



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 12, 2026 – 09:09 PM UTC

PDB ID : 8GMN / pdb_00008gmn
Title : Crystal structure of human C1s in complex with inhibitor
Authors : Dougan, D.R.; Lane, W.
Deposited on : 2023-03-26
Resolution : 2.60 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

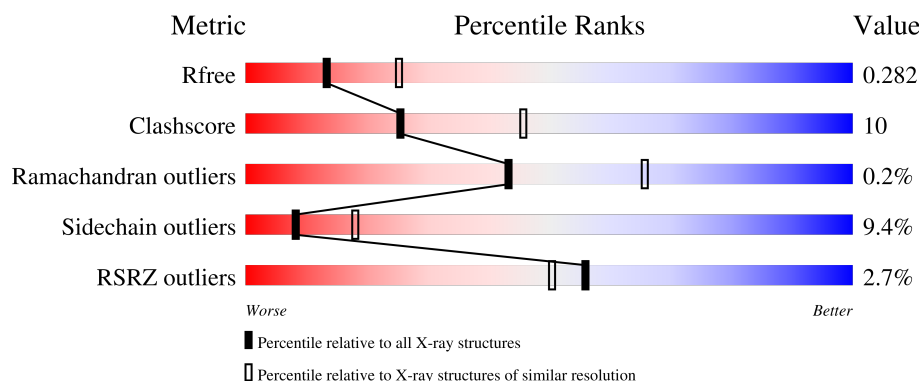
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	4008 (2.60-2.60)
Clashscore	190562	4347 (2.60-2.60)
Ramachandran outliers	187476	4277 (2.60-2.60)
Sidechain outliers	187428	4277 (2.60-2.60)
RSRZ outliers	180081	4008 (2.60-2.60)

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	371	2% 54% 18% • 26%
1	B	371	2% 57% 13% •• 26%
1	C	371	2% 48% 22% • 29%
1	D	371	2% 53% 15% • 29%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8721 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 Complement C1s subcomponent.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	3	0
			2144	1367	362	397	18			
1	B	273	Total	C	N	O	S	0	2	0
			2125	1353	358	396	18			
1	C	264	Total	C	N	O	S	0	1	0
			2051	1307	344	385	15			
1	D	264	Total	C	N	O	S	0	2	0
			2048	1308	342	380	18			

There are 164 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	318	MET	-	initiating methionine	UNP P09871
A	319	LEU	-	expression tag	UNP P09871
A	320	LEU	-	expression tag	UNP P09871
A	321	VAL	-	expression tag	UNP P09871
A	322	ASN	-	expression tag	UNP P09871
A	323	GLN	-	expression tag	UNP P09871
A	324	SER	-	expression tag	UNP P09871
A	325	HIS	-	expression tag	UNP P09871
A	326	GLN	-	expression tag	UNP P09871
A	327	GLY	-	expression tag	UNP P09871
A	328	PHE	-	expression tag	UNP P09871
A	329	ASN	-	expression tag	UNP P09871
A	330	LYS	-	expression tag	UNP P09871
A	331	GLU	-	expression tag	UNP P09871
A	332	HIS	-	expression tag	UNP P09871
A	333	THR	-	expression tag	UNP P09871
A	334	SER	-	expression tag	UNP P09871
A	335	LYS	-	expression tag	UNP P09871
A	336	MET	-	expression tag	UNP P09871
A	337	VAL	-	expression tag	UNP P09871
A	338	SER	-	expression tag	UNP P09871

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Chain	Residue	Modelled	Actual	Comment	Reference
A	339	ALA	-	expression tag	UNP P09871
A	340	ILE	-	expression tag	UNP P09871
A	341	VAL	-	expression tag	UNP P09871
A	342	LEU	-	expression tag	UNP P09871
A	343	TYR	-	expression tag	UNP P09871
A	344	VAL	-	expression tag	UNP P09871
A	345	LEU	-	expression tag	UNP P09871
A	346	LEU	-	expression tag	UNP P09871
A	347	ALA	-	expression tag	UNP P09871
A	348	ALA	-	expression tag	UNP P09871
A	349	ALA	-	expression tag	UNP P09871
A	350	ALA	-	expression tag	UNP P09871
A	351	HIS	-	expression tag	UNP P09871
A	352	SER	-	expression tag	UNP P09871
A	353	ALA	-	expression tag	UNP P09871
A	354	PHE	-	expression tag	UNP P09871
A	355	ALA	-	expression tag	UNP P09871
A	356	ASP	-	expression tag	UNP P09871
A	357	LEU	-	expression tag	UNP P09871
A	518	ALA	GLU	conflict	UNP P09871
B	318	MET	-	initiating methionine	UNP P09871
B	319	LEU	-	expression tag	UNP P09871
B	320	LEU	-	expression tag	UNP P09871
B	321	VAL	-	expression tag	UNP P09871
B	322	ASN	-	expression tag	UNP P09871
B	323	GLN	-	expression tag	UNP P09871
B	324	SER	-	expression tag	UNP P09871
B	325	HIS	-	expression tag	UNP P09871
B	326	GLN	-	expression tag	UNP P09871
B	327	GLY	-	expression tag	UNP P09871
B	328	PHE	-	expression tag	UNP P09871
B	329	ASN	-	expression tag	UNP P09871
B	330	LYS	-	expression tag	UNP P09871
B	331	GLU	-	expression tag	UNP P09871
B	332	HIS	-	expression tag	UNP P09871
B	333	THR	-	expression tag	UNP P09871
B	334	SER	-	expression tag	UNP P09871
B	335	LYS	-	expression tag	UNP P09871
B	336	MET	-	expression tag	UNP P09871
B	337	VAL	-	expression tag	UNP P09871
B	338	SER	-	expression tag	UNP P09871
B	339	ALA	-	expression tag	UNP P09871

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Chain	Residue	Modelled	Actual	Comment	Reference
B	340	ILE	-	expression tag	UNP P09871
B	341	VAL	-	expression tag	UNP P09871
B	342	LEU	-	expression tag	UNP P09871
B	343	TYR	-	expression tag	UNP P09871
B	344	VAL	-	expression tag	UNP P09871
B	345	LEU	-	expression tag	UNP P09871
B	346	LEU	-	expression tag	UNP P09871
B	347	ALA	-	expression tag	UNP P09871
B	348	ALA	-	expression tag	UNP P09871
B	349	ALA	-	expression tag	UNP P09871
B	350	ALA	-	expression tag	UNP P09871
B	351	HIS	-	expression tag	UNP P09871
B	352	SER	-	expression tag	UNP P09871
B	353	ALA	-	expression tag	UNP P09871
B	354	PHE	-	expression tag	UNP P09871
B	355	ALA	-	expression tag	UNP P09871
B	356	ASP	-	expression tag	UNP P09871
B	357	LEU	-	expression tag	UNP P09871
B	518	ALA	GLU	conflict	UNP P09871
C	318	MET	-	initiating methionine	UNP P09871
C	319	LEU	-	expression tag	UNP P09871
C	320	LEU	-	expression tag	UNP P09871
C	321	VAL	-	expression tag	UNP P09871
C	322	ASN	-	expression tag	UNP P09871
C	323	GLN	-	expression tag	UNP P09871
C	324	SER	-	expression tag	UNP P09871
C	325	HIS	-	expression tag	UNP P09871
C	326	GLN	-	expression tag	UNP P09871
C	327	GLY	-	expression tag	UNP P09871
C	328	PHE	-	expression tag	UNP P09871
C	329	ASN	-	expression tag	UNP P09871
C	330	LYS	-	expression tag	UNP P09871
C	331	GLU	-	expression tag	UNP P09871
C	332	HIS	-	expression tag	UNP P09871
C	333	THR	-	expression tag	UNP P09871
C	334	SER	-	expression tag	UNP P09871
C	335	LYS	-	expression tag	UNP P09871
C	336	MET	-	expression tag	UNP P09871
C	337	VAL	-	expression tag	UNP P09871
C	338	SER	-	expression tag	UNP P09871
C	339	ALA	-	expression tag	UNP P09871
C	340	ILE	-	expression tag	UNP P09871

