



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 02:10 PM BST

PDB ID : 6YEI
Title : Arabidopsis thaliana glutamate dehydrogenase isoform 1 in complex with NAD
Authors : Ruszkowski, M.; Grzechowiak, M.; Jaskolski, M.
Deposited on : 2020-03-24
Resolution : 2.02 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

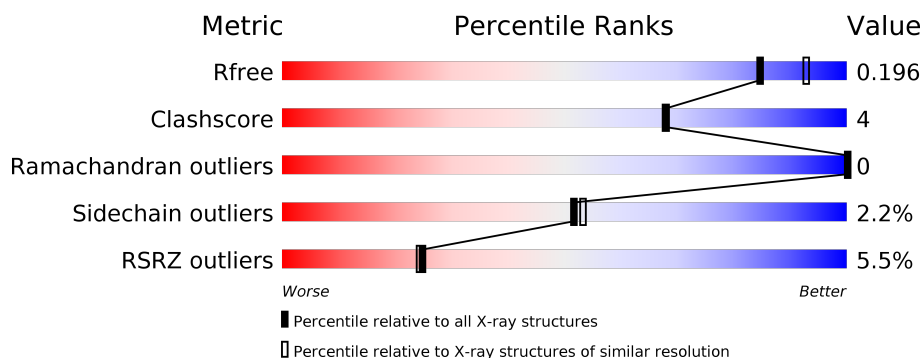
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.02 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	10434 (2.04-2.00)
Clashscore	141614	11643 (2.04-2.00)
Ramachandran outliers	138981	11493 (2.04-2.00)
Sidechain outliers	138945	11492 (2.04-2.00)
RSRZ outliers	127900	10220 (2.04-2.00)

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 on 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	414	<div> <div>90%</div> <div>9%</div> <div>•</div> </div>
1	B	414	<div> <div>%</div> <div>88%</div> <div>10%</div> <div>••</div> </div>
1	C	414	<div> <div>8%</div> <div>86%</div> <div>11%</div> <div>••</div> </div>
1	D	414	<div> <div>4%</div> <div>89%</div> <div>9%</div> <div>•</div> </div>
1	E	414	<div> <div>19%</div> <div>84%</div> <div>13%</div> <div>••</div> </div>
1	F	414	<div> <div></div> <div>93%</div> <div>6%</div> <div>•</div> </div>

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 19892 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 Glutamate dehydrogenase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	2	0
			3135	1985	549	587	14			
1	B	406	Total	C	N	O	S	0	2	0
			3116	1972	545	585	14			
1	C	407	Total	C	N	O	S	0	0	0
			3104	1967	540	583	14			
1	D	407	Total	C	N	O	S	0	0	0
			3101	1964	540	583	14			
1	E	406	Total	C	N	O	S	0	1	0
			3106	1967	542	583	14			
1	F	410	Total	C	N	O	S	0	0	0
			3125	1979	544	587	15			

There are 18 discrepancies between the modelled and reference sequences:

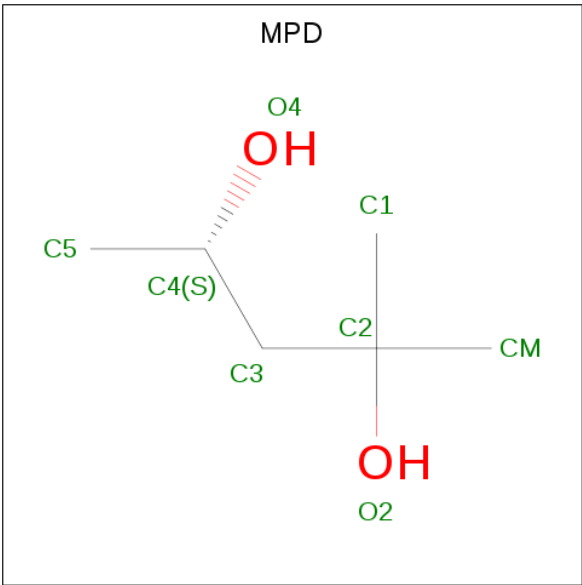
Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q43314
A	-1	ASN	-	expression tag	UNP Q43314
A	0	ALA	-	expression tag	UNP Q43314
B	-2	SER	-	expression tag	UNP Q43314
B	-1	ASN	-	expression tag	UNP Q43314
B	0	ALA	-	expression tag	UNP Q43314
C	-2	SER	-	expression tag	UNP Q43314
C	-1	ASN	-	expression tag	UNP Q43314
C	0	ALA	-	expression tag	UNP Q43314
D	-2	SER	-	expression tag	UNP Q43314
D	-1	ASN	-	expression tag	UNP Q43314
D	0	ALA	-	expression tag	UNP Q43314
E	-2	SER	-	expression tag	UNP Q43314
E	-1	ASN	-	expression tag	UNP Q43314
E	0	ALA	-	expression tag	UNP Q43314
F	-2	SER	-	expression tag	UNP Q43314
F	-1	ASN	-	expression tag	UNP Q43314

