



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 11:54 PM UTC

PDB ID : 4MNE / pdb_00004mne
Title : Crystal structure of the BRAF:MEK1 complex
Authors : Sudhamsu, J.; Haling, J.R.; Morales, T.; Brandhuber, B.; Hymowitz, S.G.
Deposited on : 2013-09-10
Resolution : 2.85 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

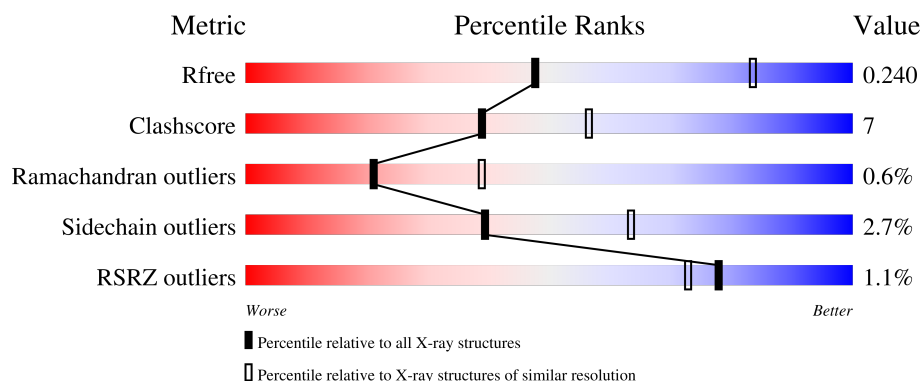
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	341	
1	D	341	
1	E	341	
1	H	341	
2	B	308	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	C	308	% 66% 18% • 16%
2	F	308	% 69% 14% 16%
2	G	308	% 66% 17% • 16%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 17682 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 Dual specificity mitogen-activated protein kinase kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	3	0
			2254	1442	381	414	17			
1	D	285	Total	C	N	O	S	0	0	0
			2226	1424	377	409	16			
1	E	286	Total	C	N	O	S	0	1	0
			2243	1435	378	413	17			
1	H	275	Total	C	N	O	S	0	0	0
			2146	1374	365	392	15			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	61	MET	-	initiating methionine	UNP Q02750
A	394	LEU	-	expression tag	UNP Q02750
A	395	GLU	-	expression tag	UNP Q02750
A	396	HIS	-	expression tag	UNP Q02750
A	397	HIS	-	expression tag	UNP Q02750
A	398	HIS	-	expression tag	UNP Q02750
A	399	HIS	-	expression tag	UNP Q02750
A	400	HIS	-	expression tag	UNP Q02750
A	401	HIS	-	expression tag	UNP Q02750
D	61	MET	-	initiating methionine	UNP Q02750
D	394	LEU	-	expression tag	UNP Q02750
D	395	GLU	-	expression tag	UNP Q02750
D	396	HIS	-	expression tag	UNP Q02750
D	397	HIS	-	expression tag	UNP Q02750
D	398	HIS	-	expression tag	UNP Q02750
D	399	HIS	-	expression tag	UNP Q02750
D	400	HIS	-	expression tag	UNP Q02750
D	401	HIS	-	expression tag	UNP Q02750
E	61	MET	-	initiating methionine	UNP Q02750
E	394	LEU	-	expression tag	UNP Q02750
E	395	GLU	-	expression tag	UNP Q02750

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
E	396	HIS	-	expression tag	UNP Q02750
E	397	HIS	-	expression tag	UNP Q02750
E	398	HIS	-	expression tag	UNP Q02750
E	399	HIS	-	expression tag	UNP Q02750
E	400	HIS	-	expression tag	UNP Q02750
E	401	HIS	-	expression tag	UNP Q02750
H	61	MET	-	initiating methionine	UNP Q02750
H	394	LEU	-	expression tag	UNP Q02750
H	395	GLU	-	expression tag	UNP Q02750
H	396	HIS	-	expression tag	UNP Q02750
H	397	HIS	-	expression tag	UNP Q02750
H	398	HIS	-	expression tag	UNP Q02750
H	399	HIS	-	expression tag	UNP Q02750
H	400	HIS	-	expression tag	UNP Q02750
H	401	HIS	-	expression tag	UNP Q02750

- Molecule 2 is a protein called Serine/threonine-protein kinase B-raf.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	270	Total	C	N	O	S	0	1	0
			2175	1394	383	385	13			
2	C	260	Total	C	N	O	S	0	1	0
			2096	1348	363	372	13			
2	F	258	Total	C	N	O	S	0	1	0
			2075	1332	361	368	14			
2	G	259	Total	C	N	O	S	0	1	0
			2082	1334	363	372	13			

There are 52 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	420	MET	-	expression tag	UNP P15056
B	421	ASP	-	expression tag	UNP P15056
B	422	ARG	-	expression tag	UNP P15056
B	423	GLY	-	expression tag	UNP P15056
B	424	SER	-	expression tag	UNP P15056
B	425	HIS	-	expression tag	UNP P15056
B	426	HIS	-	expression tag	UNP P15056
B	427	HIS	-	expression tag	UNP P15056
B	428	HIS	-	expression tag	UNP P15056
B	429	HIS	-	expression tag	UNP P15056
B	430	HIS	-	expression tag	UNP P15056

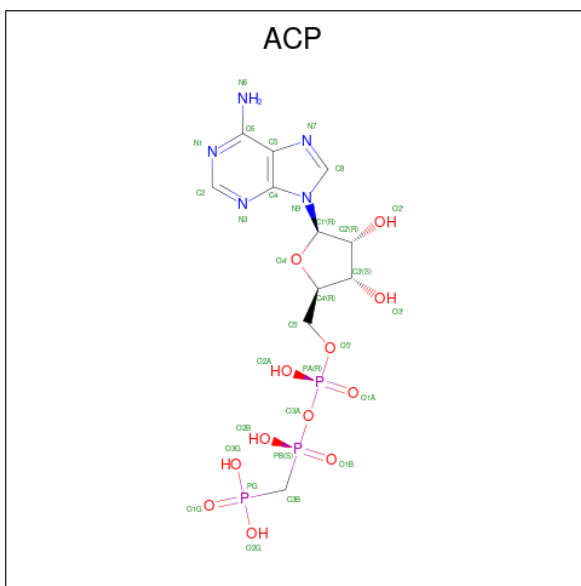
Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	431	GLY	-	expression tag	UNP P15056
B	727	LYS	-	expression tag	UNP P15056
C	420	MET	-	expression tag	UNP P15056
C	421	ASP	-	expression tag	UNP P15056
C	422	ARG	-	expression tag	UNP P15056
C	423	GLY	-	expression tag	UNP P15056
C	424	SER	-	expression tag	UNP P15056
C	425	HIS	-	expression tag	UNP P15056
C	426	HIS	-	expression tag	UNP P15056
C	427	HIS	-	expression tag	UNP P15056
C	428	HIS	-	expression tag	UNP P15056
C	429	HIS	-	expression tag	UNP P15056
C	430	HIS	-	expression tag	UNP P15056
C	431	GLY	-	expression tag	UNP P15056
C	727	LYS	-	expression tag	UNP P15056
F	420	MET	-	expression tag	UNP P15056
F	421	ASP	-	expression tag	UNP P15056
F	422	ARG	-	expression tag	UNP P15056
F	423	GLY	-	expression tag	UNP P15056
F	424	SER	-	expression tag	UNP P15056
F	425	HIS	-	expression tag	UNP P15056
F	426	HIS	-	expression tag	UNP P15056
F	427	HIS	-	expression tag	UNP P15056
F	428	HIS	-	expression tag	UNP P15056
F	429	HIS	-	expression tag	UNP P15056
F	430	HIS	-	expression tag	UNP P15056
F	431	GLY	-	expression tag	UNP P15056
F	727	LYS	-	expression tag	UNP P15056
G	420	MET	-	expression tag	UNP P15056
G	421	ASP	-	expression tag	UNP P15056
G	422	ARG	-	expression tag	UNP P15056
G	423	GLY	-	expression tag	UNP P15056
G	424	SER	-	expression tag	UNP P15056
G	425	HIS	-	expression tag	UNP P15056
G	426	HIS	-	expression tag	UNP P15056
G	427	HIS	-	expression tag	UNP P15056
G	428	HIS	-	expression tag	UNP P15056
G	429	HIS	-	expression tag	UNP P15056
G	430	HIS	-	expression tag	UNP P15056
G	431	GLY	-	expression tag	UNP P15056
G	727	LYS	-	expression tag	UNP P15056

- Molecule 3 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID:

ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).