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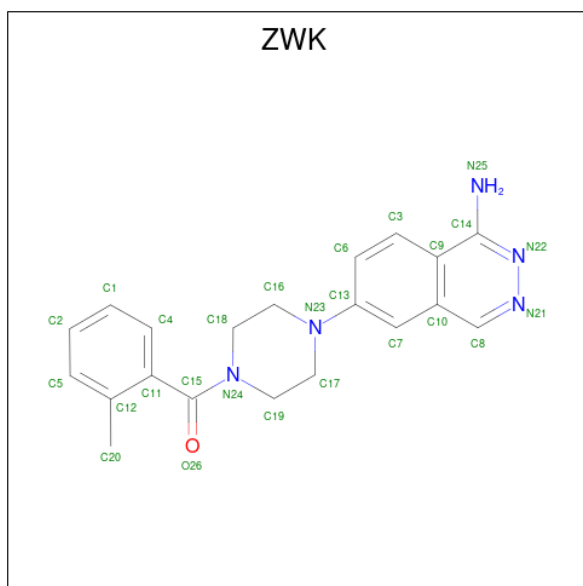
Chain	Residue	Modelled	Actual	Comment	Reference
C	341	VAL	-	expression tag	UNP P09871
C	342	LEU	-	expression tag	UNP P09871
C	343	TYR	-	expression tag	UNP P09871
C	344	VAL	-	expression tag	UNP P09871
C	345	LEU	-	expression tag	UNP P09871
C	346	LEU	-	expression tag	UNP P09871
C	347	ALA	-	expression tag	UNP P09871
C	348	ALA	-	expression tag	UNP P09871
C	349	ALA	-	expression tag	UNP P09871
C	350	ALA	-	expression tag	UNP P09871
C	351	HIS	-	expression tag	UNP P09871
C	352	SER	-	expression tag	UNP P09871
C	353	ALA	-	expression tag	UNP P09871
C	354	PHE	-	expression tag	UNP P09871
C	355	ALA	-	expression tag	UNP P09871
C	356	ASP	-	expression tag	UNP P09871
C	357	LEU	-	expression tag	UNP P09871
C	518	ALA	GLU	conflict	UNP P09871
D	318	MET	-	initiating methionine	UNP P09871
D	319	LEU	-	expression tag	UNP P09871
D	320	LEU	-	expression tag	UNP P09871
D	321	VAL	-	expression tag	UNP P09871
D	322	ASN	-	expression tag	UNP P09871
D	323	GLN	-	expression tag	UNP P09871
D	324	SER	-	expression tag	UNP P09871
D	325	HIS	-	expression tag	UNP P09871
D	326	GLN	-	expression tag	UNP P09871
D	327	GLY	-	expression tag	UNP P09871
D	328	PHE	-	expression tag	UNP P09871
D	329	ASN	-	expression tag	UNP P09871
D	330	LYS	-	expression tag	UNP P09871
D	331	GLU	-	expression tag	UNP P09871
D	332	HIS	-	expression tag	UNP P09871
D	333	THR	-	expression tag	UNP P09871
D	334	SER	-	expression tag	UNP P09871
D	335	LYS	-	expression tag	UNP P09871
D	336	MET	-	expression tag	UNP P09871
D	337	VAL	-	expression tag	UNP P09871
D	338	SER	-	expression tag	UNP P09871
D	339	ALA	-	expression tag	UNP P09871
D	340	ILE	-	expression tag	UNP P09871
D	341	VAL	-	expression tag	UNP P09871

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Chain	Residue	Modelled	Actual	Comment	Reference
D	342	LEU	-	expression tag	UNP P09871
D	343	TYR	-	expression tag	UNP P09871
D	344	VAL	-	expression tag	UNP P09871
D	345	LEU	-	expression tag	UNP P09871
D	346	LEU	-	expression tag	UNP P09871
D	347	ALA	-	expression tag	UNP P09871
D	348	ALA	-	expression tag	UNP P09871
D	349	ALA	-	expression tag	UNP P09871
D	350	ALA	-	expression tag	UNP P09871
D	351	HIS	-	expression tag	UNP P09871
D	352	SER	-	expression tag	UNP P09871
D	353	ALA	-	expression tag	UNP P09871
D	354	PHE	-	expression tag	UNP P09871
D	355	ALA	-	expression tag	UNP P09871
D	356	ASP	-	expression tag	UNP P09871
D	357	LEU	-	expression tag	UNP P09871
D	518	ALA	GLU	conflict	UNP P09871

- Molecule 2 is [4-(1-aminophthalazin-6-yl)piperazin-1-yl](2-methylphenyl)methanone (CCD ID: ZWK) (formula: C₂₀H₂₁N₅O) (labeled as "Ligand of Interest" by depositor).



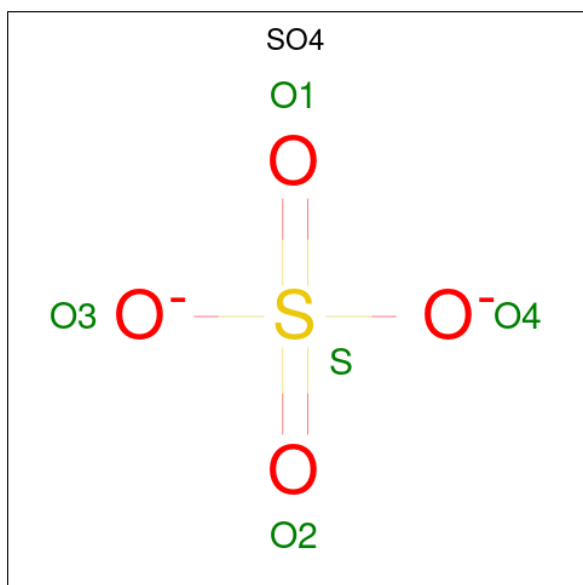
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			26	20	5	1		
2	B	1	Total	C	N	O	0	0
			26	20	5	1		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			26	20	5	1		
2	D	1	Total	C	N	O	0	0
			26	20	5	1		

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	O	S	0	0
			5	4	1		
3	C	1	Total	O	S	0	0
			5	4	1		

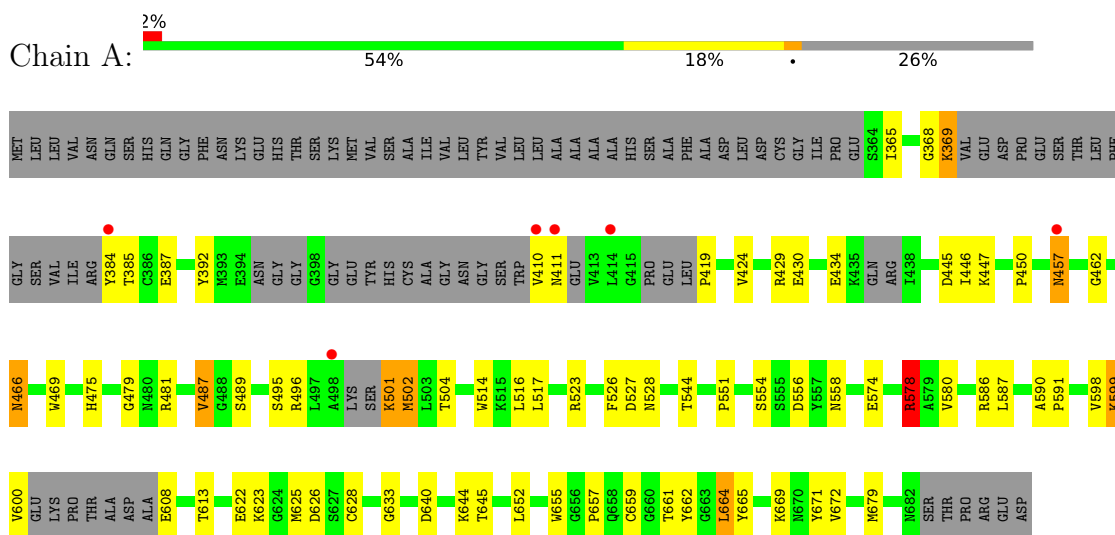
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	83	Total	O	0	0
			83	83		
4	B	81	Total	O	0	0
			81	81		
4	C	42	Total	O	0	0
			42	42		
4	D	33	Total	O	0	0
			33	33		