Continued on next page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	0	ALA	-	expression tag	UNP Q43314

- # NAD
-
- The image displays the chemical structure of Nicotinamide Adenine Dinucleotide (NAD). It consists of two nucleotides linked by a pyrophosphate bridge. The first nucleotide is composed of a nicotinamide ring (labeled with 'N' and 'C' atoms) and a ribose sugar (labeled with 'C' and 'O' atoms). The second nucleotide is composed of an adenine ring (labeled with 'N' and 'C' atoms) and a ribose sugar (labeled with 'C' and 'O' atoms). The pyrophosphate bridge connects the 3' carbon of the first ribose to the 5' carbon of the second ribose. The structure is shown in a 3D representation with various atoms labeled with their chemical symbols (N, C, O, P, H).

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $\text{C}_6\text{H}_{14}\text{O}_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	A	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	C	1	Total	C	O	0	0
			8	6	2		
3	C	1	Total	C	O	0	0
			8	6	2		
3	D	1	Total	C	O	0	0
			8	6	2		
3	D	1	Total	C	O	0	0
			8	6	2		
3	D	1	Total	C	O	0	0
			8	6	2		
3	D	1	Total	C	O	0	0
			8	6	2		
3	E	1	Total	C	O	0	0
			8	6	2		

Continued on next page...

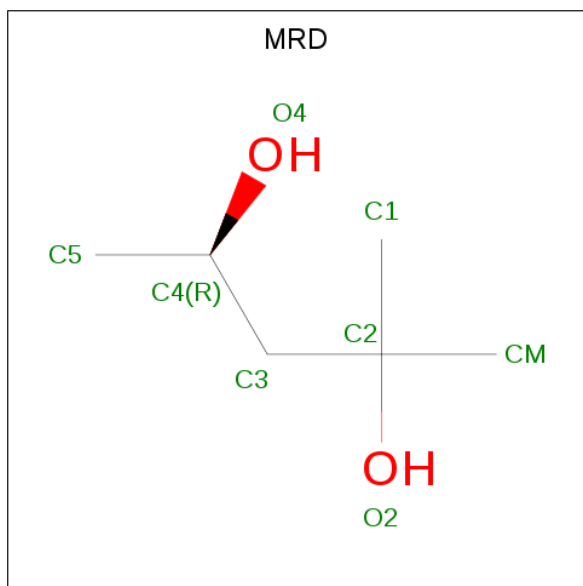
Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	C	O	0	0
			8	6	2		

- Molecule 4 is POTASSIUM ION (three-letter code: K) (formula: K) (labeled as "Ligand of Interest" by author).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	K	0	0
			2	2		
4	D	1	Total	K	0	0
			1	1		
4	C	1	Total	K	0	0
			1	1		
4	E	2	Total	K	0	0
			2	2		

- Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			8	6	2		
5	B	1	Total	C	O	0	0
			8	6	2		
5	C	1	Total	C	O	0	0
			8	6	2		

Continued on next page...

Continued from previous page...

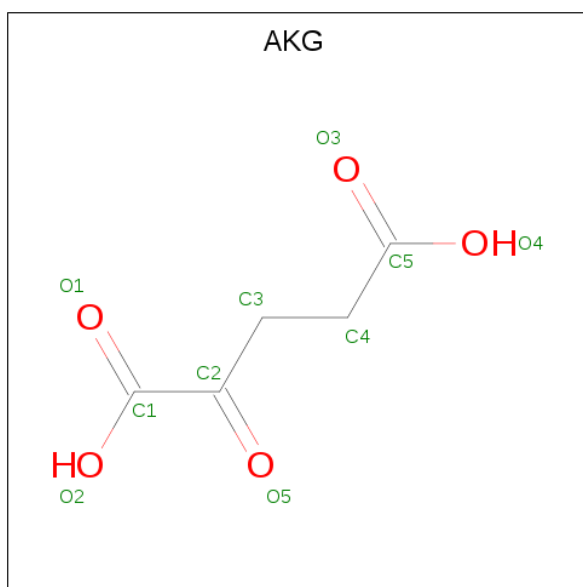
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	D	1	Total	C	O	0	0
			8	6	2		
5	E	1	Total	C	O	0	0
			8	6	2		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 7 is 2-OXOGLUTARIC ACID (three-letter code: AKG) (formula: $C_5H_6O_5$) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	F	1	Total	C	O	0	0
			10	5	5		

