



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:39 AM UTC

PDB ID : 9EOY / pdb_00009eoy
Title : Structure of Thr354Asn, Glu355Gln, Thr412Asn, Ile414Met, Ile464His, and Phe467Met mutant human CaMKII alpha hub bound to PIPA
Authors : Narayanan, D.; Larsen, A.S.G.; Solbak, S.M.O.; Wellendorph, P.; Gee, C.L.; Kastrup, J.S.
Deposited on : 2024-03-15
Resolution : 2.10 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

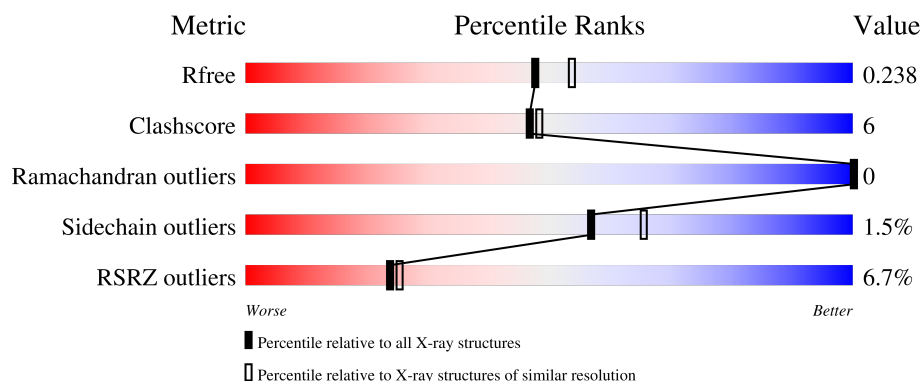
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	135	7% 85% 13% .
1	B	135	4% 83% 13% ..
1	C	135	8% 79% 18% ..
1	D	135	14% 76% 21% ..

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Mol	Chain	Length	Quality of chain
1	E	135	5% 82% 15% ..
1	F	135	4% 84% 13% .
1	G	135	4% 91% ...

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7710 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 Calcium/calmodulin-dependent protein kinase type II subunit alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	132	Total	C	N	O	S	0	1	0
			1077	675	196	198	8			
1	B	133	Total	C	N	O	S	0	2	0
			1096	687	205	196	8			
1	C	132	Total	C	N	O	S	0	0	0
			1071	671	196	196	8			
1	D	132	Total	C	N	O	S	0	0	0
			1071	671	196	196	8			
1	E	133	Total	C	N	O	S	0	1	0
			1083	679	199	196	9			
1	F	132	Total	C	N	O	S	0	0	0
			1071	671	196	196	8			
1	G	130	Total	C	N	O	S	0	1	0
			1062	667	194	192	9			

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	341	GLY	-	expression tag	UNP Q9UQM7
A	342	PRO	-	expression tag	UNP Q9UQM7
A	343	HIS	-	expression tag	UNP Q9UQM7
A	344	MET	-	expression tag	UNP Q9UQM7
A	354	ASN	THR	engineered mutation	UNP Q9UQM7
A	355	GLN	GLU	engineered mutation	UNP Q9UQM7
A	412	ASN	THR	engineered mutation	UNP Q9UQM7
A	414	MET	ILE	engineered mutation	UNP Q9UQM7
A	464	HIS	ILE	engineered mutation	UNP Q9UQM7
A	467	MET	PHE	engineered mutation	UNP Q9UQM7
B	341	GLY	-	expression tag	UNP Q9UQM7
B	342	PRO	-	expression tag	UNP Q9UQM7
B	343	HIS	-	expression tag	UNP Q9UQM7
B	344	MET	-	expression tag	UNP Q9UQM7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	354	ASN	THR	engineered mutation	UNP Q9UQM7
B	355	GLN	GLU	engineered mutation	UNP Q9UQM7
B	412	ASN	THR	engineered mutation	UNP Q9UQM7
B	414	MET	ILE	engineered mutation	UNP Q9UQM7
B	464	HIS	ILE	engineered mutation	UNP Q9UQM7
B	467	MET	PHE	engineered mutation	UNP Q9UQM7
C	341	GLY	-	expression tag	UNP Q9UQM7
C	342	PRO	-	expression tag	UNP Q9UQM7
C	343	HIS	-	expression tag	UNP Q9UQM7
C	344	MET	-	expression tag	UNP Q9UQM7
C	354	ASN	THR	engineered mutation	UNP Q9UQM7
C	355	GLN	GLU	engineered mutation	UNP Q9UQM7
C	412	ASN	THR	engineered mutation	UNP Q9UQM7
C	414	MET	ILE	engineered mutation	UNP Q9UQM7
C	464	HIS	ILE	engineered mutation	UNP Q9UQM7
C	467	MET	PHE	engineered mutation	UNP Q9UQM7
D	341	GLY	-	expression tag	UNP Q9UQM7
D	342	PRO	-	expression tag	UNP Q9UQM7
D	343	HIS	-	expression tag	UNP Q9UQM7
D	344	MET	-	expression tag	UNP Q9UQM7
D	354	ASN	THR	engineered mutation	UNP Q9UQM7
D	355	GLN	GLU	engineered mutation	UNP Q9UQM7
D	412	ASN	THR	engineered mutation	UNP Q9UQM7
D	414	MET	ILE	engineered mutation	UNP Q9UQM7
D	464	HIS	ILE	engineered mutation	UNP Q9UQM7
D	467	MET	PHE	engineered mutation	UNP Q9UQM7
E	341	GLY	-	expression tag	UNP Q9UQM7
E	342	PRO	-	expression tag	UNP Q9UQM7
E	343	HIS	-	expression tag	UNP Q9UQM7
E	344	MET	-	expression tag	UNP Q9UQM7
E	354	ASN	THR	engineered mutation	UNP Q9UQM7
E	355	GLN	GLU	engineered mutation	UNP Q9UQM7
E	412	ASN	THR	engineered mutation	UNP Q9UQM7
E	414	MET	ILE	engineered mutation	UNP Q9UQM7
E	464	HIS	ILE	engineered mutation	UNP Q9UQM7
E	467	MET	PHE	engineered mutation	UNP Q9UQM7
F	341	GLY	-	expression tag	UNP Q9UQM7
F	342	PRO	-	expression tag	UNP Q9UQM7
F	343	HIS	-	expression tag	UNP Q9UQM7
F	344	MET	-	expression tag	UNP Q9UQM7
F	354	ASN	THR	engineered mutation	UNP Q9UQM7
F	355	GLN	GLU	engineered mutation	UNP Q9UQM7