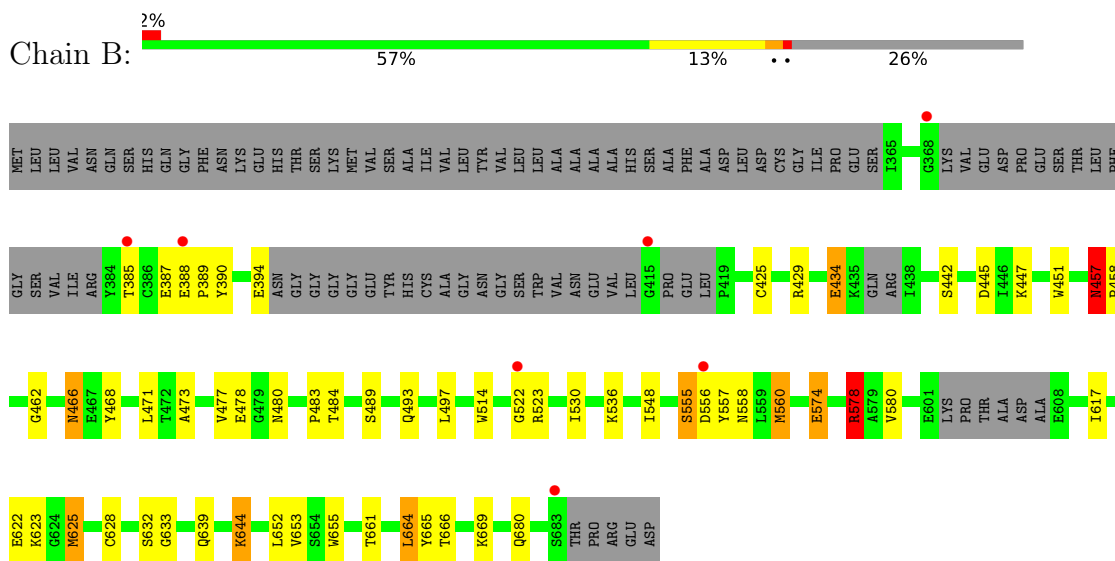
3 Residue-property plots

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: Complement C1s subcomponent

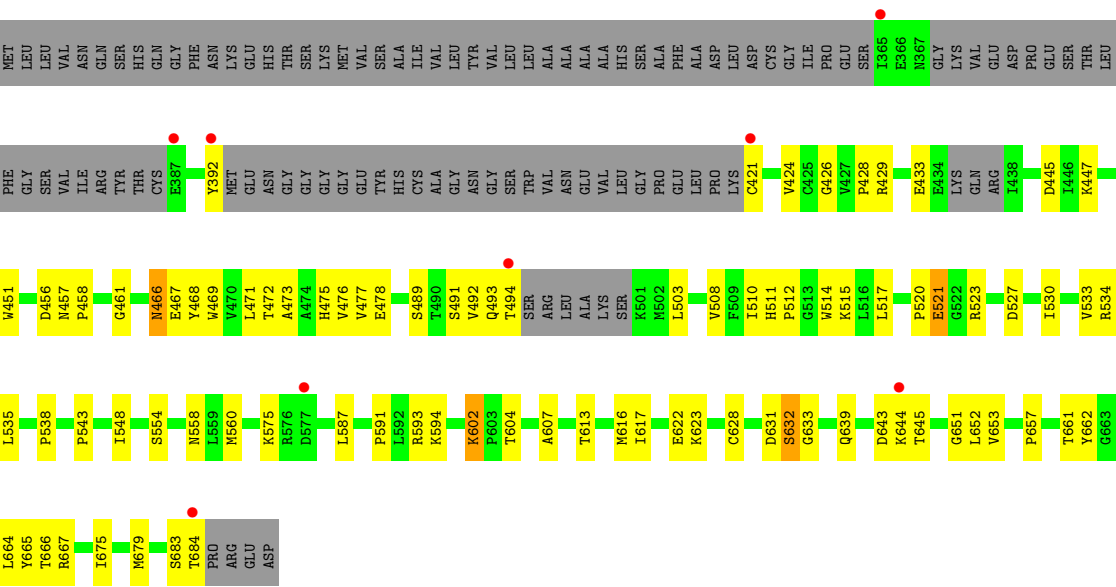


• Molecule 1: Complement C1s subcomponent

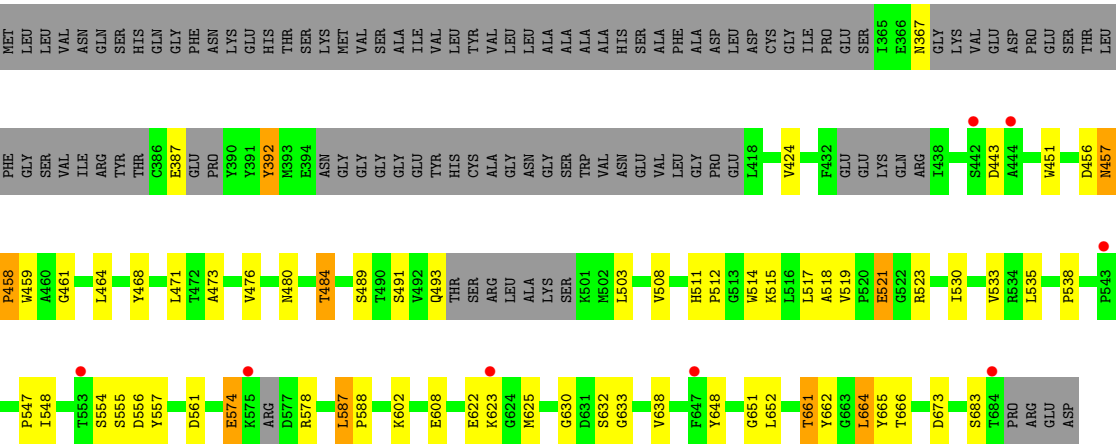


• Molecule 1: Complement C1s subcomponent





● Molecule 1: Complement C1s subcomponent



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	50.47Å 77.65Å 108.48Å 86.13° 79.09° 71.08°	Depositor
Resolution (Å)	35.00 – 2.60 35.00 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.1 (35.00-2.60) 94.1 (35.00-2.60)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.34 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.8.0257	Depositor
R, R_{free}	0.224 , 0.281 0.225 , 0.282	Depositor DCC
R_{free} test set	2196 reflections (4.67%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 41.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.069 for h,h-k,h-l 0.001 for -h,-h+k,-l 0.001 for -h,-k,-h+l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	8721	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.94% 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: SO4, ZWK

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	0.60	1/2197 (0.0%)	1.15	4/2970 (0.1%)
1	B	0.59	0/2181	1.18	6/2952 (0.2%)
1	C	0.55	0/2103	1.06	0/2855
1	D	0.54	0/2102	1.04	2/2849 (0.1%)
All	All	0.57	1/8583 (0.0%)	1.11	12/11626 (0.1%)

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
1	A	0	1
1	B	0	3
1	C	0	1
1	D	0	1
All	All	0	6

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	475	HIS	CE1-NE2	5.13	1.37	1.32

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	662	TYR	CA-C-N	-6.62	116.58	122.47
1	A	662	TYR	C-N-CA	-6.62	116.58	122.47
1	B	574	GLU	N-CA-C	-6.42	105.45	113.28
1	A	504	THR	CB-CA-C	6.28	118.43	109.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	493	GLN	CA-C-N	6.01	128.33	120.28
1	B	493	GLN	C-N-CA	6.01	128.33	120.28
1	A	578	ARG	CG-CD-NE	5.53	124.16	112.00
1	B	434	GLU	CB-CG-CD	5.33	121.66	112.60
1	D	602	LYS	CB-CA-C	5.16	118.18	109.67
1	B	580	VAL	N-CA-C	-5.14	107.39	111.81
1	D	673	ASP	CA-CB-CG	5.04	117.64	112.60
1	B	578	ARG	CG-CD-NE	5.02	123.04	112.00