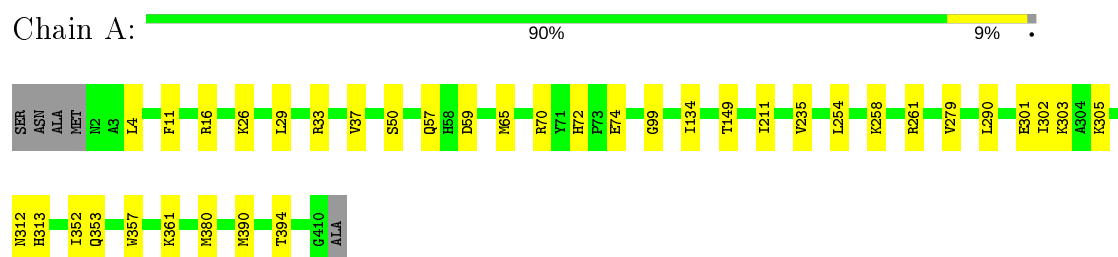
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	162	Total	O	0	0
			162	162		
8	B	138	Total	O	0	0
			138	138		
8	C	105	Total	O	0	0
			105	105		
8	D	117	Total	O	0	0
			117	117		
8	E	72	Total	O	0	0
			72	72		
8	F	163	Total	O	0	0
			163	163		

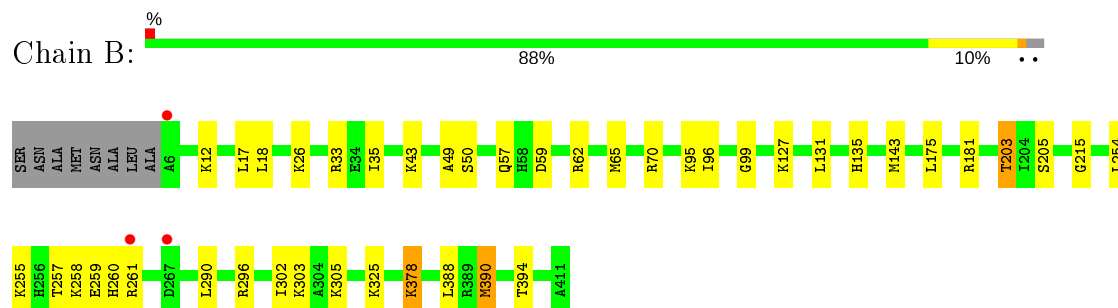
3 Residue-property plots [i](#)

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.

