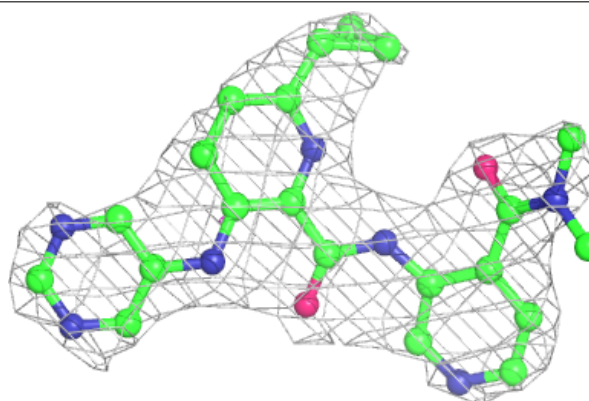


**Electron density around K5R C 803:**

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

**Electron density around K5R A 804:**

$2mF_o-DF_c$  (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.