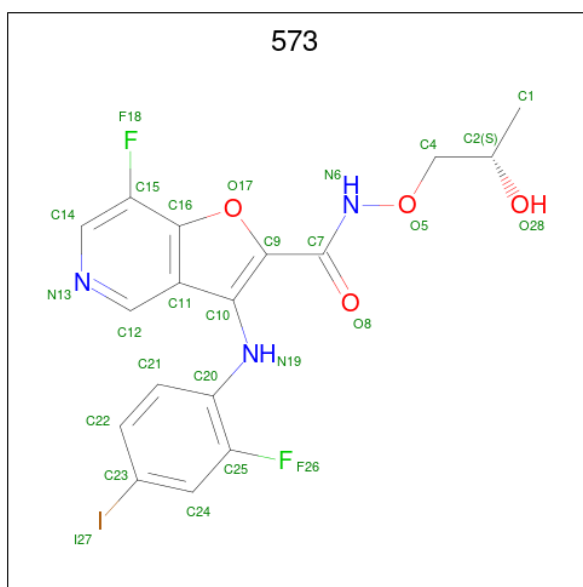


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	11	5	12	3		
3	D	1	Total	C	N	O	P	0	0
			31	11	5	12	3		
3	E	1	Total	C	N	O	P	0	0
			31	11	5	12	3		
3	H	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	D	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		
4	H	1	Total	Mg	0	0
			1	1		

- Molecule 5 is 7-fluoro-3-[(2-fluoro-4-iodophenyl)amino]-N-[(2S)-2-hydroxypropyl]oxy}furo[3,2-c]pyridine-2-carboxamide (CCD ID: 573) (formula: $C_{17}H_{14}F_2IN_3O_4$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
5	A	1	Total 27	C 17	F 2	I 1	N 3	O 4	0	0
5	D	1	Total 27	C 17	F 2	I 1	N 3	O 4	0	0
5	E	1	Total 27	C 17	F 2	I 1	N 3	O 4	0	0
5	H	1	Total 27	C 17	F 2	I 1	N 3	O 4	0	0
5	H	1	Total 27	C 17	F 2	I 1	N 3	O 4	0	0

- Molecule 6 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	F	1	Total Cl 1 1	0	0

- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	12	Total O 12 12	0	0
7	B	28	Total O 28 28	0	0
7	C	17	Total O 17 17	0	0

Continued on next page...

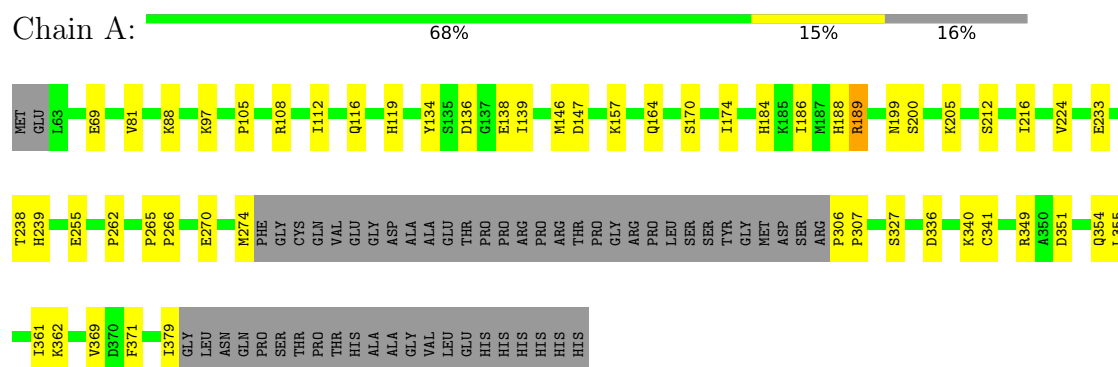
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	D	19	Total 19	O 19	0	0
7	E	8	Total 8	O 8	0	0
7	F	18	Total 18	O 18	0	0
7	G	12	Total 12	O 12	0	0
7	H	7	Total 7	O 7	0	0

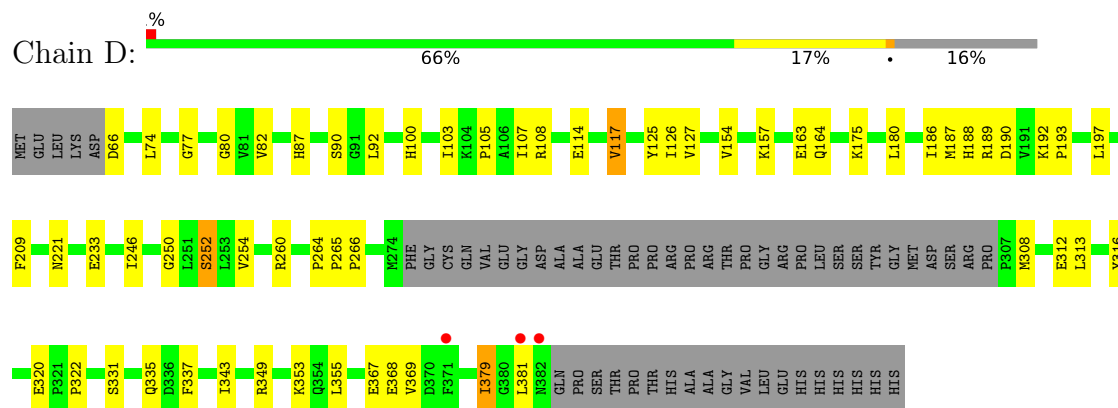
3 Residue-property plots [i](#)

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

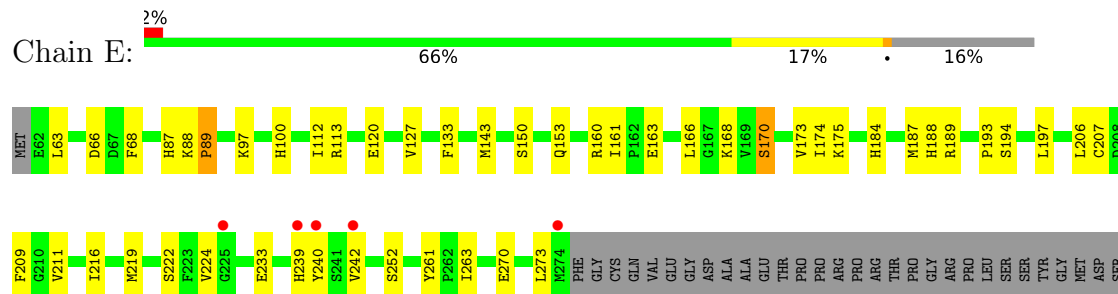
- Molecule 1: Dual specificity mitogen-activated protein kinase kinase 1



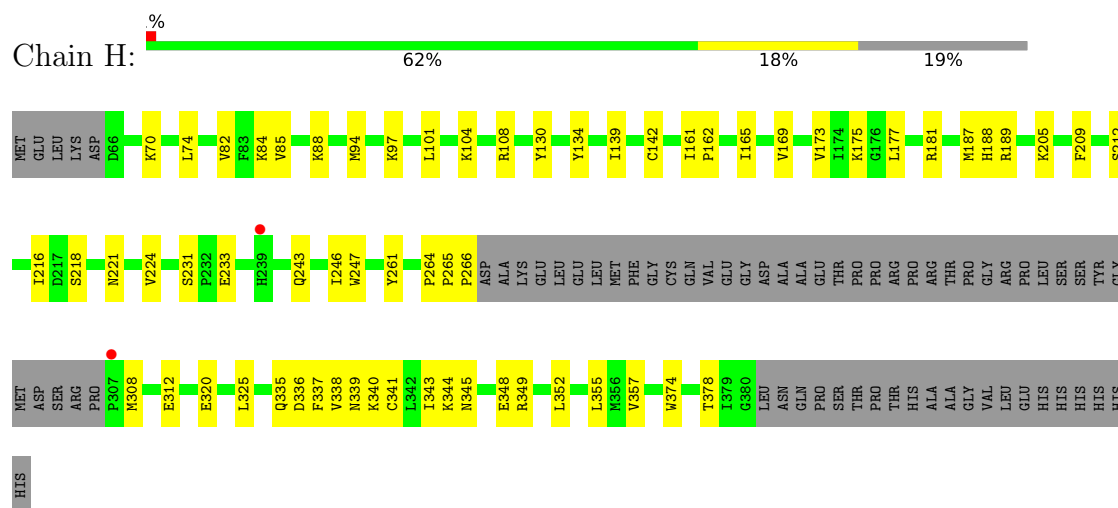
- Molecule 1: Dual specificity mitogen-activated protein kinase kinase 1



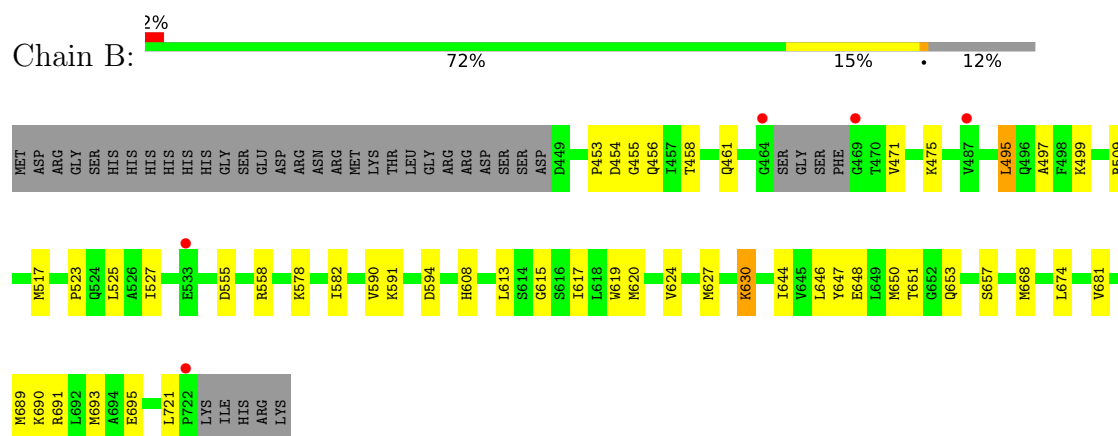
- Molecule 1: Dual specificity mitogen-activated protein kinase kinase 1