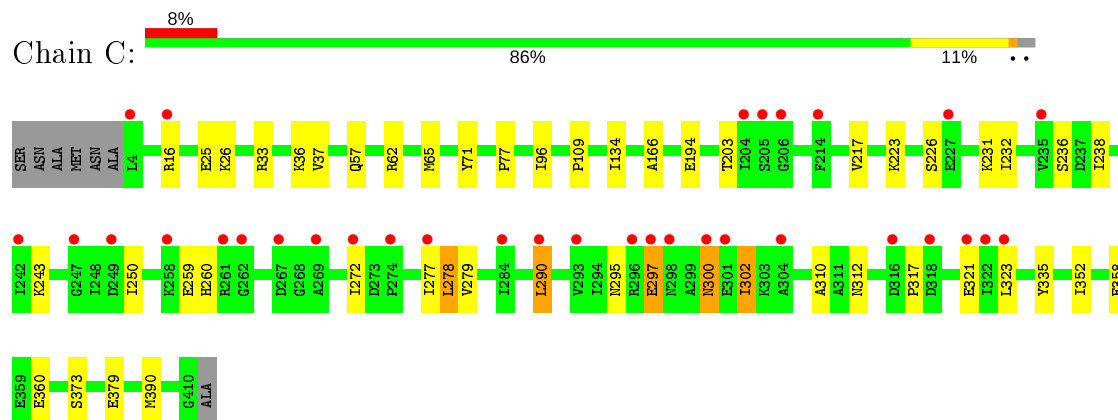
- Molecule 1: Glutamate dehydrogenase 1



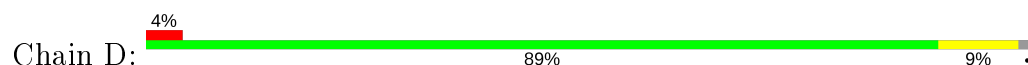
- Molecule 1: Glutamate dehydrogenase 1

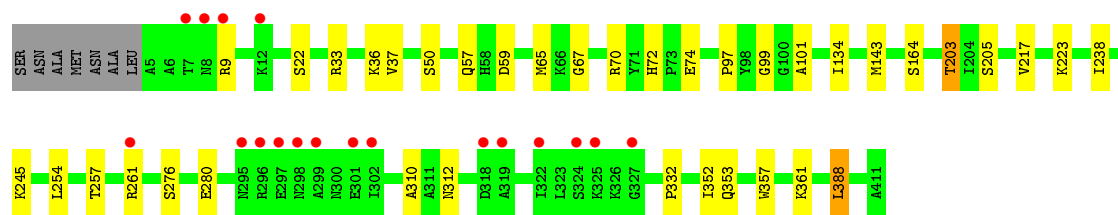


- Molecule 1: Glutamate dehydrogenase 1

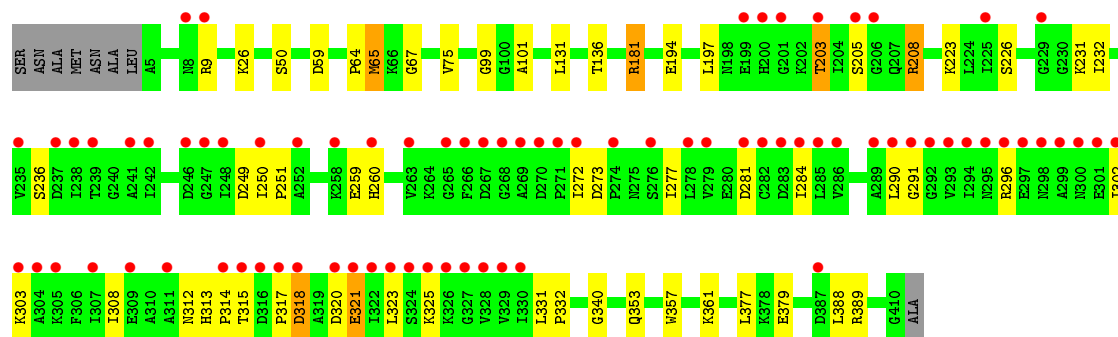
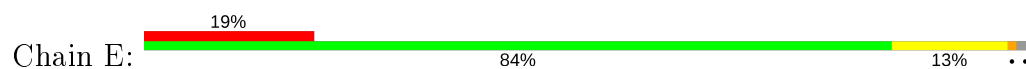


- Molecule 1: Glutamate dehydrogenase 1

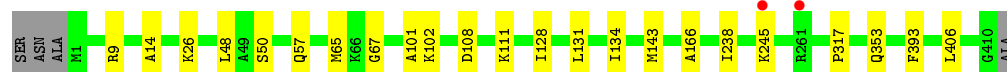




● Molecule 1: Glutamate dehydrogenase 1



● Molecule 1: Glutamate dehydrogenase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.84Å 99.81Å 317.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	70.26 – 2.02 158.97 – 2.02	Depositor EDS
% Data completeness (in resolution range)	83.3 (70.26-2.02) 83.3 (158.97-2.02)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.73 (at 2.02Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.160 , 0.196 0.160 , 0.196	Depositor DCC
R_{free} test set	1646 reflections (1.00%)	wwPDB-VP
Wilson B-factor (Å ²)	35.2	Xtriage
Anisotropy	0.005	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 52.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	19892	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.45% 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: MPD, NAD, K, EDO, MRD, AKG

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	0.44	0/3201	0.59	0/4329
1	B	0.43	0/3178	0.58	0/4296
1	C	0.39	0/3166	0.59	0/4281
1	D	0.42	0/3163	0.57	0/4277
1	E	0.38	0/3169	0.55	0/4286
1	F	0.43	0/3187	0.59	0/4309
All	All	0.42	0/19064	0.58	0/25778

There are no bond length outliers.

There are no bond angle outliers.