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Chain	Residue	Modelled	Actual	Comment	Reference
F	412	ASN	THR	engineered mutation	UNP Q9UQM7
F	414	MET	ILE	engineered mutation	UNP Q9UQM7
F	464	HIS	ILE	engineered mutation	UNP Q9UQM7
F	467	MET	PHE	engineered mutation	UNP Q9UQM7
G	341	GLY	-	expression tag	UNP Q9UQM7
G	342	PRO	-	expression tag	UNP Q9UQM7
G	343	HIS	-	expression tag	UNP Q9UQM7
G	344	MET	-	expression tag	UNP Q9UQM7
G	354	ASN	THR	engineered mutation	UNP Q9UQM7
G	355	GLN	GLU	engineered mutation	UNP Q9UQM7
G	412	ASN	THR	engineered mutation	UNP Q9UQM7
G	414	MET	ILE	engineered mutation	UNP Q9UQM7
G	464	HIS	ILE	engineered mutation	UNP Q9UQM7
G	467	MET	PHE	engineered mutation	UNP Q9UQM7

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



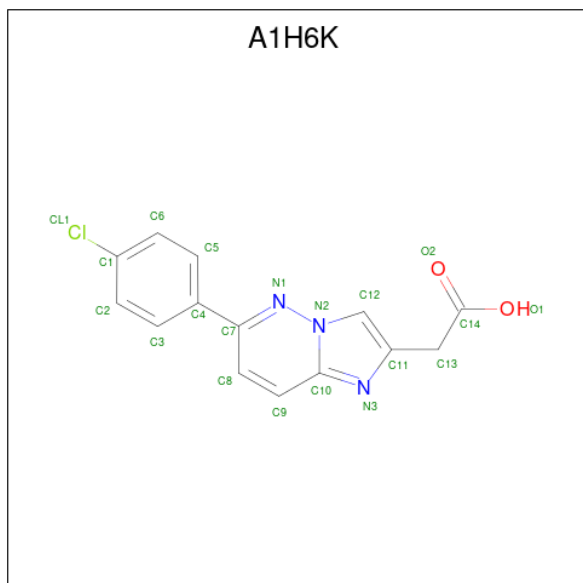
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	B	1	Total	C	O	0	0
			4	2	2		
2	C	1	Total	C	O	0	0
			4	2	2		
2	E	1	Total	C	O	0	0
			4	2	2		

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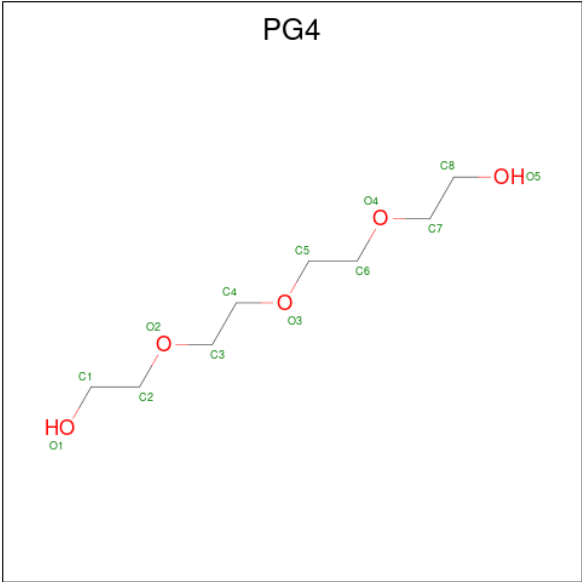
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	C	O	0	0
			4	2	2		
2	G	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is 2-[6-(4-chlorophenyl)imidazo[1,2-b]pyridazin-2-yl]ethanoic acid (CCD ID: A1H6K) (formula: $C_{14}H_{10}ClN_3O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total	C	Cl	N	O	0	0
			20	14	1	3	2		
3	D	1	Total	C	Cl	N	O	0	0
			20	14	1	3	2		