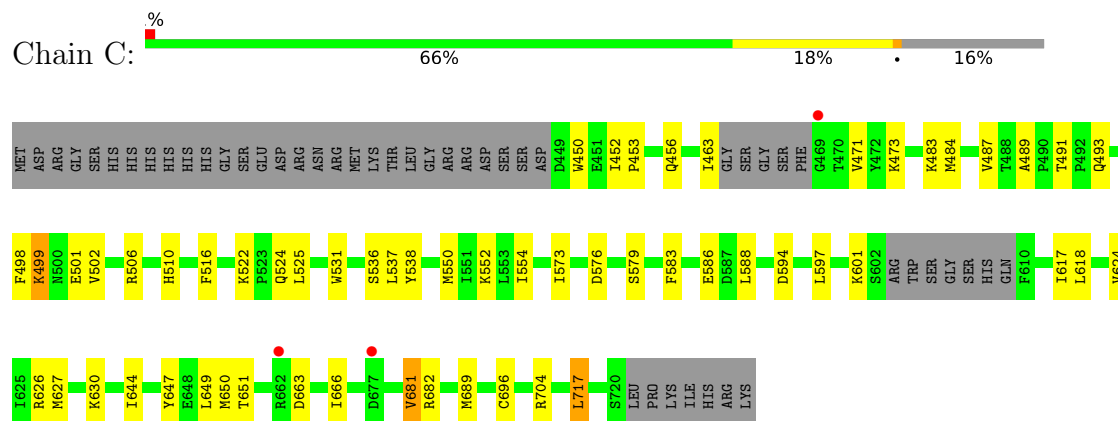
- Molecule 1: Dual specificity mitogen-activated protein kinase kinase 1



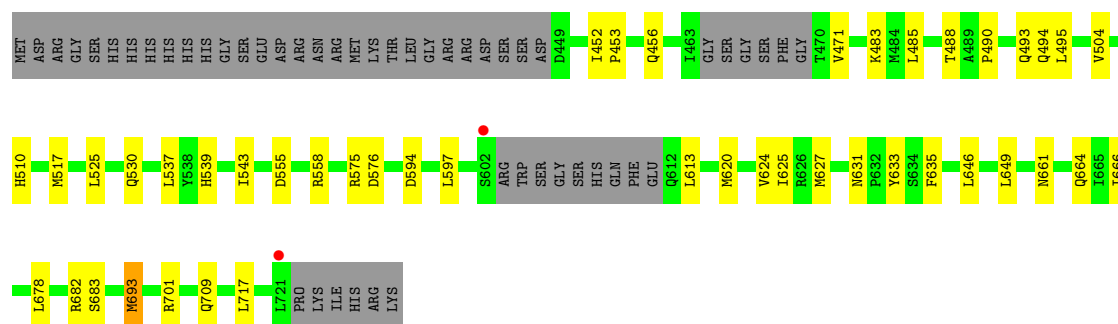
- Molecule 2: Serine/threonine-protein kinase B-raf



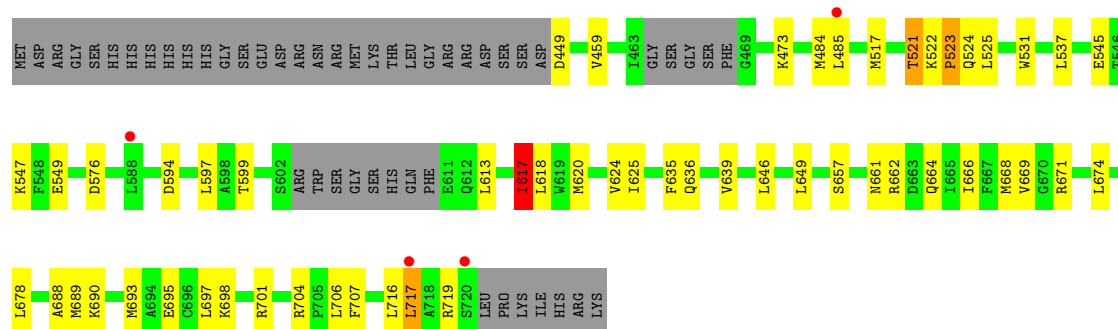
- Molecule 2: Serine/threonine-protein kinase B-raf



- Molecule 2: Serine/threonine-protein kinase B-raf



• Molecule 2: Serine/threonine-protein kinase B-raf



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.50Å 135.66Å 256.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.59 – 2.85 39.59 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.6 (39.59-2.85) 94.4 (39.59-2.85)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.185 , 0.240 0.186 , 0.240	Depositor DCC
R_{free} test set	2000 reflections (2.50%)	wwPDB-VP
Wilson B-factor (Å ²)	54.8	Xtriage
Anisotropy	0.340	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 32.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	17682	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 573, MG, ACP, CL

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	0.54	0/2308	0.93	3/3112 (0.1%)
1	D	0.57	0/2272	0.92	6/3063 (0.2%)
1	E	0.51	0/2292	0.91	3/3089 (0.1%)
1	H	0.49	0/2192	0.91	8/2956 (0.3%)
2	B	0.58	0/2226	0.90	3/3004 (0.1%)
2	C	0.57	0/2143	0.91	2/2890 (0.1%)
2	F	0.56	0/2120	0.91	6/2860 (0.2%)
2	G	0.55	0/2127	0.93	4/2869 (0.1%)
All	All	0.55	0/17680	0.92	35/23843 (0.1%)

There are no bond length outliers.

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	522	LYS	CA-C-N	-9.03	110.52	119.64
2	C	522	LYS	C-N-CA	-9.03	110.52	119.64
1	E	161	ILE	CA-C-N	8.08	128.55	119.83
1	E	161	ILE	C-N-CA	8.08	128.55	119.83
1	D	381	LEU	N-CA-C	-6.83	105.89	114.56

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	2254	0	2277	32	0
1	D	2226	0	2254	31	0
1	E	2243	0	2273	36	0
1	H	2146	0	2172	37	0
2	B	2175	0	2217	29	0
2	C	2096	0	2140	32	0
2	F	2075	0	2129	21	0
2	G	2082	0	2128	29	0
3	A	31	0	14	0	0
3	D	31	0	14	1	0
3	E	31	0	14	3	0
3	H	31	0	14	0	0
4	A	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	H	1	0	0	0	0
5	A	27	0	14	2	0
5	D	27	0	14	0	0
5	E	27	0	14	1	0
5	H	54	0	28	6	0
6	F	1	0	0	0	0
7	A	12	0	0	0	0
7	B	28	0	0	0	0
7	C	17	0	0	0	0
7	D	19	0	0	0	0
7	E	8	0	0	0	0
7	F	18	0	0	1	0
7	G	12	0	0	0	0
7	H	7	0	0	0	0
All	All	17682	0	17716	240	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 7.

The worst 5 of 240 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:H:320:GLU:O	1:H:344:LYS:NZ	1.91	1.04
1:E:66:ASP:O	1:E:88:LYS:NZ	1.94	0.99
2:B:555:ASP:OD1	2:B:558[A]:ARG:NH1	2.00	0.93
1:D:157:LYS:HE3	1:D:379:ILE:HG23	1.53	0.91
1:E:163:GLU:OE2	1:E:331:SER:HB3	1.76	0.86

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	285/341 (84%)	269 (94%)	14 (5%)	2 (1%)	18	35
1	D	281/341 (82%)	266 (95%)	13 (5%)	2 (1%)	18	35
1	E	283/341 (83%)	262 (93%)	20 (7%)	1 (0%)	30	48
1	H	271/341 (80%)	262 (97%)	8 (3%)	1 (0%)	30	48
2	B	267/308 (87%)	254 (95%)	11 (4%)	2 (1%)	18	35
2	C	255/308 (83%)	242 (95%)	12 (5%)	1 (0%)	30	48
2	F	253/308 (82%)	243 (96%)	9 (4%)	1 (0%)	30	48
2	G	254/308 (82%)	236 (93%)	15 (6%)	3 (1%)	10	22
All	All	2149/2596 (83%)	2034 (95%)	102 (5%)	13 (1%)	21	39

5 of 13 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136	ASP
2	C	594	ASP
1	D	221	ASN
1	A	189	ARG
2	B	594	ASP

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	251/294 (85%)	249 (99%)	2 (1%)	73	86
1	D	247/294 (84%)	237 (96%)	10 (4%)	28	53
1	E	250/294 (85%)	242 (97%)	8 (3%)	34	59
1	H	238/294 (81%)	233 (98%)	5 (2%)	47	70
2	B	239/272 (88%)	232 (97%)	7 (3%)	37	61
2	C	231/272 (85%)	225 (97%)	6 (3%)	40	65
2	F	230/272 (85%)	224 (97%)	6 (3%)	40	65
2	G	230/272 (85%)	223 (97%)	7 (3%)	36	60
All	All	1916/2264 (85%)	1865 (97%)	51 (3%)	39	63