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	457	ASN	Peptide
1	B	425[A]	CYS	Peptide
1	B	457	ASN	Peptide
1	B	522	GLY	Peptide
1	C	457	ASN	Peptide
1	D	457	ASN	Peptide

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	2144	0	2088	51	0
1	B	2125	0	2065	33	0
1	C	2051	0	1988	43	0
1	D	2048	0	1991	39	0
2	A	26	0	0	3	0
2	B	26	0	0	0	0
2	C	26	0	0	1	0
2	D	26	0	0	0	0
3	B	5	0	0	0	0
3	C	5	0	0	0	0
4	A	83	0	0	7	0
4	B	81	0	0	4	0
4	C	42	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	33	0	0	0	0
All	All	8721	0	8132	159	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

All (159) 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:516:LEU:HD13	1:D:521:GLU:HG3	1.23	1.19
1:A:655:TRP:CZ2	1:A:664:LEU:HD12	2.00	0.96
1:A:516:LEU:HD13	1:D:521:GLU:CG	1.96	0.95
1:A:655:TRP:CE2	1:A:664:LEU:HD12	2.02	0.94
1:A:516:LEU:CD1	1:D:521:GLU:HG3	2.01	0.89
1:D:574:GLU:H	1:D:574:GLU:CD	1.82	0.88
1:B:480:ASN:HB3	4:B:838:HOH:O	1.76	0.83
1:A:446:ILE:HG23	4:A:829:HOH:O	1.80	0.81
1:A:430:GLU:OE1	1:A:447:LYS:HD3	1.81	0.80
1:C:468:TYR:OH	1:C:538:PRO:HG3	1.86	0.75
1:D:508:VAL:HG22	1:D:533:VAL:HG22	1.72	0.70
1:C:445:ASP:OD1	1:C:447:LYS:HE2	1.91	0.70
1:A:544:THR:HA	4:A:829:HOH:O	1.91	0.69
1:A:369:LYS:HG2	1:A:384:TYR:HA	1.74	0.69
1:A:496:ARG:NH2	4:A:802:HOH:O	2.27	0.68
1:B:578:ARG:HH11	1:B:578:ARG:CG	2.06	0.68
1:A:655:TRP:NE1	1:A:664:LEU:HD12	2.08	0.68
1:D:468:TYR:OH	1:D:538:PRO:HG3	1.94	0.67
1:C:392:TYR:HD2	1:C:424:VAL:HG22	1.59	0.66
1:C:617:ILE:HG12	1:C:667:ARG:NH1	2.10	0.66
1:B:578:ARG:HH11	1:B:578:ARG:HG2	1.60	0.65
1:C:515:LYS:HE3	1:C:517:LEU:HD21	1.79	0.65
1:A:628:CYS:HB3	4:A:858:HOH:O	1.99	0.62
1:B:639:GLN:NE2	1:B:644:LYS:HG2	2.14	0.62
1:D:392:TYR:HD2	1:D:424:VAL:HG22	1.65	0.61
1:B:462:GLY:HA2	1:B:633:GLY:O	2.01	0.60
1:C:468:TYR:CZ	1:C:538:PRO:HG3	2.36	0.60
1:A:655:TRP:CZ2	1:A:664:LEU:CD1	2.80	0.60
1:A:429:ARG:HH22	1:B:560:MET:HE1	1.65	0.60
1:A:558:ASN:OD1	1:A:669:LYS:HE2	2.01	0.59
1:A:554:SER:OG	1:A:556:ASP:OD1	2.20	0.58
1:D:461:GLY:O	1:D:633:GLY:HA3	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:587:LEU:HD21	1:D:625:MET:O	2.04	0.58
1:D:473:ALA:HB3	1:D:476:VAL:HG23	1.86	0.57
1:A:466:ASN:HD21	1:A:469:TRP:HD1	1.52	0.57
1:A:586:ARG:O	1:A:625:MET:SD	2.63	0.57
1:C:521:GLU:H	1:C:521:GLU:CD	2.13	0.56
1:C:489:SER:OG	1:C:491:SER:O	2.23	0.56
1:D:468:TYR:CZ	1:D:538:PRO:HG3	2.41	0.56
1:A:551:PRO:HG2	1:A:672:VAL:CG2	2.36	0.55
1:C:471:LEU:HD11	1:C:530:ILE:HD11	1.88	0.55
1:B:466:ASN:ND2	1:B:468:TYR:H	2.04	0.55
1:D:459:TRP:O	1:D:630:GLY:HA2	2.06	0.55
1:C:651:GLY:HA2	1:C:666:THR:O	2.06	0.55
1:C:473:ALA:HB3	1:C:476:VAL:HG23	1.88	0.54
1:B:558:ASN:OD1	1:B:669:LYS:HE2	2.07	0.54
1:C:527:ASP:CG	1:C:613:THR:HG21	2.33	0.54
1:C:508:VAL:HG22	1:C:533:VAL:HG22	1.90	0.54
1:D:652:LEU:O	1:D:665:TYR:HA	2.07	0.54
1:C:520:PRO:HD2	1:C:521:GLU:OE2	2.08	0.53
1:C:451:TRP:CE2	1:C:548:ILE:HD12	2.43	0.53
1:D:503:LEU:HB3	1:D:535:LEU:HD22	1.91	0.53
1:D:471:LEU:HD11	1:D:530:ILE:HD11	1.91	0.53
1:C:503:LEU:HB3	1:C:535:LEU:HD22	1.91	0.53
1:B:466:ASN:ND2	1:B:466:ASN:C	2.67	0.52
1:D:514:TRP:CZ2	1:D:523:ARG:CZ	2.94	0.51
1:A:599:LYS:N	4:A:803:HOH:O	2.42	0.51
1:C:616:MET:HB3	1:C:664:LEU:HD12	1.92	0.51
1:C:466:ASN:ND2	1:C:468:TYR:H	2.08	0.50
1:C:643:ASP:OD1	1:C:645:THR:HG22	2.11	0.50
1:A:590:ALA:HB1	1:A:591:PRO:HD2	1.93	0.50
1:A:527:ASP:CG	1:A:613:THR:HG21	2.37	0.49
1:D:587:LEU:HD22	1:D:588:PRO:HD2	1.95	0.49
1:A:514:TRP:CZ2	1:A:523:ARG:CZ	2.95	0.49
1:B:652:LEU:HB2	1:B:666:THR:HB	1.94	0.49
1:B:655:TRP:CE2	1:B:664:LEU:HD23	2.48	0.49
1:D:456:ASP:HB3	1:D:484:THR:OG1	2.12	0.49
1:B:639:GLN:HE22	1:B:644:LYS:HG2	1.78	0.48
1:B:655:TRP:CZ2	1:B:664:LEU:HD23	2.49	0.48
1:A:640:ASP:OD1	1:A:640:ASP:C	2.56	0.48
1:D:651:GLY:HA2	1:D:666:THR:O	2.13	0.48
1:B:471:LEU:HD11	1:B:530:ILE:HD11	1.94	0.48
1:B:625:MET:HE3	1:B:625:MET:HB2	1.61	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:659:CYS:HA	2:A:700:ZWK:N21	2.28	0.47
1:C:602:LYS:HG2	1:C:607:ALA:HB3	1.96	0.47
1:A:481:ARG:NH2	1:D:521:GLU:OE1	2.48	0.47
1:B:458:PRO:HD2	4:B:807:HOH:O	2.14	0.47
1:D:574:GLU:CD	1:D:574:GLU:N	2.60	0.47
1:C:653:VAL:HG22	1:C:665:TYR:HE2	1.78	0.47
1:A:369:LYS:N	1:A:385:THR:O	2.48	0.47
1:C:468:TYR:HH	1:C:538:PRO:HG3	1.77	0.46
1:A:578:ARG:CG	1:A:578:ARG:HH11	2.28	0.46
1:C:461:GLY:O	1:C:633:GLY:HA3	2.15	0.46