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	3135	0	3155	22	0
1	B	3116	0	3132	26	0
1	C	3104	0	3124	33	0
1	D	3101	0	3118	24	0
1	E	3106	0	3120	32	0
1	F	3125	0	3147	16	0
2	A	44	0	26	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	44	0	26	1	0
2	C	44	0	26	2	0
2	D	44	0	26	1	0
2	E	44	0	26	0	0
2	F	44	0	26	1	0
3	A	32	0	56	1	0
3	B	24	0	42	2	0
3	C	16	0	28	3	0
3	D	32	0	56	3	0
3	E	16	0	28	2	0
4	A	2	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	2	0	0	0	0
5	A	8	0	14	1	0
5	B	8	0	14	0	0
5	C	8	0	14	0	0
5	D	8	0	14	0	0
5	E	8	0	14	0	0
6	D	4	0	6	0	0
6	F	4	0	6	0	0
7	F	10	0	4	1	0
8	A	162	0	0	3	0
8	B	138	0	0	5	0
8	C	105	0	0	1	0
8	D	117	0	0	1	0
8	E	72	0	0	0	0
8	F	163	0	0	1	0
All	All	19892	0	19248	145	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 4.

All (145) 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:C:26:LYS:HE2	1:D:50:SER:HB2	1.67	0.76
1:C:77:PRO:HG3	3:C:503:MPD:HM1	1.67	0.75
1:F:143:MET:HE2	2:F:501:NAD:H3D	1.70	0.72
1:C:62:ARG:NH2	1:C:96:ILE:O	2.22	0.72
1:E:318:ASP:OD1	1:E:318:ASP:N	2.22	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:26:LYS:HE2	1:F:50:SER:HB2	1.74	0.69
1:C:300:ASN:N	1:C:300:ASN:OD1	2.29	0.66
1:E:9:ARG:HH22	1:E:317:PRO:HG2	1.61	0.66
1:B:254:LEU:O	1:B:258:LYS:HG2	1.99	0.63
1:D:223:LYS:HE3	3:D:505:MPD:H52	1.81	0.62
1:D:254:LEU:HD13	3:D:505:MPD:H32	1.82	0.61
1:C:226:SER:HB3	1:C:232:ILE:HD12	1.82	0.61
1:B:57:GLN:HB3	1:B:65:MET:SD	2.42	0.60
1:C:134:ILE:HG12	8:C:622:HOH:O	2.02	0.60
1:B:127:LYS:NZ	8:B:601:HOH:O	2.27	0.59
1:C:278:LEU:H	1:C:278:LEU:HD13	1.67	0.59
1:C:134:ILE:HD12	1:C:166:ALA:HB3	1.84	0.59
1:A:254:LEU:O	1:A:258:LYS:HG2	2.02	0.59
1:C:236:SER:HB3	1:C:277:ILE:HD13	1.84	0.58
1:C:302:ILE:HD11	1:C:323:LEU:HD21	1.85	0.58
1:C:295:ASN:OD1	1:C:297:GLU:HG2	2.04	0.57
1:E:291:GLY:HA2	1:E:314:PRO:HA	1.85	0.57
1:E:131:LEU:HD21	1:F:131:LEU:HD11	1.87	0.57
1:A:57:GLN:HB3	1:A:65:MET:SD	2.43	0.57
1:A:305:LYS:NZ	8:A:601:HOH:O	2.31	0.57
1:C:57:GLN:HB3	1:C:65:MET:SD	2.45	0.56
1:D:57:GLN:HB3	1:D:65:MET:SD	2.46	0.56
1:B:203:THR:HG23	1:B:205:SER:H	1.71	0.55
1:E:296:ARG:HH21	1:E:318:ASP:CG	2.09	0.55
1:B:35:ILE:HD13	1:B:131:LEU:HD13	1.88	0.55
1:E:259:GLU:HG3	1:E:260:HIS:ND1	2.22	0.55
1:F:102:LYS:NZ	7:F:502:AKG:O5	2.36	0.54
1:E:321:GLU:OE2	1:E:325:LYS:HE3	2.08	0.54
1:D:203:THR:HG23	1:D:205:SER:H	1.72	0.54
1:E:65:MET:HE2	1:E:136:THR:O	2.08	0.53
1:E:203:THR:HG23	1:E:205:SER:H	1.72	0.53
3:E:503:MPD:O4	3:E:503:MPD:O2	2.25	0.53
1:B:12:LYS:NZ	8:B:602:HOH:O	2.40	0.53
1:B:62:ARG:NH2	1:B:96:ILE:O	2.41	0.53
1:C:37:VAL:HG12	1:D:33:ARG:HG3	1.90	0.52
1:F:134:ILE:HG12	8:F:680:HOH:O	2.09	0.52