5 of 51 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	170	SER
2	F	504	VAL
1	H	338	VAL
1	E	211	VAL
1	E	344	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 16 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	145	HIS
2	G	709	GLN
1	E	153	GLN
2	G	580	ASN
1	D	239	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 5 are monoatomic - leaving 9 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	573	D	903	-	28,29,29	1.15	2 (7%)	30,41,41	2.49	12 (40%)
5	573	E	903	-	28,29,29	1.19	3 (10%)	30,41,41	2.41	11 (36%)
5	573	A	903	-	28,29,29	1.08	2 (7%)	30,41,41	2.14	7 (23%)
3	ACP	E	901	4	31,33,33	1.70	8 (25%)	47,52,52	1.86	12 (25%)
3	ACP	D	901	4	31,33,33	1.61	7 (22%)	47,52,52	1.80	12 (25%)
3	ACP	A	901	4	31,33,33	1.70	9 (29%)	47,52,52	1.91	11 (23%)
3	ACP	H	901	4	31,33,33	1.70	8 (25%)	47,52,52	1.82	12 (25%)
5	573	H	904	-	28,29,29	1.19	2 (7%)	30,41,41	2.31	10 (33%)
5	573	H	903	-	28,29,29	1.06	3 (10%)	30,41,41	2.44	8 (26%)

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	573	D	903	-	-	3/14/14/14	0/3/3/3
5	573	E	903	-	-	0/14/14/14	0/3/3/3
5	573	A	903	-	-	0/14/14/14	0/3/3/3
3	ACP	E	901	4	-	9/19/38/38	0/3/3/3
3	ACP	D	901	4	-	4/19/38/38	0/3/3/3
3	ACP	A	901	4	-	1/19/38/38	0/3/3/3
3	ACP	H	901	4	-	3/19/38/38	0/3/3/3
5	573	H	904	-	-	2/14/14/14	0/3/3/3

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	573	H	903	-	-	0/14/14/14	0/3/3/3

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	901	ACP	C5-C4	4.79	1.47	1.39
3	D	901	ACP	C5-C4	4.77	1.47	1.39
3	H	901	ACP	C5-C4	4.71	1.47	1.39
3	A	901	ACP	C5-C4	4.59	1.47	1.39
5	D	903	573	C9-C7	-3.77	1.41	1.48

The worst 5 of 95 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	H	903	573	O17-C9-C7	8.09	126.26	115.90
5	D	903	573	O17-C9-C7	7.68	125.73	115.90
5	E	903	573	O17-C9-C7	7.55	125.57	115.90
5	A	903	573	O17-C9-C7	6.97	124.82	115.90
5	H	904	573	C16-O17-C9	6.69	113.15	105.66

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

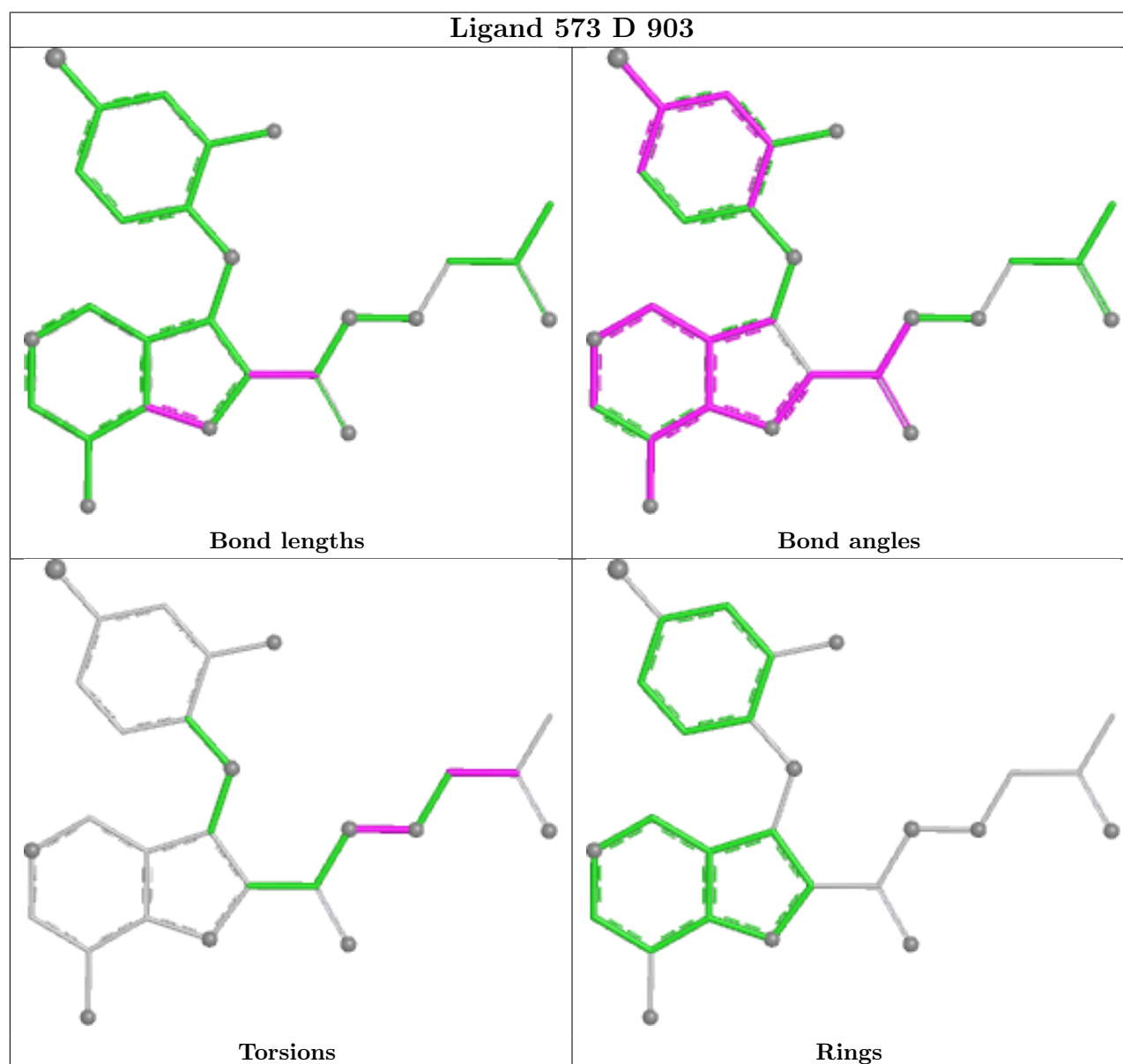
Mol	Chain	Res	Type	Atoms
3	D	901	ACP	C5'-O5'-PA-O3A
3	E	901	ACP	PB-C3B-PG-O1G
3	E	901	ACP	PB-C3B-PG-O2G
3	E	901	ACP	PB-C3B-PG-O3G
3	E	901	ACP	PG-C3B-PB-O1B

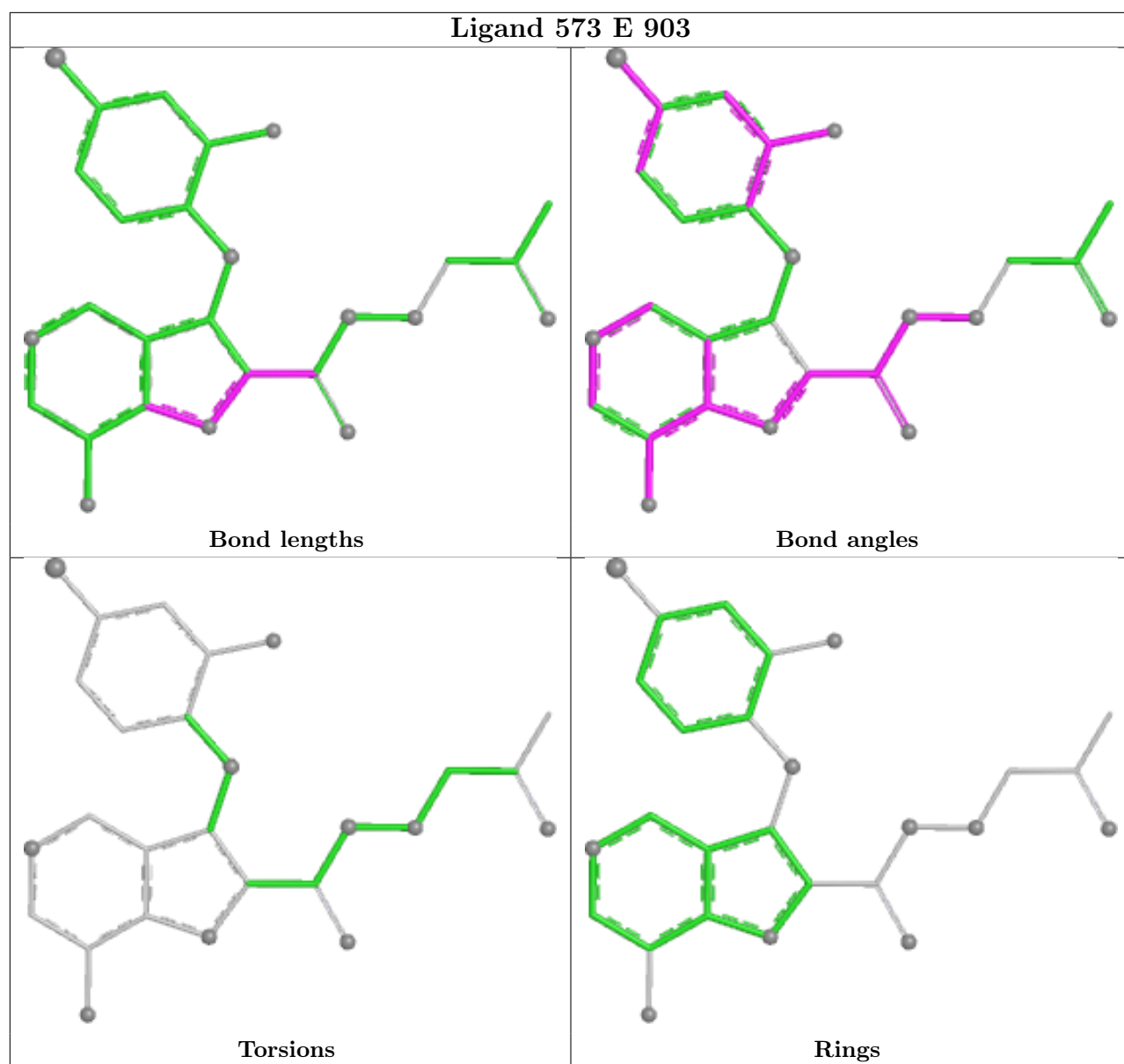
There are no ring outliers.