1:D:521:GLU:H	1:D:521:GLU:CD	2.24	0.46
1:D:451:TRP:CE2	1:D:548:ILE:HD12	2.50	0.46
1:B:617:ILE:HB	1:B:665:TYR:HB2	1.97	0.46
1:A:652:LEU:O	1:A:665:TYR:HA	2.15	0.46
1:C:632:SER:HA	1:C:653:VAL:HB	1.98	0.46
1:C:591:PRO:HG2	1:C:594:LYS:HE2	1.98	0.46
1:A:502:MET:HE2	1:A:502:MET:HB3	1.81	0.45
1:C:472:THR:OG1	1:C:473:ALA:N	2.49	0.45
1:B:652:LEU:O	1:B:665:TYR:HA	2.15	0.45
1:C:392:TYR:CD1	1:C:392:TYR:C	2.95	0.45
1:C:493:GLN:O	1:C:494:THR:C	2.60	0.45
1:A:644:LYS:HG3	1:A:645:THR:HG23	1.99	0.45
1:B:389:PRO:HG2	1:B:429:ARG:NH1	2.31	0.45
1:A:487:VAL:HG12	4:A:818:HOH:O	2.15	0.45
1:B:628:CYS:HB3	4:B:849:HOH:O	2.17	0.45
1:C:652:LEU:O	1:C:665:TYR:HA	2.16	0.44
1:C:675:ILE:O	1:C:679:MET:HG3	2.17	0.44
1:D:367:ASN:C	1:D:387:GLU:HG3	2.42	0.44
1:D:511:HIS:HA	1:D:512:PRO:HD3	1.86	0.44
1:B:457:ASN:HD22	1:B:457:ASN:HA	1.54	0.44
1:C:558:ASN:HA	4:C:837:HOH:O	2.17	0.44
1:A:625:MET:HB2	1:A:625:MET:HE3	1.58	0.44
1:B:451:TRP:CE2	1:B:548:ILE:HD12	2.53	0.44
1:C:477:VAL:O	1:C:478:GLU:C	2.60	0.44
1:C:604:THR:HG22	1:C:607:ALA:HB2	2.00	0.44
1:C:657:PRO:HD2	1:C:662:TYR:O	2.18	0.43
1:D:392:TYR:CD1	1:D:392:TYR:C	2.95	0.43
1:D:515:LYS:HE3	1:D:517:LEU:HD21	2.00	0.43
1:A:469:TRP:CE2	1:A:679:MET:HG2	2.53	0.43
1:A:600:VAL:HG11	1:A:657:PRO:O	2.17	0.43
1:B:477:VAL:O	1:B:478:GLU:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:523:ARG:HD2	1:A:526:PHE:CZ	2.54	0.43
1:A:365:ILE:HG21	1:A:419:PRO:O	2.19	0.43
1:A:392:TYR:HD2	1:A:424:VAL:HG22	1.83	0.43
1:A:445:ASP:O	1:A:446:ILE:C	2.62	0.43
1:D:464:LEU:O	1:D:547:PRO:HA	2.18	0.43
1:D:555:SER:C	1:D:557:TYR:H	2.27	0.43
1:B:457:ASN:N	4:B:807:HOH:O	2.52	0.43
1:C:469:TRP:CH2	1:C:534:ARG:HB2	2.53	0.43
1:C:466:ASN:HD21	1:C:469:TRP:HD1	1.65	0.42
1:B:473:ALA:H	1:B:633:GLY:HA2	1.83	0.42
1:C:514:TRP:CZ2	1:C:523:ARG:CZ	3.03	0.42
1:C:429:ARG:HG3	1:C:543:PRO:HA	2.02	0.42
1:B:514:TRP:CZ2	1:B:523:ARG:CZ	3.02	0.42
1:C:511:HIS:HA	1:C:512:PRO:HD3	1.91	0.42
1:B:632:SER:HA	1:B:653:VAL:HB	2.02	0.42
1:A:466:ASN:ND2	1:A:469:TRP:HD1	2.17	0.42
1:A:528:ASN:HA	1:A:671:TYR:OH	2.19	0.42
1:A:655:TRP:HA	2:A:700:ZWK:C6	2.49	0.42
1:C:426:GLY:O	1:C:428:PRO:HD3	2.19	0.42
1:A:517:LEU:O	1:D:519:VAL:HG21	2.20	0.42
1:D:661:THR:HB	1:D:662:TYR:H	1.75	0.42
1:D:457:ASN:HB3	1:D:480:ASN:ND2	2.34	0.42
1:A:626:ASP:OD2	2:A:700:ZWK:N22	2.53	0.41
1:A:445:ASP:C	1:A:447:LYS:N	2.77	0.41
1:A:462:GLY:HA2	1:A:633:GLY:O	2.20	0.41
1:B:497:LEU:HD23	1:B:497:LEU:HA	1.97	0.41
1:B:389:PRO:HD2	1:B:390:TYR:CE2	2.56	0.41
1:D:392:TYR:CD2	1:D:424:VAL:HG22	2.52	0.41
1:A:479:GLY:HA2	1:D:518:ALA:O	2.20	0.41
1:B:445:ASP:C	1:B:447:LYS:N	2.77	0.41
1:C:475:HIS:HD2	2:C:702:ZWK:C2	2.34	0.41
1:C:628:CYS:O	1:C:631:ASP:HB2	2.21	0.41
1:A:501:LYS:HD3	1:A:501:LYS:HA	1.87	0.41
1:A:598:VAL:HA	4:A:803:HOH:O	2.19	0.41
1:D:489:SER:OG	1:D:491:SER:O	2.36	0.41
1:B:480:ASN:ND2	1:B:483:PRO:HA	2.36	0.40
1:B:555:SER:C	1:B:557:TYR:H	2.28	0.40
1:D:491:SER:OG	1:D:493:GLN:HG2	2.20	0.40
1:C:467:GLU:O	1:C:538:PRO:HA	2.22	0.40
1:D:664:LEU:HD13	1:D:664:LEU:HA	1.81	0.40
1:A:447:LYS:O	1:A:450:PRO:HD3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:555:SER:C	1:B:557:TYR:N	2.79	0.40
1:D:511:HIS:HB2	1:D:530:ILE:HG23	2.02	0.40
1:D:638:VAL:HG12	1:D:648:TYR:CE1	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	260/371 (70%)	250 (96%)	10 (4%)	0	100	100
1	B	263/371 (71%)	251 (95%)	12 (5%)	0	100	100
1	C	254/371 (68%)	243 (96%)	10 (4%)	1 (0%)	30	51
1	D	250/371 (67%)	234 (94%)	15 (6%)	1 (0%)	30	51
All	All	1027/1484 (69%)	978 (95%)	47 (5%)	2 (0%)	43	66

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	458	PRO
1	D	458	PRO

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	231/307 (75%)	209 (90%)	22 (10%)	8	18
1	B	229/307 (75%)	206 (90%)	23 (10%)	7	16
1	C	220/307 (72%)	199 (90%)	21 (10%)	8	18
1	D	221/307 (72%)	203 (92%)	18 (8%)	11	24
All	All	901/1228 (73%)	817 (91%)	84 (9%)	8	18

All (84) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	369	LYS
1	A	387	GLU
1	A	410	VAL
1	A	411	ASN
1	A	434	GLU
1	A	457	ASN
1	A	466	ASN
1	A	487	VAL
1	A	489	SER
1	A	495	SER
1	A	501	LYS
1	A	502	MET
1	A	574	GLU
1	A	578	ARG
1	A	580	VAL
1	A	587	LEU
1	A	599	LYS
1	A	608	GLU
1	A	622	GLU
1	A	623	LYS
1	A	661	THR
1	A	664	LEU
1	B	385	THR
1	B	387	GLU
1	B	388	GLU
1	B	394	GLU
1	B	434	GLU
1	B	442	SER
1	B	457	ASN
1	B	466	ASN
1	B	484	THR
1	B	489	SER
1	B	536	LYS