1:B:259:GLU:HG3	1:B:260:HIS:ND1	2.25	0.52
1:E:226:SER:HB3	1:E:232:ILE:HD13	1.91	0.52
1:A:390:MET:O	1:A:394:THR:HG23	2.10	0.51
1:C:36:LYS:HD2	3:C:503:MPD:H32	1.92	0.51
1:F:67:GLY:HA3	1:F:101:ALA:O	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:358:GLU:HB3	1:C:360:GLU:OE1	2.11	0.51
1:C:243:LYS:HB2	1:C:272:ILE:HD13	1.92	0.50
1:C:317:PRO:O	1:C:321:GLU:HG3	2.12	0.50
1:D:134:ILE:CG2	1:D:352:ILE:HD11	2.42	0.50
1:C:217:VAL:HG11	1:C:310:ALA:HB1	1.94	0.49
1:E:223:LYS:HA	1:E:250:ILE:HG21	1.94	0.49
1:E:302:ILE:HD13	1:E:323:LEU:HD21	1.94	0.49
1:C:335:TYR:HE1	1:C:373:SER:HG	1.58	0.49
1:F:134:ILE:HD12	1:F:166:ALA:HB3	1.94	0.49
1:C:33:ARG:HG2	1:D:37:VAL:HG12	1.94	0.49
1:D:332:PRO:HD3	1:D:388:LEU:HB3	1.95	0.48
1:A:312:ASN:HB3	1:A:313[B]:HIS:CD2	2.49	0.48
1:C:278:LEU:HD23	1:C:279:VAL:HG13	1.96	0.48
1:A:134:ILE:CG2	1:A:352:ILE:HD11	2.43	0.48
1:E:50:SER:HB2	1:F:26:LYS:HE2	1.96	0.48
1:B:43:LYS:HD2	1:B:49:ALA:HB2	1.95	0.48
1:B:388:LEU:HG	3:B:504:MPD:H11	1.95	0.48
1:D:59:ASP:O	1:D:99:GLY:HA3	2.14	0.47
1:B:70:ARG:HG3	1:B:143:MET:HB3	1.96	0.47
1:D:72:HIS:CE1	1:D:74:GLU:HB2	2.49	0.47
1:E:236:SER:HB3	1:E:277:ILE:HD13	1.97	0.47
1:F:57:GLN:HB3	1:F:65:MET:SD	2.54	0.47
1:A:149:THR:OG1	5:A:508:MRD:O4	2.22	0.47
1:D:217:VAL:HG11	1:D:310:ALA:HB1	1.97	0.46
1:E:59:ASP:O	1:E:99:GLY:HA3	2.14	0.46
1:A:72:HIS:CE1	1:A:74:GLU:HB2	2.50	0.46
1:E:377:LEU:HD21	1:E:388:LEU:HD22	1.98	0.46
1:B:261:ARG:HG2	1:B:261:ARG:O	2.14	0.46
1:E:67:GLY:HA3	1:E:101:ALA:O	2.16	0.46
1:A:37:VAL:HG12	1:B:33[B]:ARG:HG3	1.97	0.46
3:B:502:MPD:H31	1:D:97:PRO:CB	2.47	0.45
1:E:181:ARG:NH2	1:E:340:GLY:O	2.46	0.45
1:E:357:TRP:CE2	1:E:361:LYS:HE3	2.51	0.45
1:F:9:ARG:HD3	1:F:317:PRO:HG2	1.98	0.45
1:C:194:GLU:OE1	1:C:203:THR:HG23	2.16	0.45
1:F:128:ILE:HA	1:F:131:LEU:HD23	1.97	0.45
1:C:226:SER:HB3	1:C:232:ILE:CD1	2.47	0.45
1:D:261:ARG:O	1:D:261:ARG:HG2	2.17	0.45
1:C:278:LEU:O	1:C:302:ILE:HG22	2.17	0.45
1:E:203:THR:HG23	1:E:205:SER:N	2.31	0.45
1:A:59:ASP:O	1:A:99:GLY:HA3	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:134:ILE:HD11	1:D:164:SER:HB3	1.99	0.45
1:A:301:GLU:O	1:A:303:LYS:HD2	2.18	0.44
1:B:18:LEU:HD21	1:B:394:THR:HG23	1.99	0.44
1:B:95:LYS:HB2	8:B:687:HOH:O	2.16	0.44
1:E:290:LEU:HD23	1:E:290:LEU:H	1.81	0.44
1:A:279:VAL:HB	1:A:301:GLU:HG2	2.00	0.44
1:A:261:ARG:O	1:A:261:ARG:HG2	2.16	0.44
1:F:14:ALA:HB2	1:F:393:PHE:HB3	1.99	0.44
1:C:16:ARG:NH1	1:C:25:GLU:OE1	2.51	0.44
1:C:259:GLU:HG3	1:C:260:HIS:ND1	2.33	0.43
1:C:134:ILE:CG2	1:C:352:ILE:HD11	2.48	0.43
1:C:71:TYR:HB3	1:C:109:PRO:HG3	2.00	0.43
1:B:181:ARG:HA	1:B:181:ARG:HD2	1.80	0.43
1:A:33:ARG:NH1	8:A:604:HOH:O	2.48	0.43