6 monomers are involved in 13 short contacts:

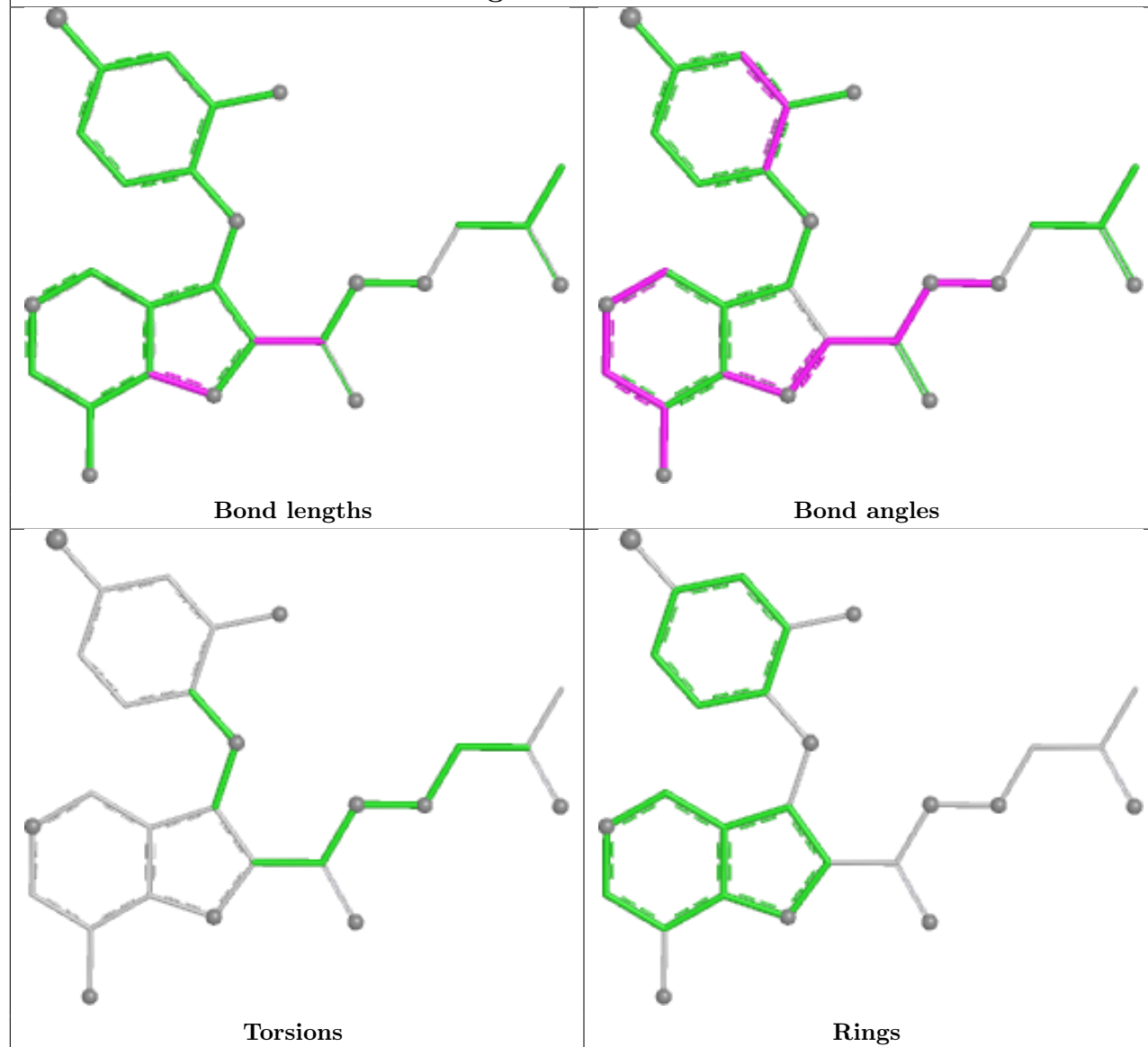
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	903	573	1	0
5	A	903	573	2	0
3	E	901	ACP	3	0
3	D	901	ACP	1	0
5	H	904	573	3	0
5	H	903	573	3	0

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.