- Molecule 4 is TETRAETHYLENE GLYCOL (CCD ID: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			13	8	5		

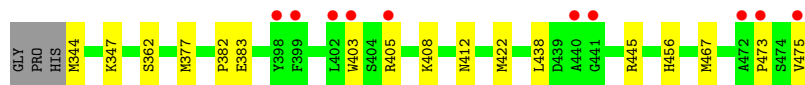
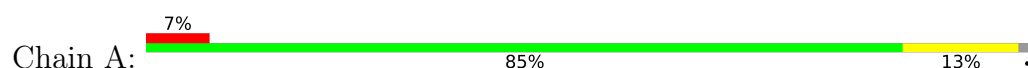
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	14	Total	O	0	0
			14	14		
5	B	13	Total	O	0	0
			13	13		
5	C	8	Total	O	0	0
			8	8		
5	D	11	Total	O	0	0
			11	11		
5	E	17	Total	O	0	0
			17	17		
5	F	17	Total	O	0	0
			17	17		
5	G	22	Total	O	0	0
			22	22		

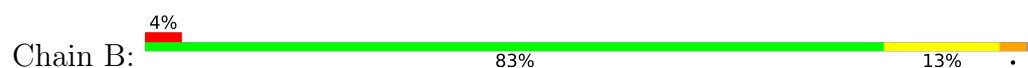
3 Residue-property plots

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.

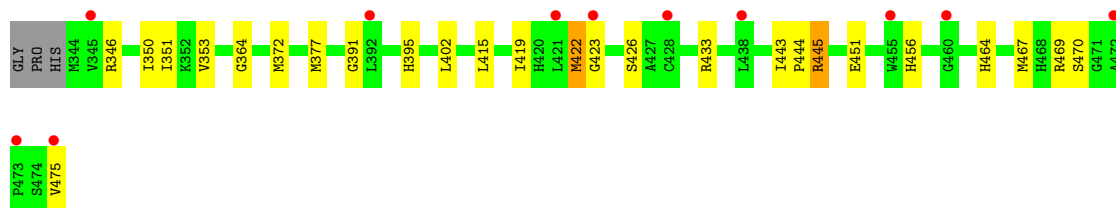
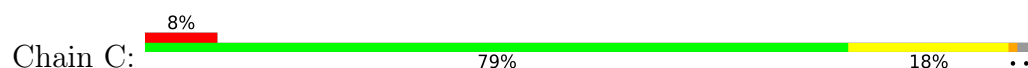
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha



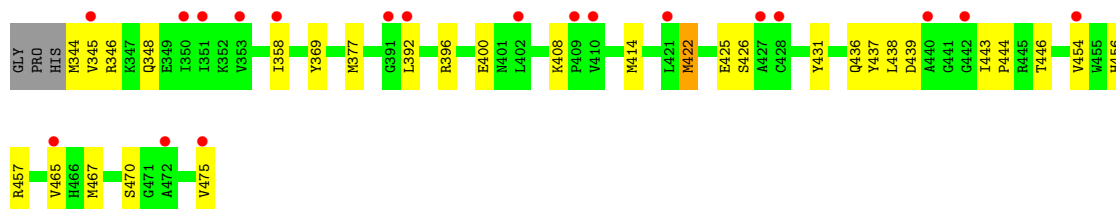
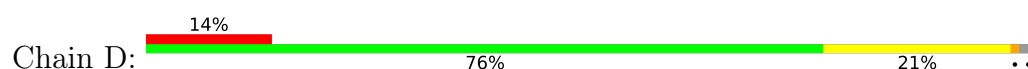
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha



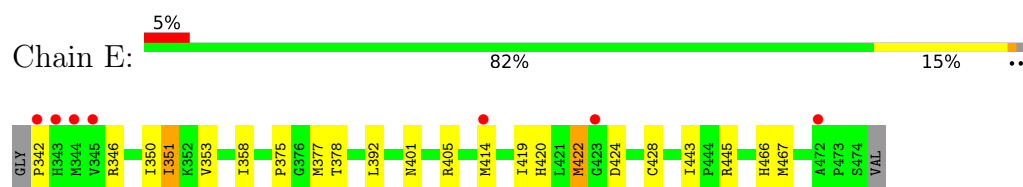
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha