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Mol	Chain	Res	Type
1	B	555	SER
1	B	556	ASP
1	B	560	MET
1	B	574	GLU
1	B	578	ARG
1	B	622	GLU
1	B	623	LYS
1	B	625	MET
1	B	644	LYS
1	B	661	THR
1	B	664	LEU
1	B	680	GLN
1	C	421	CYS
1	C	433	GLU
1	C	456	ASP
1	C	466	ASN
1	C	492	VAL
1	C	510	ILE
1	C	521	GLU
1	C	554	SER
1	C	560	MET
1	C	575	LYS
1	C	587	LEU
1	C	593	ARG
1	C	602	LYS
1	C	622	GLU
1	C	623	LYS
1	C	632	SER
1	C	639	GLN
1	C	644	LYS
1	C	661	THR
1	C	683	SER
1	C	684	THR
1	D	392	TYR
1	D	443	ASP
1	D	458	PRO
1	D	484	THR
1	D	521	GLU
1	D	554	SER
1	D	556	ASP
1	D	561	ASP
1	D	574	GLU

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Mol	Chain	Res	Type
1	D	578	ARG
1	D	587	LEU
1	D	608	GLU
1	D	622	GLU
1	D	623	LYS
1	D	632	SER
1	D	661	THR
1	D	664	LEU
1	D	683	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	457	ASN
1	A	466	ASN
1	B	452	GLN
1	B	457	ASN
1	B	466	ASN
1	B	480	ASN
1	B	639	GLN
1	C	466	ASN
1	C	642	ASN
1	D	480	ASN

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 ⓘ

6 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	$\# Z > 2$
2	ZWK	B	702	-	29,29,29	1.58	4 (13%)	38,41,41	1.65	7 (18%)
3	SO4	C	701	-	4,4,4	0.35	0	6,6,6	0.15	0
2	ZWK	C	702	-	29,29,29	1.56	3 (10%)	38,41,41	1.41	8 (21%)
3	SO4	B	701	-	4,4,4	0.33	0	6,6,6	0.16	0
2	ZWK	D	700	-	29,29,29	1.39	3 (10%)	38,41,41	1.32	6 (15%)
2	ZWK	A	700	-	29,29,29	1.64	5 (17%)	38,41,41	1.72	9 (23%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ZWK	B	702	-	-	0/12/22/22	0/4/4/4
2	ZWK	D	700	-	-	4/12/22/22	0/4/4/4
2	ZWK	C	702	-	-	2/12/22/22	0/4/4/4
2	ZWK	A	700	-	-	0/12/22/22	0/4/4/4

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	702	ZWK	C14-C9	-5.85	1.39	1.45
2	B	702	ZWK	C14-C9	-5.33	1.40	1.45
2	A	700	ZWK	C14-C9	-4.76	1.40	1.45
2	D	700	ZWK	C14-C9	-4.56	1.40	1.45
2	A	700	ZWK	C11-C15	-3.13	1.46	1.50
2	A	700	ZWK	C18-N24	3.03	1.52	1.47
2	A	700	ZWK	C8-N21	2.66	1.36	1.31
2	D	700	ZWK	C8-N21	2.51	1.36	1.31
2	A	700	ZWK	C17-N23	2.38	1.50	1.46
2	D	700	ZWK	C11-C15	-2.28	1.47	1.50
2	B	702	ZWK	C17-N23	2.28	1.50	1.46
2	C	702	ZWK	C11-C15	-2.24	1.47	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	702	ZWK	C18-N24	2.23	1.51	1.47
2	B	702	ZWK	C8-N21	2.23	1.35	1.31
2	C	702	ZWK	C8-N21	2.21	1.35	1.31

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	700	ZWK	O26-C15-C11	-4.07	112.07	120.06
2	A	700	ZWK	C4-C11-C12	4.02	124.58	119.86
2	B	702	ZWK	C7-C13-N23	-3.72	117.89	122.11
2	B	702	ZWK	C19-N24-C18	3.60	120.03	112.68
2	A	700	ZWK	C19-N24-C18	3.37	119.55	112.68
2	A	700	ZWK	O26-C15-N24	3.33	127.61	122.35
2	B	702	ZWK	C16-N23-C17	3.33	119.06	111.57
2	C	702	ZWK	O26-C15-N24	3.20	127.41	122.35
2	B	702	ZWK	C10-C8-N21	-3.20	121.26	124.54
2	C	702	ZWK	C19-N24-C18	3.19	119.19	112.68
2	D	700	ZWK	C19-N24-C18	3.17	119.15	112.68
2	B	702	ZWK	C18-C16-N23	2.96	117.01	110.78
2	C	702	ZWK	C16-N23-C17	2.92	118.14	111.57
2	A	700	ZWK	C1-C2-C5	2.89	123.80	120.24
2	A	700	ZWK	C16-N23-C17	2.83	117.93	111.57
2	C	702	ZWK	C19-C17-N23	-2.82	104.84	110.78
2	C	702	ZWK	C18-C16-N23	2.78	116.64	110.78
2	A	700	ZWK	C2-C1-C4	-2.62	117.01	120.24
2	D	700	ZWK	C16-N23-C17	2.52	117.23	111.57
2	A	700	ZWK	C19-N24-C15	-2.41	115.34	122.79
2	D	700	ZWK	O26-C15-N24	2.29	125.96	122.35
2	C	702	ZWK	C10-C8-N21	-2.23	122.25	124.54
2	C	702	ZWK	C4-C11-C12	2.17	122.41	119.86
2	D	700	ZWK	C19-C17-N23	-2.11	106.34	110.78
2	B	702	ZWK	C5-C12-C11	2.09	120.27	117.75
2	D	700	ZWK	C4-C11-C12	2.05	122.27	119.86
2	C	702	ZWK	O26-C15-C11	-2.04	116.06	120.06
2	B	702	ZWK	O26-C15-N24	2.04	125.57	122.35
2	D	700	ZWK	C19-N24-C15	-2.04	116.49	122.79
2	A	700	ZWK	C12-C11-C15	-2.02	117.49	120.42

There are no chirality outliers.

All (6) torsion outliers are listed below:

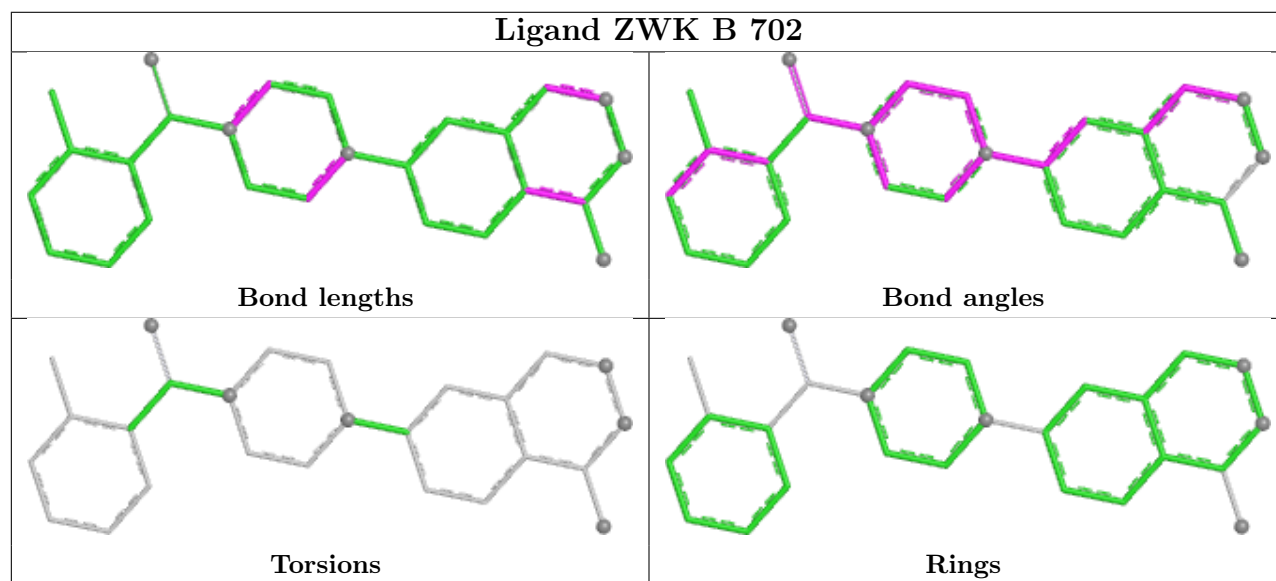
Mol	Chain	Res	Type	Atoms
2	D	700	ZWK	C11-C15-N24-C19
2	D	700	ZWK	O26-C15-N24-C19
2	C	702	ZWK	C11-C15-N24-C19
2	C	702	ZWK	O26-C15-N24-C19
2	D	700	ZWK	O26-C15-N24-C18
2	D	700	ZWK	C11-C15-N24-C18