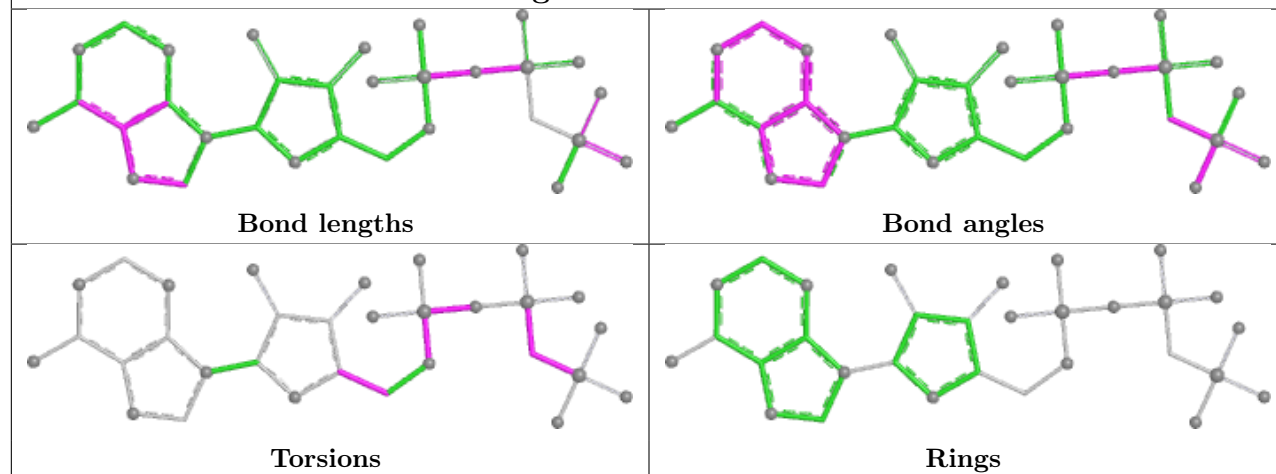


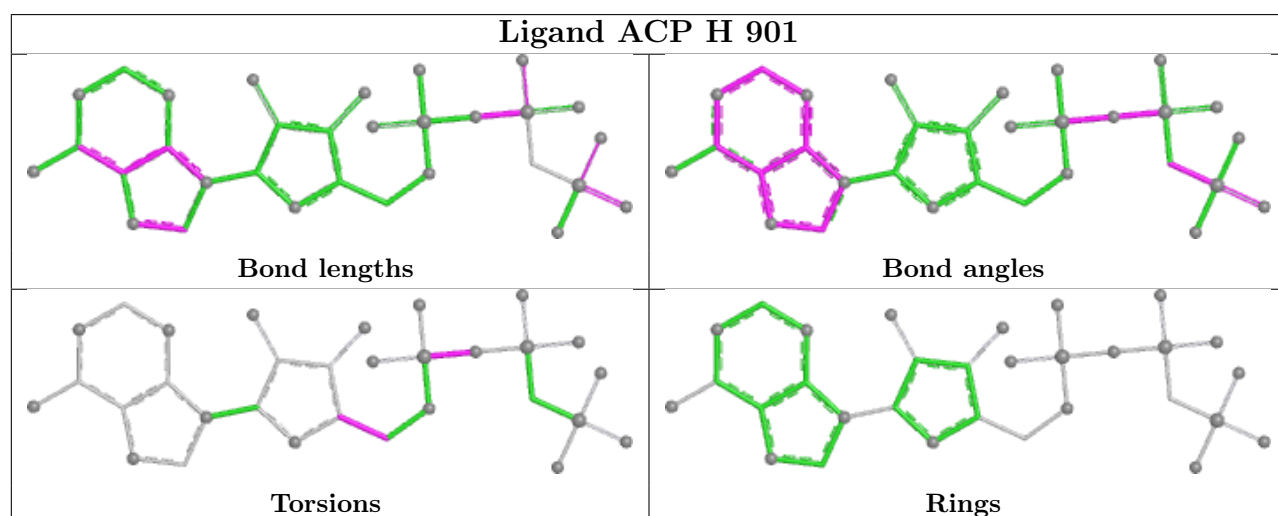
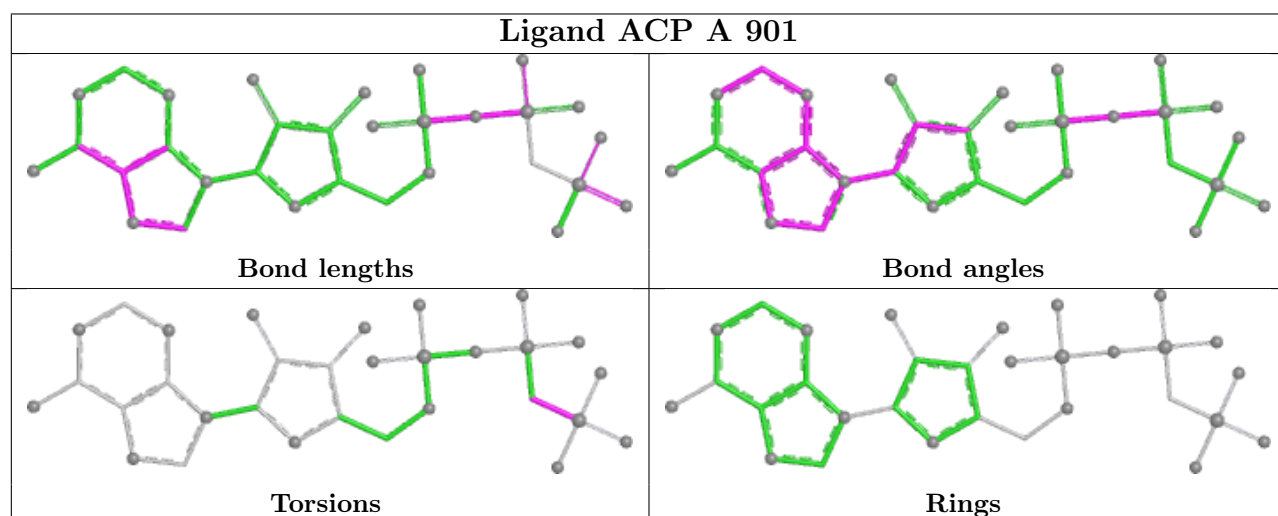
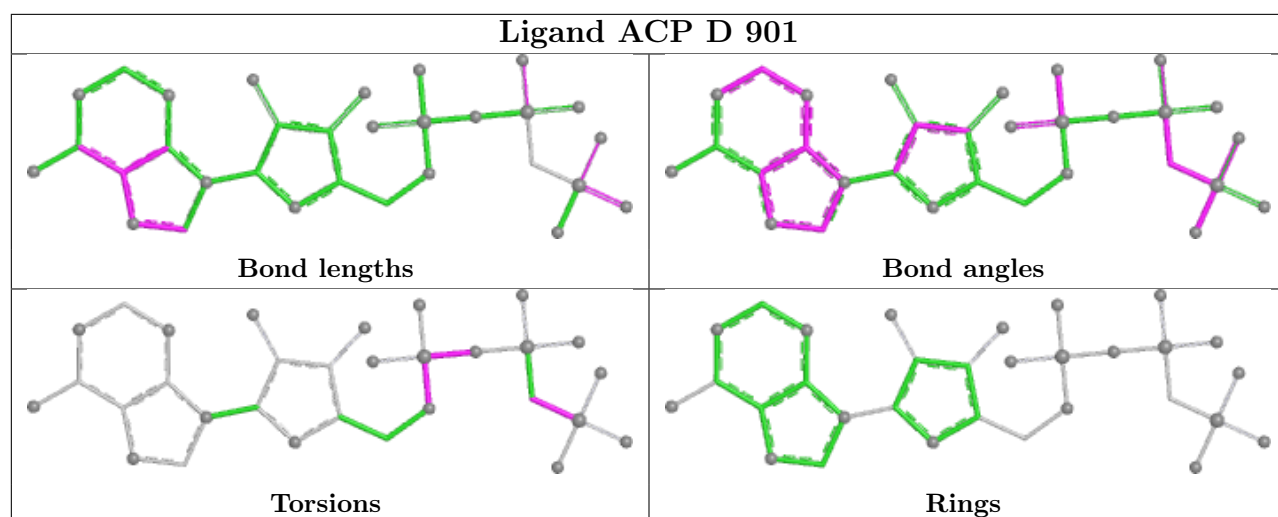