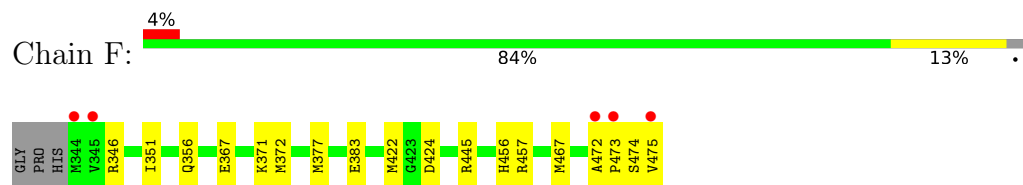
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha



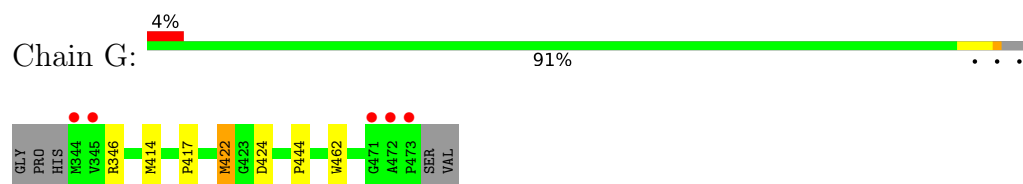
- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha



- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha



- Molecule 1: Calcium/calmodulin-dependent protein kinase type II subunit alpha



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	103.05Å 182.92Å 107.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.48 – 2.10 46.48 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.48-2.10) 100.0 (46.48-2.10)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487)	Depositor
R, R_{free}	0.224 , 0.251 0.225 , 0.238	Depositor DCC
R_{free} test set	2988 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	48.1	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 58.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.005 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.016 for 1/2*h+1/2*k,3/2*h-1/2*k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7710	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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: PG4, ACT, A1H6K

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	0.11	0/1108	0.35	0/1497
1	B	0.18	0/1132	0.39	0/1528
1	C	0.13	0/1099	0.40	0/1484
1	D	0.13	0/1099	0.36	0/1484
1	E	0.10	0/1116	0.33	0/1508
1	F	0.12	0/1099	0.35	0/1484
1	G	0.10	0/1093	0.34	0/1476
All	All	0.13	0/7746	0.36	0/10461

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	1
1	C	0	2
1	F	0	1
All	All	0	5

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	445	ARG	Sidechain
1	B	445	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	C	433	ARG	Sidechain
1	C	445	ARG	Sidechain
1	F	445	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	1077	0	1033	12	0
1	B	1096	0	1059	15	0
1	C	1071	0	1027	19	0
1	D	1071	0	1027	23	0
1	E	1083	0	1038	13	0
1	F	1071	0	1027	9	0
1	G	1062	0	1022	5	0
2	A	4	0	3	0	0
2	B	4	0	3	0	0
2	C	4	0	3	0	0
2	E	4	0	3	0	0
2	F	4	0	3	0	0
2	G	4	0	3	0	0
3	C	20	0	0	0	0
3	D	20	0	0	0	0
4	C	13	0	18	2	0
5	A	14	0	0	0	0
5	B	13	0	0	0	0
5	C	8	0	0	0	0
5	D	11	0	0	0	0
5	E	17	0	0	0	0
5	F	17	0	0	0	0
5	G	22	0	0	0	0
All	All	7710	0	7269	85	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 6.