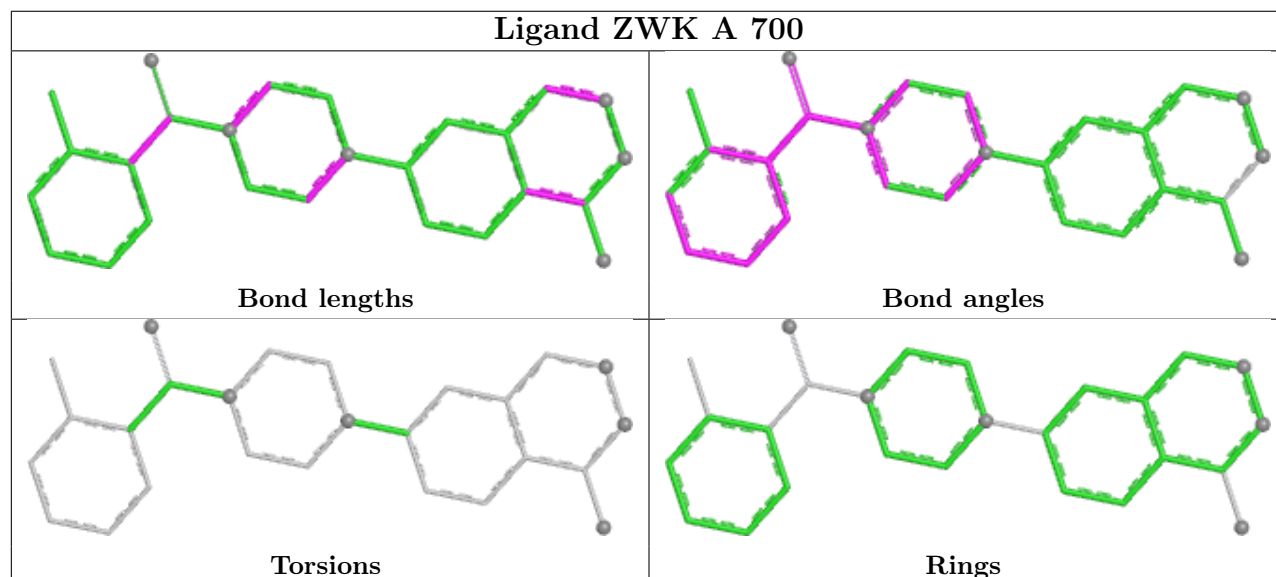
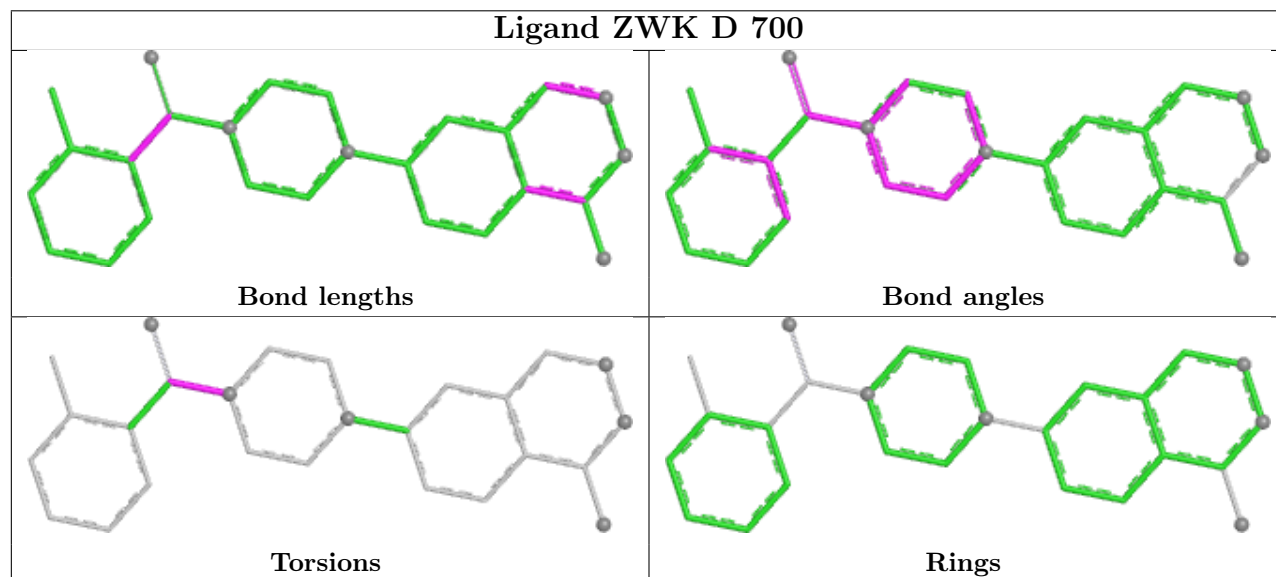
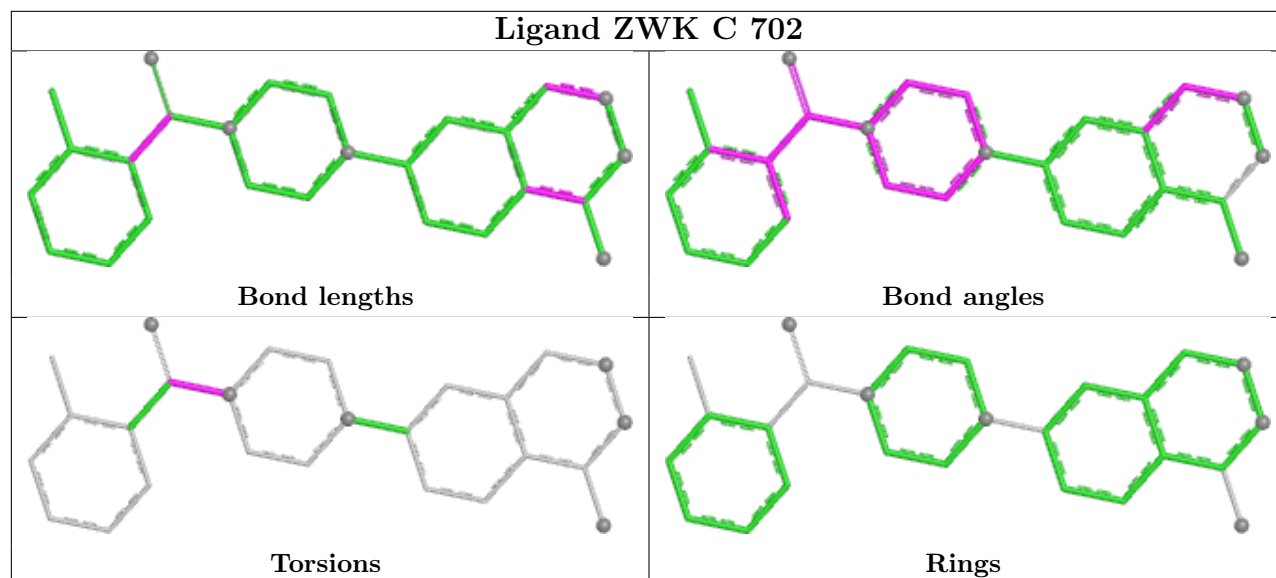
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	702	ZWK	1	0
2	A	700	ZWK	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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	276/371 (74%)	-0.10	6 (2%) 62 57	20, 36, 78, 111	1 (0%)
1	B	273/371 (73%)	-0.14	7 (2%) 57 51	21, 36, 73, 87	1 (0%)
1	C	264/371 (71%)	0.20	8 (3%) 52 47	23, 53, 96, 113	0
1	D	264/371 (71%)	0.40	8 (3%) 52 47	23, 64, 98, 126	1 (0%)
All	All	1077/1484 (72%)	0.09	29 (2%) 56 50	20, 45, 90, 126	3 (0%)