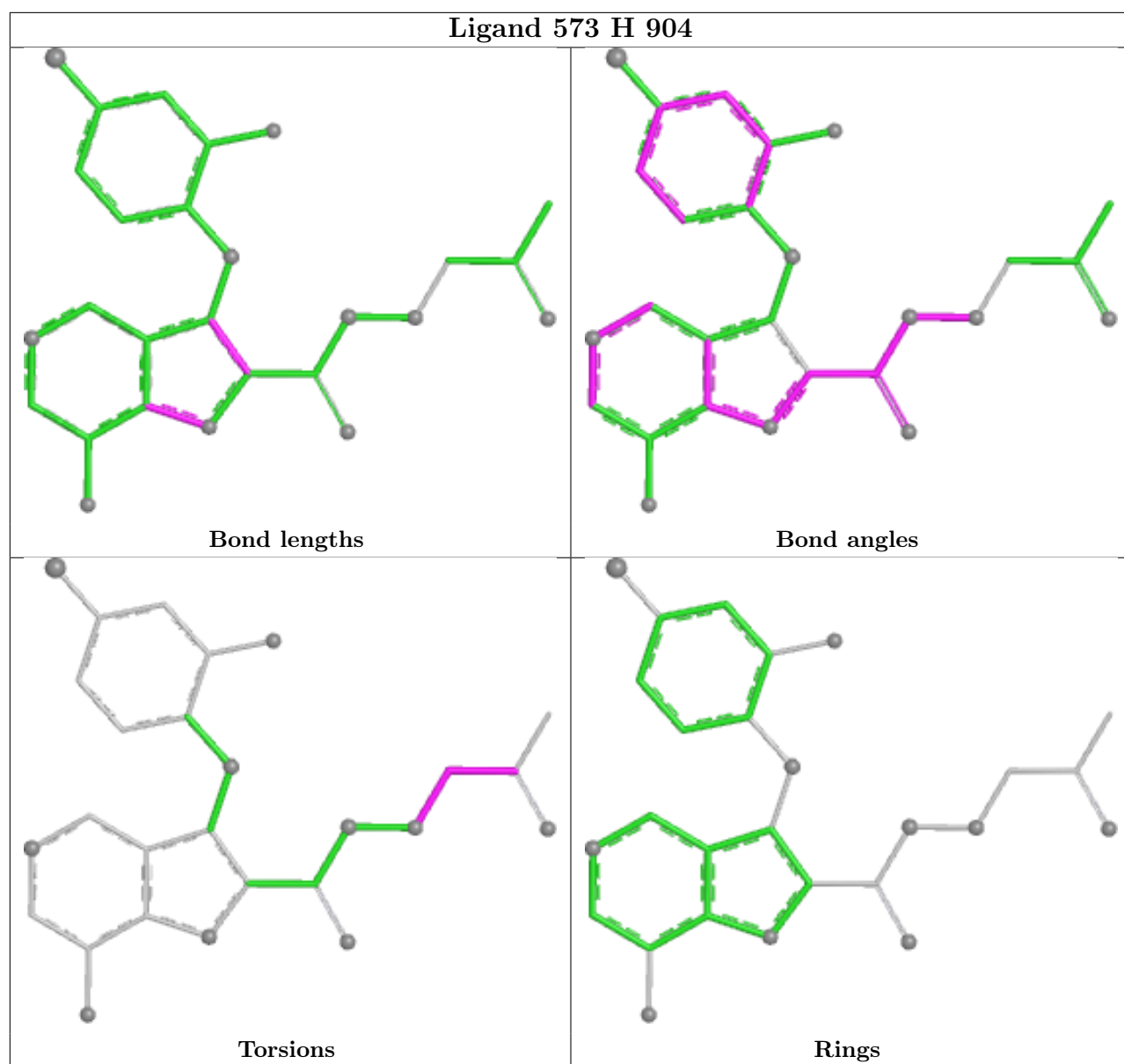
Ligand 573 A 903

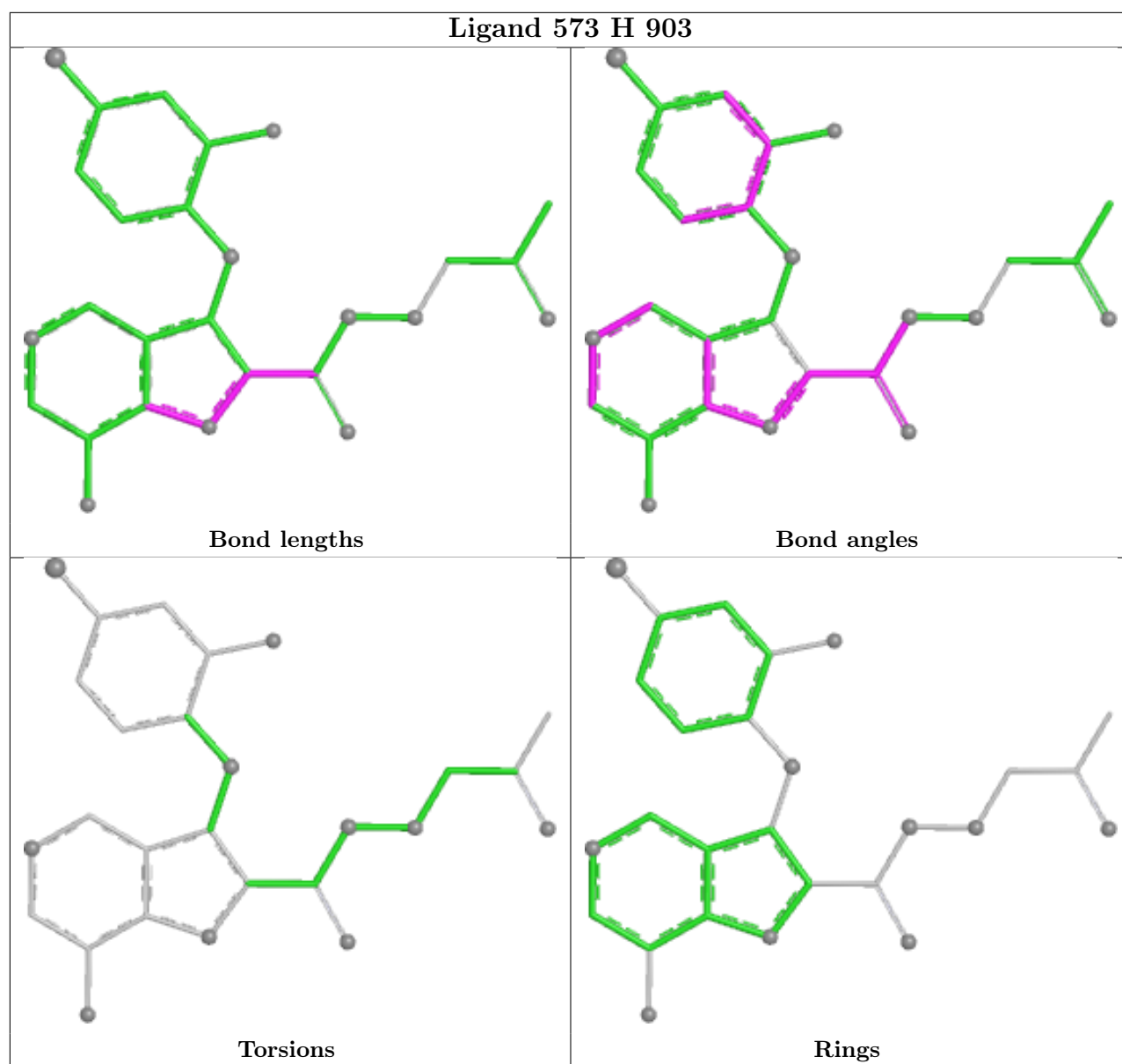


Ligand ACP E 901









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	286/341 (83%)	-0.45	0 100 100	19, 45, 78, 127	3 (1%)
1	D	285/341 (83%)	-0.46	3 (1%) 78 73	24, 41, 83, 139	0
1	E	286/341 (83%)	-0.28	6 (2%) 63 55	25, 49, 89, 143	1 (0%)
1	H	275/341 (80%)	-0.20	2 (0%) 84 80	29, 54, 89, 146	0
2	B	270/308 (87%)	-0.53	5 (1%) 66 59	12, 33, 85, 143	1 (0%)
2	C	260/308 (84%)	-0.45	3 (1%) 76 71	18, 39, 80, 129	1 (0%)
2	F	258/308 (83%)	-0.58	2 (0%) 82 78	18, 37, 84, 137	1 (0%)
2	G	259/308 (84%)	-0.43	4 (1%) 72 65	20, 40, 84, 125	1 (0%)
All	All	2179/2596 (83%)	-0.42	25 (1%) 78 73	12, 43, 87, 146	8 (0%)

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	722	PRO	3.6
2	F	721	LEU	3.5
2	B	464	GLY	3.4
2	G	588	LEU	3.3
1	E	240	TYR	2.9

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

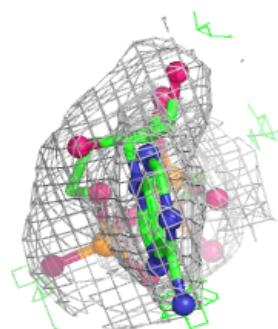
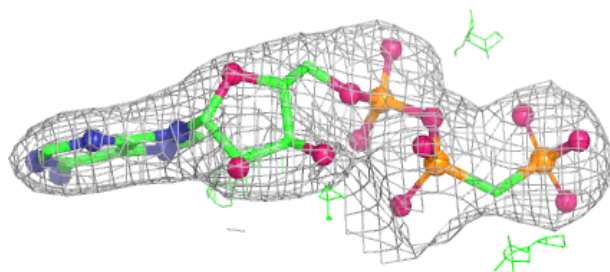
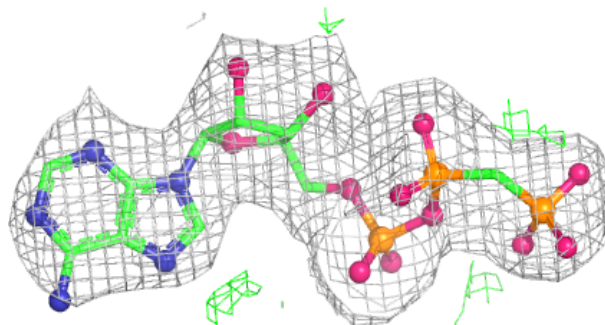
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
6	CL	F	801	1/1	0.81	0.19	71,71,71,71	0
3	ACP	E	901	31/31	0.96	0.07	34,46,57,64	0
5	573	H	904	27/27	0.97	0.10	41,54,74,83	0
3	ACP	H	901	31/31	0.97	0.05	41,49,56,58	0
3	ACP	A	901	31/31	0.98	0.06	31,44,50,51	0
3	ACP	D	901	31/31	0.98	0.05	33,38,43,46	0
4	MG	H	902	1/1	0.99	0.02	52,52,52,52	0
5	573	A	903	27/27	0.99	0.07	35,39,45,51	0
5	573	D	903	27/27	0.99	0.07	33,39,47,51	0
5	573	E	903	27/27	0.99	0.07	42,47,58,61	0
5	573	H	903	27/27	0.99	0.06	36,42,49,51	0
4	MG	A	902	1/1	0.99	0.03	45,45,45,45	0
4	MG	E	902	1/1	0.99	0.03	68,68,68,68	0
4	MG	D	902	1/1	1.00	0.02	47,47,47,47	0

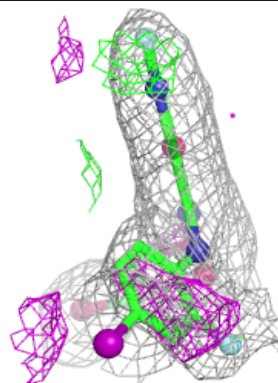
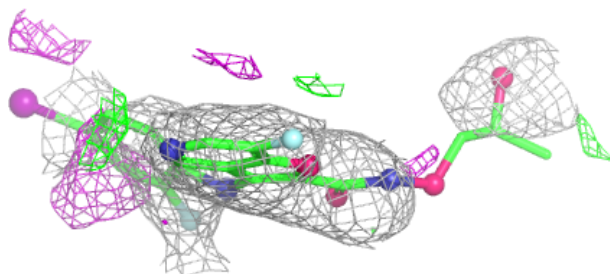
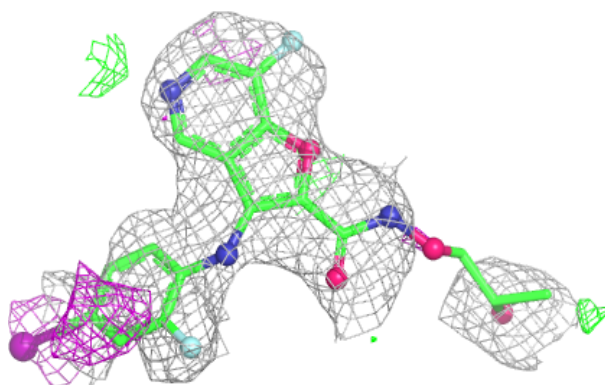
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ACP E 901:

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

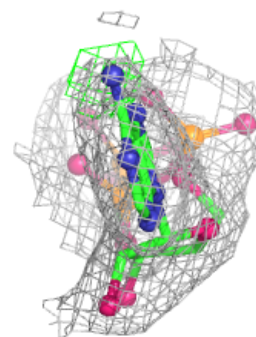
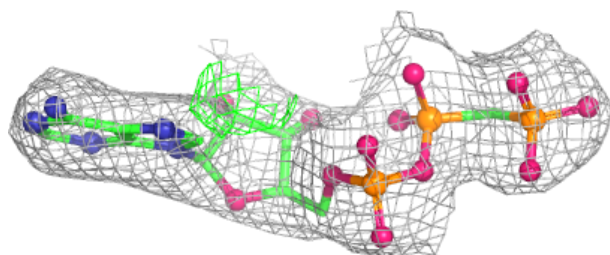
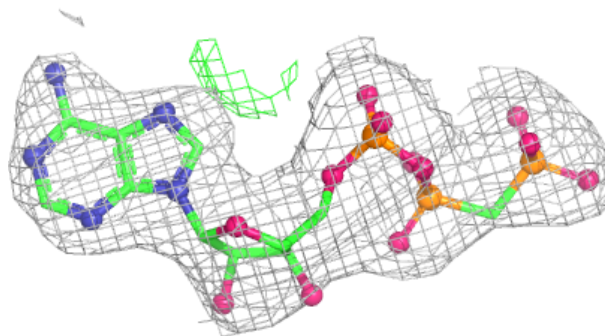
**Electron density around 573 H 904:**