All (85) 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:405:ARG:HH11	1:A:405:ARG:HG3	1.53	0.73
1:F:346:ARG:HH22	1:F:457:ARG:HH22	1.36	0.71
1:E:342:PRO:HG2	1:E:346:ARG:HH11	1.57	0.69
1:B:402:LEU:HD11	1:D:444:PRO:HD2	1.76	0.68
1:E:422:MET:HG2	1:F:456:HIS:HB2	1.76	0.68
1:C:391:GLY:O	1:C:395:HIS:ND1	2.27	0.67
1:B:391:GLY:O	1:B:395:HIS:ND1	2.28	0.66
1:A:456:HIS:HB2	1:B:422:MET:HG2	1.76	0.66
1:B:397:PHE:HE2	1:D:444:PRO:HB3	1.63	0.62
1:C:456:HIS:HB2	1:D:422:MET:HG2	1.80	0.62
1:A:403:TRP:HZ2	1:A:475:VAL:HG13	1.66	0.61
1:A:422:MET:HG2	1:B:456:HIS:HB2	1.82	0.60
1:A:344:MET:HB2	1:A:347:LYS:HG3	1.85	0.58
1:A:382:PRO:HB2	1:A:473:PRO:HA	1.86	0.57
1:A:408:LYS:HD3	1:A:438:LEU:HB2	1.84	0.57
1:D:436:GLN:HG2	1:D:446:THR:HG22	1.87	0.57
1:B:351:ILE:HG13	1:B:419:ILE:HD11	1.86	0.57
1:F:383:GLU:OE2	1:F:474:SER:HB3	2.05	0.57
1:D:408:LYS:HE3	1:D:438:LEU:H	1.71	0.56
1:B:444:PRO:C	1:B:445:ARG:HD2	2.31	0.55
1:C:346:ARG:NH2	1:C:423:GLY:O	2.38	0.55
1:D:369:TYR:HE1	1:D:392:LEU:HD12	1.71	0.55
1:C:364:GLY:HA3	4:C:503:PG4:H72	1.88	0.54
1:E:351:ILE:HG13	1:E:419:ILE:HD11	1.87	0.54
1:D:396:ARG:NE	1:D:400:GLU:OE1	2.41	0.54
1:A:377:MET:HE1	1:A:467:MET:HG2	1.89	0.54
1:C:422:MET:HG2	1:D:456:HIS:HB2	1.90	0.53
1:A:383:GLU:OE2	1:A:475:VAL:HG12	2.08	0.53
1:C:351:ILE:HG13	1:C:419:ILE:HD11	1.89	0.53
1:E:377:MET:HE1	1:E:467:MET:HG2	1.91	0.52
1:F:424:ASP:O	1:F:457:ARG:NH2	2.42	0.52
1:C:377:MET:HG3	1:C:391:GLY:HA3	1.92	0.52
1:A:362:SER:OG	1:A:412:ASN:ND2	2.43	0.51
1:D:358:ILE:HD12	1:D:414:MET:HE2	1.93	0.50
1:E:443:ILE:HD11	1:E:445:ARG:HH21	1.76	0.50
1:D:344:MET:HG2	1:D:346:ARG:HB3	1.94	0.50
1:C:377:MET:HE1	1:C:467:MET:HG2	1.93	0.49
1:D:377:MET:HE1	1:D:467:MET:HG2	1.94	0.49
1:G:346:ARG:HH11	1:G:462:TRP:HZ2	1.60	0.49
1:C:443:ILE:HD11	1:C:445:ARG:NH2	2.27	0.48
1:E:420:HIS:HB2	1:E:428[B]:CYS:SG	2.54	0.48
1:F:377:MET:HE1	1:F:467:MET:HG2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:422:MET:HE3	1:D:422:MET:HB2	1.75	0.47
1:E:350:ILE:HA	1:E:353:VAL:HG12	1.96	0.47
1:G:346:ARG:HH12	1:G:424:ASP:C	2.22	0.47
1:E:346:ARG:NH2	1:E:424:ASP:OD1	2.49	0.46
1:G:414[A]:MET:HG2	1:G:417:PRO:HG3	1.98	0.46
1:B:375:PRO:HA	1:B:392:LEU:HD12	1.98	0.46
1:D:439:ASP:OD1	1:D:443:ILE:HG12	2.16	0.46
1:B:377:MET:HE1	1:B:467:MET:HG2	1.98	0.45
1:D:437:TYR:CD2	1:D:475:VAL:HG11	2.52	0.45
1:D:437:TYR:O	1:D:444:PRO:HA	2.17	0.45
1:B:373:CYS:HB2	1:B:392:LEU:HD21	1.99	0.45
1:F:475:VAL:HG13	1:G:444:PRO:HG2	1.98	0.45
1:D:425:GLU:HA	1:D:457:ARG:HB2	1.99	0.44
1:E:378:THR:OG1	1:E:466:HIS:ND1	2.45	0.44
1:C:422:MET:HB3	1:D:426:SER:OG	2.18	0.43
1:F:356:GLN:HB2	1:F:372:MET:HE1	2.00	0.43
1:C:470:SER:HB3	1:D:470:SER:HB3	1.99	0.43
1:D:454:VAL:O	1:D:465:VAL:HG12	2.18	0.43
1:D:439:ASP:CG	1:D:443:ILE:HG12	2.43	0.43
1:E:358:ILE:HD12	1:E:414:MET:HE2	2.01	0.43
1:E:443:ILE:CD1	1:E:445:ARG:HH21	2.31	0.43
1:B:349:GLU:HA	1:B:352:LYS:NZ	2.34	0.42
1:C:443:ILE:HA	1:C:444:PRO:HD3	1.86	0.42
1:D:345:VAL:HA	1:D:348:GLN:HB2	2.01	0.42
1:E:401:ASN:HA	1:E:405:ARG:HH22	1.84	0.42
1:A:382:PRO:CB	1:A:473:PRO:HA	2.50	0.42
1:B:377:MET:HE2	1:B:391:GLY:HA3	2.02	0.42
1:D:414:MET:HG3	1:D:431:TYR:CD2	2.55	0.42
1:F:472:ALA:HA	1:F:473:PRO:HD3	1.88	0.42
1:C:350:ILE:HA	1:C:353:VAL:HG12	2.01	0.41
1:E:375:PRO:HA	1:E:392:LEU:HD12	2.02	0.41
1:D:358:ILE:HD11	1:D:431:TYR:OH	2.21	0.41
1:C:402:LEU:HB2	4:C:503:PG4:H51	2.02	0.41
1:F:367:GLU:O	1:F:371:LYS:HG3	2.21	0.41
1:A:422:MET:HG2	1:B:456:HIS:CB	2.50	0.41
1:C:353:VAL:O	1:C:372:MET:HE1	2.21	0.41
1:C:451:GLU:OE2	1:C:469:ARG:HD3	2.21	0.41
1:C:464:HIS:CE1	1:C:467:MET:HB3	2.56	0.41
1:B:344:MET:O	1:B:348:GLN:HG2	2.20	0.41
1:C:415:LEU:HD23	1:C:415:LEU:HA	1.89	0.41
1:C:422:MET:HB2	1:C:426:SER:OG	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:422:MET:HE2	1:G:422:MET:HB2	1.97	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	131/135 (97%)	128 (98%)	3 (2%)	0	100	100
1	B	133/135 (98%)	130 (98%)	3 (2%)	0	100	100
1	C	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
1	D	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
1	E	132/135 (98%)	130 (98%)	2 (2%)	0	100	100
1	F	130/135 (96%)	126 (97%)	4 (3%)	0	100	100
1	G	129/135 (96%)	126 (98%)	3 (2%)	0	100	100
All	All	915/945 (97%)	892 (98%)	23 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	116/117 (99%)	116 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	118/117 (101%)	114 (97%)	4 (3%)	32	35
1	C	115/117 (98%)	113 (98%)	2 (2%)	53	62
1	D	115/117 (98%)	114 (99%)	1 (1%)	70	78
1	E	117/117 (100%)	115 (98%)	2 (2%)	53	62
1	F	115/117 (98%)	113 (98%)	2 (2%)	53	62
1	G	114/117 (97%)	113 (99%)	1 (1%)	70	78
All	All	810/819 (99%)	798 (98%)	12 (2%)	57	65