1:A:305:LYS:HA	1:A:305:LYS:HD3	1.70	0.43
1:D:357:TRP:CE2	1:D:361:LYS:HE3	2.54	0.43
1:F:108:ASP:OD2	1:F:111:LYS:HE2	2.18	0.43
1:B:255:LYS:O	1:B:259:GLU:HG2	2.19	0.43
1:B:17:LEU:CD1	1:B:390:MET:HG3	2.49	0.43
1:C:290:LEU:HD11	2:C:501:NAD:C6A	2.48	0.43
1:D:312:ASN:ND2	2:D:502:NAD:H6N	2.34	0.43
1:D:36:LYS:HG2	3:D:503:MPD:H32	2.01	0.43
1:C:312:ASN:ND2	2:C:501:NAD:H6N	2.33	0.42
1:E:197:LEU:HD11	1:E:284:ILE:HD11	2.01	0.42
1:C:335:TYR:HE1	1:C:373:SER:OG	2.02	0.42
1:D:70:ARG:HG3	1:D:143:MET:HB3	2.00	0.42
1:A:357:TRP:CE2	1:A:361:LYS:HE3	2.54	0.42
1:B:215:GLY:HA3	2:B:501:NAD:O5B	2.19	0.42
1:D:67:GLY:HA3	1:D:101:ALA:O	2.20	0.42
1:A:50:SER:HB2	1:B:26:LYS:HE2	2.02	0.42
1:E:249:ASP:OD1	1:E:251:PRO:HD2	2.20	0.42
1:A:211:ILE:O	1:A:235:VAL:HA	2.20	0.42
1:D:353:GLN:HB3	1:F:353:GLN:HE21	1.84	0.42
1:E:208:ARG:HA	1:E:231:LYS:O	2.19	0.42
1:A:353:GLN:HB3	1:E:353:GLN:HE21	1.83	0.42
1:F:406:LEU:HD12	1:F:406:LEU:HA	1.90	0.42
1:B:59:ASP:O	1:B:99:GLY:HA3	2.20	0.42
1:C:238:ILE:HD12	1:C:238:ILE:HA	1.89	0.42
1:F:238:ILE:HD12	1:F:238:ILE:HA	1.86	0.42
1:B:378:LYS:HE3	1:B:378:LYS:HB3	1.73	0.42
1:E:272:ILE:HG22	1:E:273:ASP:N	2.35	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:276:SER:O	1:D:280:GLU:HG2	2.20	0.41
1:E:75:VAL:HG11	3:E:503:MPD:H52	2.01	0.41
1:B:70:ARG:HD3	8:B:719:HOH:O	2.20	0.41
1:D:70:ARG:HD2	8:D:711:HOH:O	2.20	0.41
1:E:308:ILE:HG23	1:E:331:LEU:HD23	2.02	0.41
1:D:238:ILE:HD12	1:D:238:ILE:HA	1.90	0.41
3:A:504:MPD:O4	3:A:504:MPD:O2	2.36	0.41
3:C:503:MPD:H11	3:C:503:MPD:O4	2.21	0.41
1:E:332:PRO:HG3	1:E:389:ARG:HA	2.03	0.41
1:A:26:LYS:HE2	1:B:50:SER:HB2	2.03	0.41
1:B:135:HIS:HD2	8:B:729:HOH:O	2.04	0.41
1:E:312:ASN:HB3	1:E:313[B]:HIS:CE1	2.55	0.41
1:A:11:PHE:CE2	1:A:29:LEU:HG	2.55	0.40
1:A:70:ARG:HD2	8:A:742:HOH:O	2.20	0.40
1:E:281:ASP:OD1	1:E:303:LYS:HG2	2.21	0.40
1:C:223:LYS:HA	1:C:250:ILE:HG21	2.04	0.40
1:B:203:THR:HG23	1:B:205:SER:N	2.35	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	409/414 (99%)	401 (98%)	8 (2%)	0	100	100
1	B	406/414 (98%)	397 (98%)	9 (2%)	0	100	100
1	C	405/414 (98%)	397 (98%)	8 (2%)	0	100	100
1	D	405/414 (98%)	395 (98%)	10 (2%)	0	100	100
1	E	405/414 (98%)	395 (98%)	10 (2%)	0	100	100
1	F	408/414 (99%)	399 (98%)	9 (2%)	0	100	100
All	All	2438/2484 (98%)	2384 (98%)	54 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	332/333 (100%)	327 (98%)	5 (2%)	65	68
1	B	330/333 (99%)	319 (97%)	11 (3%)	38	36
1	C	329/333 (99%)	321 (98%)	8 (2%)	49	49
1	D	328/333 (98%)	322 (98%)	6 (2%)	59	61
1	E	329/333 (99%)	318 (97%)	11 (3%)	38	36
1	F	331/333 (99%)	329 (99%)	2 (1%)	86	89
All	All	1979/1998 (99%)	1936 (98%)	43 (2%)	52	53