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	410	VAL	4.0
1	D	684	THR	3.4
1	C	494	THR	3.2
1	C	684	THR	3.1
1	B	415	GLY	3.0
1	B	368	GLY	2.8
1	C	392	TYR	2.7
1	B	385	THR	2.7
1	A	414	LEU	2.7
1	D	444	ALA	2.6
1	A	498	ALA	2.5
1	D	647	PHE	2.4
1	C	365	ILE	2.4
1	A	457	ASN	2.4
1	B	683	SER	2.4
1	D	543	PRO	2.4
1	B	388	GLU	2.3
1	C	387	GLU	2.2
1	D	575	LYS	2.2
1	C	421	CYS	2.2
1	A	411	ASN	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	556	ASP	2.2
1	C	577	ASP	2.2
1	A	384	TYR	2.1
1	D	442	SER	2.1
1	D	623	LYS	2.1
1	D	553	THR	2.0
1	C	644	LYS	2.0
1	B	522	GLY	2.0

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](#)

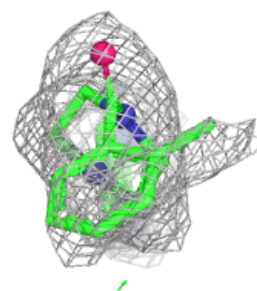
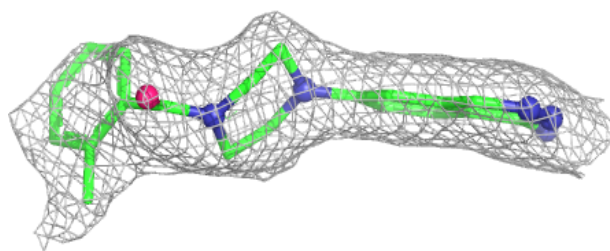
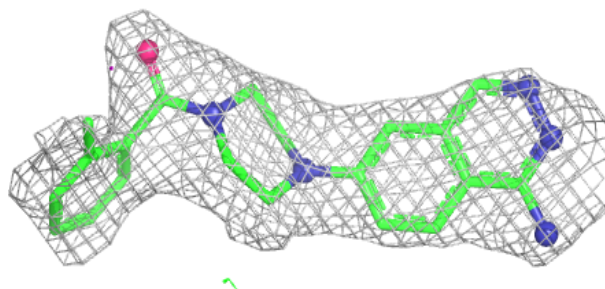
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
3	SO4	B	701	5/5	0.75	0.11	72,76,82,84	0
3	SO4	C	701	5/5	0.81	0.11	87,94,96,97	0
2	ZWK	D	700	26/26	0.91	0.13	53,59,76,76	0
2	ZWK	C	702	26/26	0.92	0.12	44,50,65,68	0
2	ZWK	A	700	26/26	0.94	0.08	27,30,34,38	0
2	ZWK	B	702	26/26	0.95	0.08	26,29,34,37	0

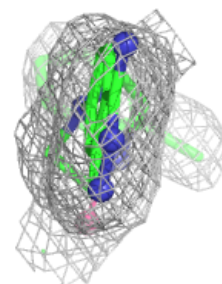
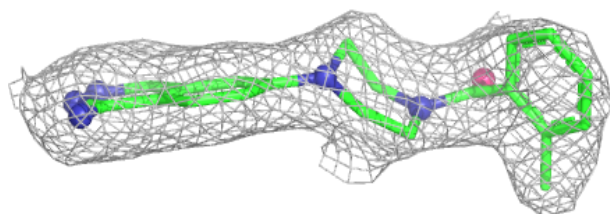
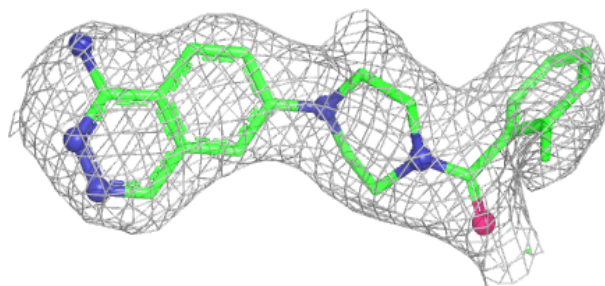
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ZWK D 700:

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

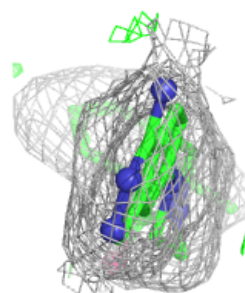
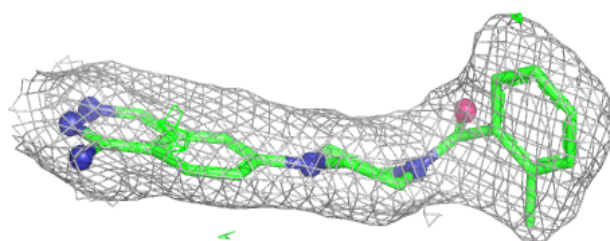
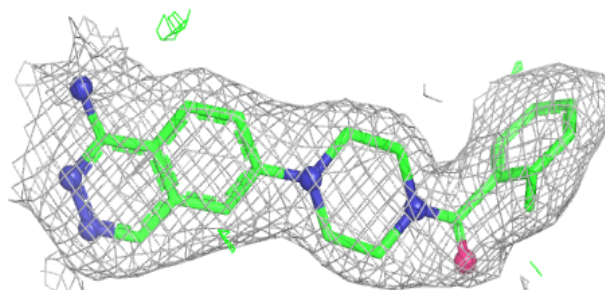
**Electron density around ZWK C 702:**

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

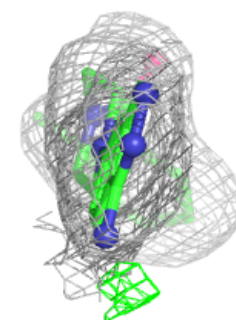
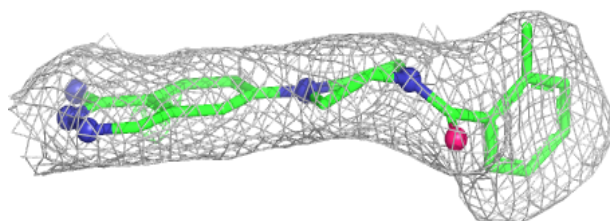
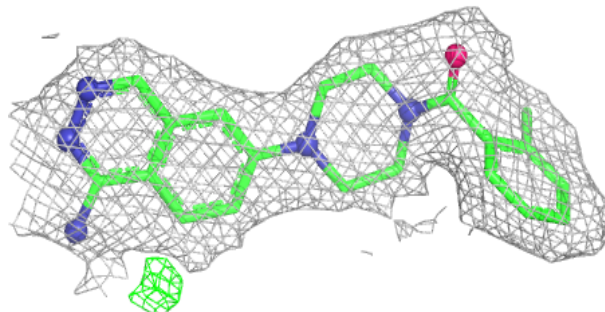


Electron density around ZWK A 700:

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

**Electron density around ZWK B 702:**

$2mF_o-DF_c$ (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.