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	344	MET
1	B	351	ILE
1	B	422	MET
1	B	443	ILE
1	C	422	MET
1	C	475	VAL
1	D	422	MET
1	E	351	ILE
1	E	422	MET
1	F	351	ILE
1	F	422	MET
1	G	422	MET

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	406	ASN
1	A	412	ASN
1	B	356	GLN
1	B	436	GLN
1	C	355	GLN
1	D	411	HIS
1	E	436	GLN
1	G	356	GLN
1	G	395	HIS
1	G	420	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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$
3	A1H6K	C	502	-	22,22,22	1.56	5 (22%)	26,31,31	0.76	0
2	ACT	E	501	-	3,3,3	1.35	0	3,3,3	1.38	0
2	ACT	B	501	-	3,3,3	1.33	0	3,3,3	1.37	0
2	ACT	G	501	-	3,3,3	1.36	0	3,3,3	1.51	0
2	ACT	C	501	-	3,3,3	1.36	0	3,3,3	1.37	0
3	A1H6K	D	501	-	22,22,22	1.52	5 (22%)	26,31,31	1.67	4 (15%)
2	ACT	F	501	-	3,3,3	1.36	0	3,3,3	1.51	0
4	PG4	C	503	-	12,12,12	0.14	0	11,11,11	0.14	0
2	ACT	A	501	-	3,3,3	1.36	0	3,3,3	1.37	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	PG4	C	503	-	-	5/10/10/10	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	A1H6K	C	502	-	-	4/8/8/8	0/3/3/3
3	A1H6K	D	501	-	-	4/8/8/8	0/3/3/3

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	502	A1H6K	C7-N1	3.16	1.36	1.31
3	C	502	A1H6K	C11-N3	-2.95	1.33	1.38
3	D	501	A1H6K	C11-N3	-2.82	1.33	1.38
3	D	501	A1H6K	C7-N1	2.72	1.36	1.31
3	D	501	A1H6K	C9-C8	2.38	1.41	1.35
3	C	502	A1H6K	C8-C7	-2.35	1.40	1.44
3	D	501	A1H6K	C8-C7	-2.22	1.40	1.44
3	D	501	A1H6K	N2-N1	-2.19	1.34	1.38
3	C	502	A1H6K	C9-C8	2.14	1.40	1.35
3	C	502	A1H6K	C12-C11	2.10	1.40	1.36

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	501	A1H6K	C5-C4-C7	-4.32	116.03	120.87
3	D	501	A1H6K	C3-C4-C7	3.69	125.00	120.87
3	D	501	A1H6K	C4-C7-N1	-3.39	110.46	115.33
3	D	501	A1H6K	C4-C7-C8	2.57	126.72	122.39

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	502	A1H6K	N3-C11-C13-C14
3	C	502	A1H6K	C12-C11-C13-C14
3	D	501	A1H6K	N3-C11-C13-C14
3	D	501	A1H6K	C12-C11-C13-C14
4	C	503	PG4	C6-C5-O3-C4
4	C	503	PG4	C1-C2-O2-C3
3	C	502	A1H6K	C11-C13-C14-O1
3	C	502	A1H6K	C11-C13-C14-O2
3	D	501	A1H6K	C11-C13-C14-O1
4	C	503	PG4	O3-C5-C6-O4
4	C	503	PG4	C5-C6-O4-C7
4	C	503	PG4	C4-C3-O2-C2