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

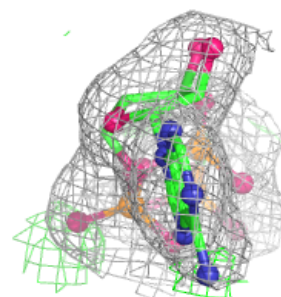
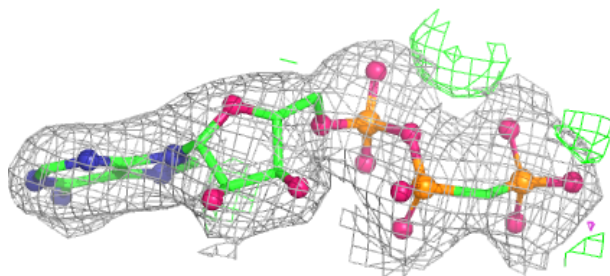
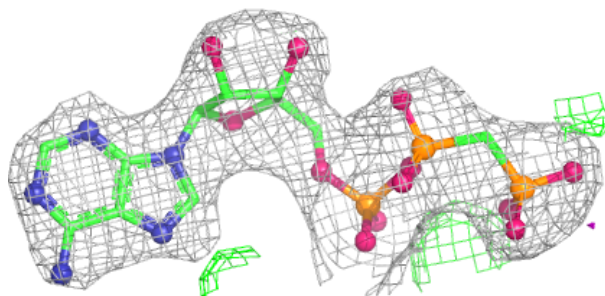


Electron density around ACP H 901:

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

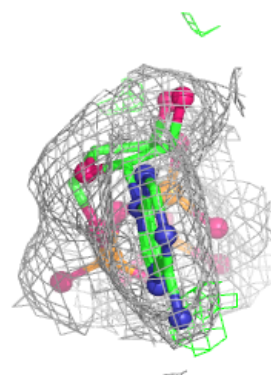
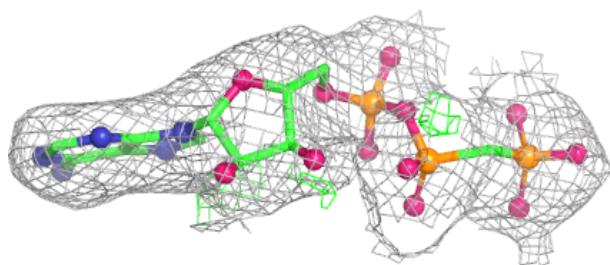
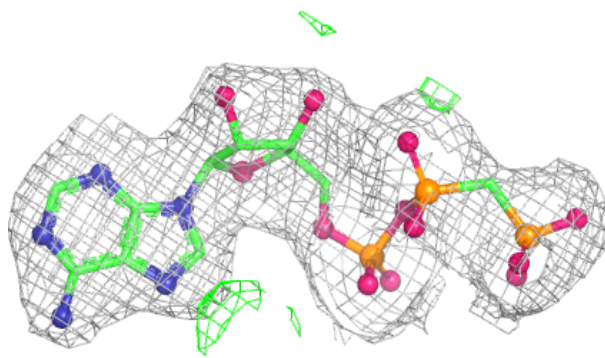
**Electron density around ACP A 901:**

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

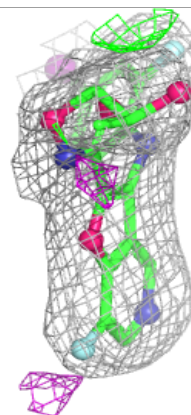
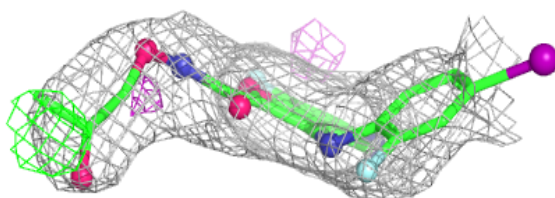
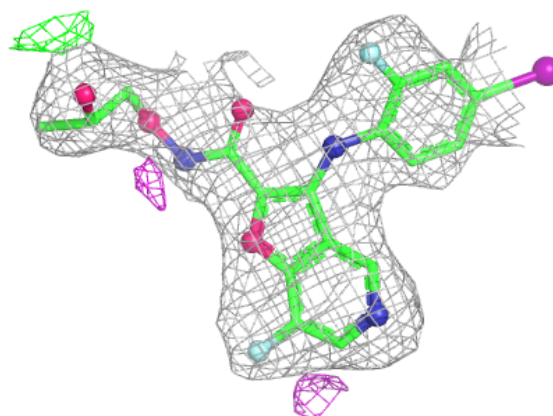


Electron density around ACP D 901:

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

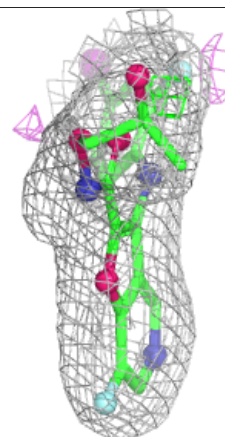
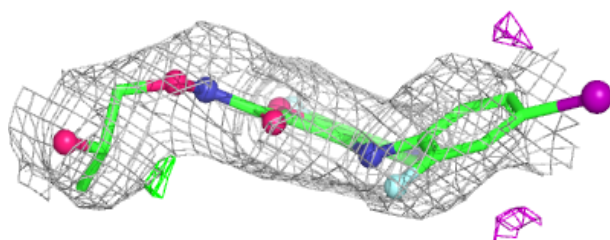
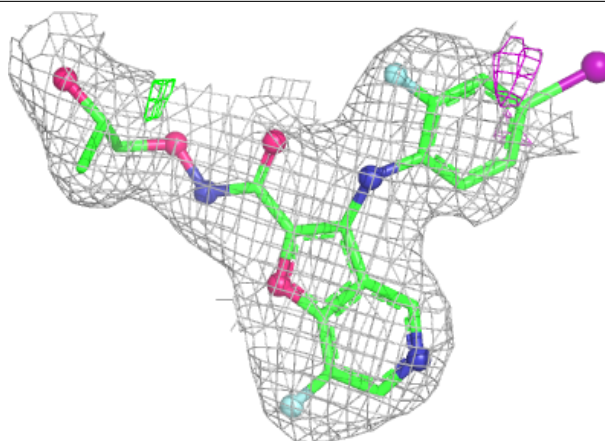
**Electron density around 573 A 903:**

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



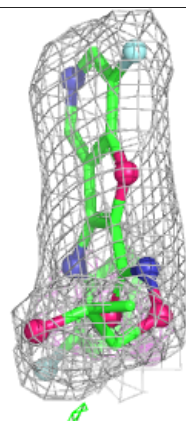
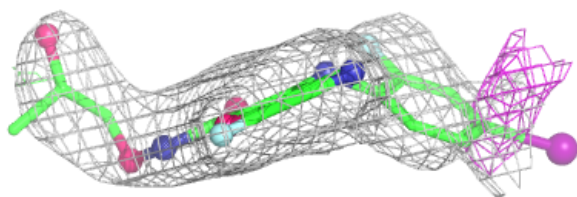
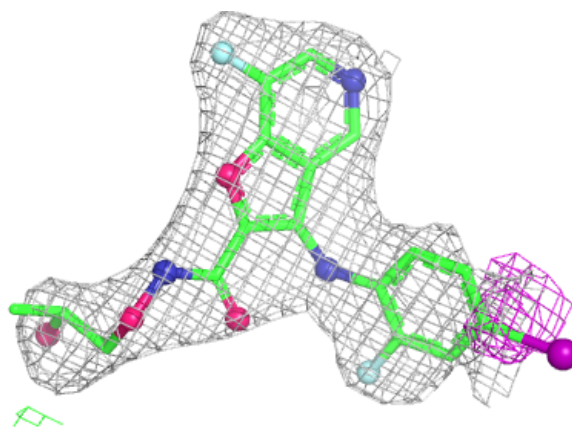
Electron density around 573 D 903:

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



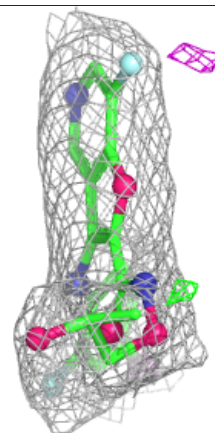
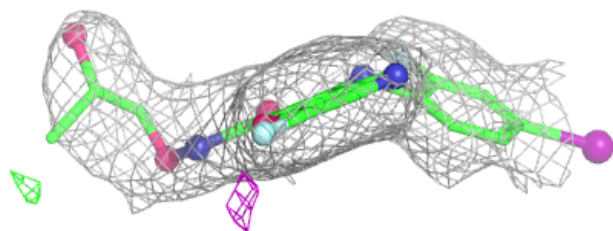
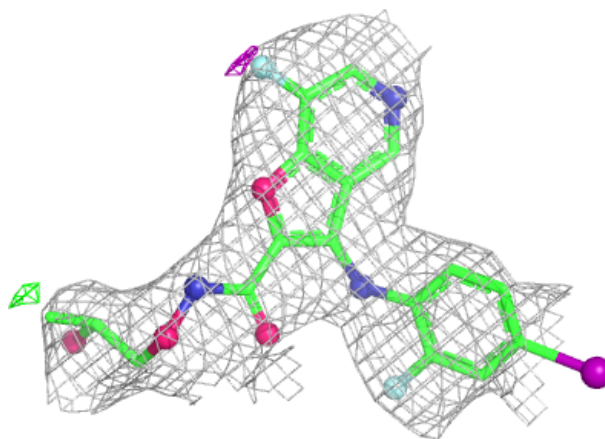
Electron density around 573 E 903:

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



Electron density around 573 H 903:

$2mF_o-DF_c$ (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.