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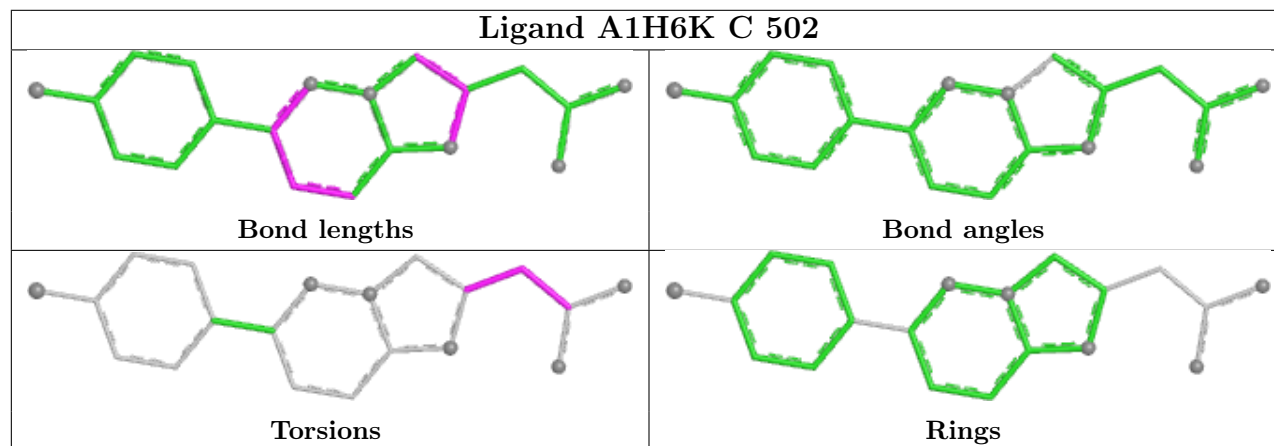
Mol	Chain	Res	Type	Atoms
3	D	501	A1H6K	C11-C13-C14-O2

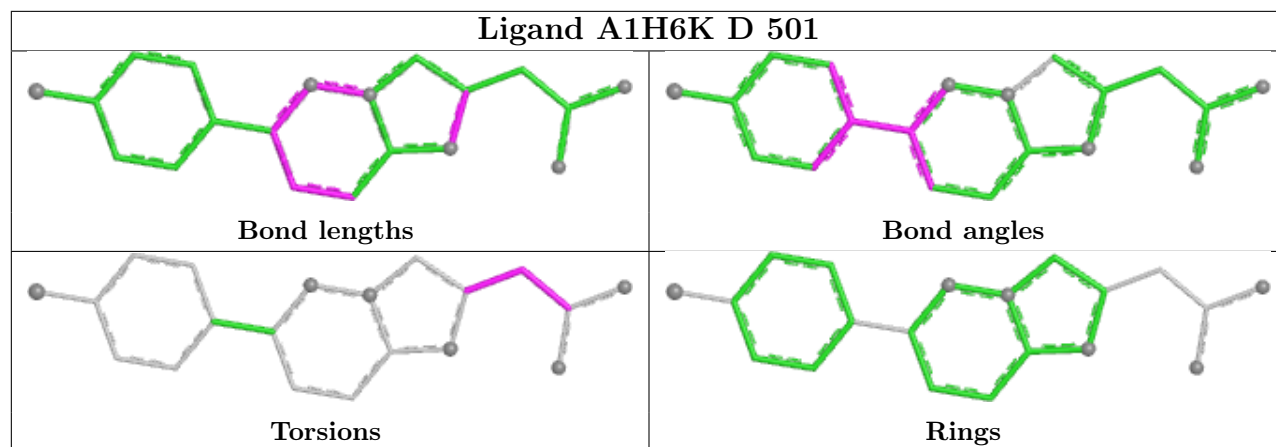
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	C	503	PG4	2	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 [i](#)

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ > 2		OWAB(Å ²)	Q < 0.9
1	A	132/135 (97%)	0.67	10 (7%)	20 21	34, 83, 127, 175	1 (0%)
1	B	133/135 (98%)	0.48	5 (3%)	44 46	49, 83, 132, 165	2 (1%)
1	C	132/135 (97%)	0.87	11 (8%)	17 18	49, 92, 136, 167	0
1	D	132/135 (97%)	1.04	19 (14%)	6 6	51, 99, 146, 162	0
1	E	133/135 (98%)	0.40	7 (5%)	32 34	36, 76, 121, 165	1 (0%)
1	F	132/135 (97%)	0.26	5 (3%)	44 46	37, 66, 117, 135	0
1	G	130/135 (96%)	0.20	5 (3%)	44 46	39, 66, 119, 148	1 (0%)
All	All	924/945 (97%)	0.56	62 (6%)	24 25	34, 81, 134, 175	5 (0%)

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	472	ALA	4.2
1	G	345	VAL	4.2
1	D	465	VAL	4.1
1	A	402	LEU	3.9
1	E	414	MET	3.7
1	A	403	TRP	3.7
1	E	344	MET	3.6
1	D	402	LEU	3.6
1	E	343	HIS	3.3
1	E	472	ALA	3.3
1	A	398	TYR	3.3
1	A	475	VAL	3.2
1	A	399	PHE	3.2
1	A	472	ALA	3.1
1	C	475	VAL	3.1
1	D	353	VAL	3.1
1	E	423	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	475	VAL	2.9
1	G	473	PRO	2.8
1	D	391	GLY	2.7
1	D	440	ALA	2.6
1	D	409	PRO	2.6
1	F	345	VAL	2.6
1	D	358	ILE	2.6
1	G	472	ALA	2.6
1	B	473	PRO	2.6
1	F	473	PRO	2.6
1	C	345	VAL	2.5
1	E	345	VAL	2.5
1	C	455	TRP	2.5
1	C	423	GLY	2.5
1	D	345	VAL	2.4
1	C	421	LEU	2.4
1	E	342	PRO	2.4
1	C	460	GLY	2.3
1	F	344	MET	2.3
1	D	442	GLY	2.3
1	D	350	ILE	2.3
1	C	473	PRO	2.3
1	D	454	VAL	2.3
1	C	438	LEU	2.2
1	G	344	MET	2.2
1	D	392	LEU	2.2
1	C	428	CYS	2.2
1	D	410	VAL	2.1
1	A	440	ALA	2.1
1	B	472	ALA	2.1
1	D	472	ALA	2.1
1	F	472	ALA	2.1
1	D	421	LEU	2.1
1	D	428	CYS	2.1
1	A	473	PRO	2.1
1	B	342	PRO	2.1
1	B	391	GLY	2.1
1	A	405	ARG	2.1
1	G	471	GLY	2.1
1	F	475	VAL	2.1
1	C	392	LEU	2.1
1	D	351	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	427	ALA	2.1
1	A	441	GLY	2.0
1	B	442	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](#)

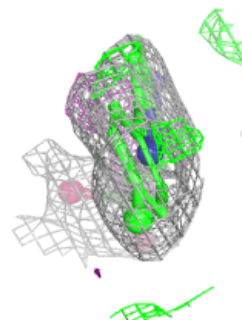
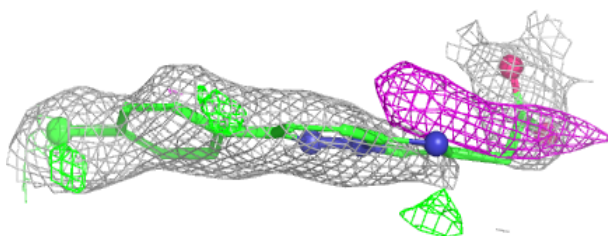
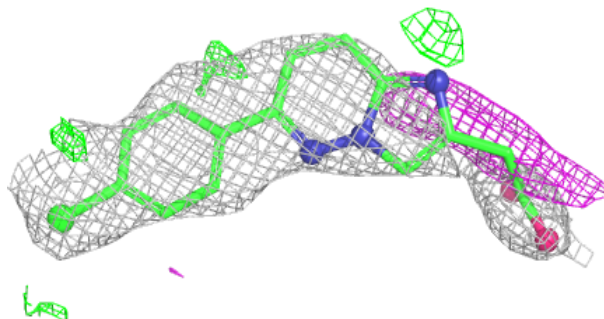
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	ACT	C	501	4/4	0.81	0.14	73,76,77,78	0
3	A1H6K	D	501	20/20	0.81	0.18	51,65,83,86	20
4	PG4	C	503	13/13	0.85	0.14	78,89,103,103	0
3	A1H6K	C	502	20/20	0.87	0.14	79,85,93,103	20
2	ACT	A	501	4/4	0.90	0.11	47,54,55,56	0
2	ACT	B	501	4/4	0.91	0.12	62,67,72,76	0
2	ACT	G	501	4/4	0.92	0.10	49,60,60,65	0
2	ACT	E	501	4/4	0.94	0.08	50,50,54,56	0
2	ACT	F	501	4/4	0.97	0.06	44,46,50,52	0

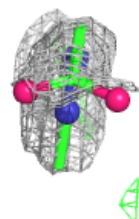
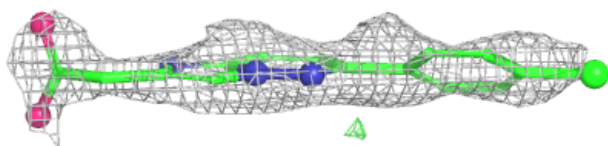
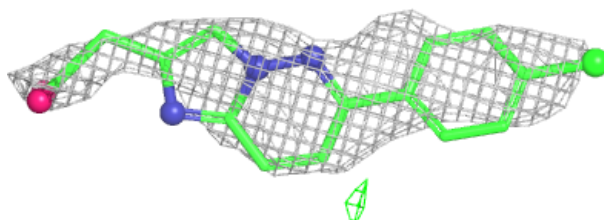
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1H6K D 501:

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

**Electron density around A1H6K C 502:**

$2mF_o-DF_c$ (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.