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	LEU
1	A	16	ARG
1	A	290	LEU
1	A	302	ILE
1	A	380	MET
1	B	175	LEU
1	B	203	THR
1	B	257	THR
1	B	290	LEU
1	B	296	ARG
1	B	302	ILE
1	B	303	LYS
1	B	305	LYS
1	B	325	LYS
1	B	378	LYS
1	B	390	MET
1	C	231	LYS
1	C	278	LEU
1	C	290	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	297	GLU
1	C	300	ASN
1	C	302	ILE
1	C	379	GLU
1	C	390	MET
1	D	9	ARG
1	D	22	SER
1	D	203	THR
1	D	245	LYS
1	D	257	THR
1	D	388	LEU
1	E	64	PRO
1	E	65	MET
1	E	181	ARG
1	E	194	GLU
1	E	203	THR
1	E	208	ARG
1	E	315	THR
1	E	318	ASP
1	E	320	ASP
1	E	321	GLU
1	E	379	GLU
1	F	48	LEU
1	F	245	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	312	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 monosaccharides in this entry.

5.6 Ligand geometry

Of 35 ligands modelled in this entry, 6 are monoatomic - leaving 29 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	$\# Z > 2$
3	MPD	A	505	-	7,7,7	0.12	0	9,10,10	0.28	0
2	NAD	F	501	-	42,48,48	0.61	0	50,73,73	0.85	3 (6%)
3	MPD	E	503	-	7,7,7	0.15	0	9,10,10	0.35	0
3	MPD	C	503	-	7,7,7	0.16	0	9,10,10	0.51	0
3	MPD	A	502	-	7,7,7	0.12	0	9,10,10	0.32	0
2	NAD	A	501	-	42,48,48	0.64	0	50,73,73	0.88	2 (4%)
2	NAD	C	501	-	42,48,48	0.56	0	50,73,73	0.79	1 (2%)
3	MPD	A	504	-	7,7,7	0.10	0	9,10,10	0.34	0
3	MPD	D	504	-	7,7,7	0.10	0	9,10,10	0.27	0
2	NAD	B	501	-	42,48,48	0.58	0	50,73,73	0.77	2 (4%)
3	MPD	C	502	-	7,7,7	0.15	0	9,10,10	0.28	0
7	AKG	F	502	-	3,9,9	0.60	0	4,11,11	1.68	2 (50%)
3	MPD	B	503	-	7,7,7	0.14	0	9,10,10	0.36	0
3	MPD	D	505	-	7,7,7	0.13	0	9,10,10	0.69	0
3	MPD	D	506	-	7,7,7	0.05	0	9,10,10	0.43	0
2	NAD	E	502	-	42,48,48	0.65	0	50,73,73	0.86	3 (6%)
3	MPD	B	502	-	7,7,7	0.13	0	9,10,10	0.59	0
5	MRD	D	508	-	7,7,7	0.12	0	9,10,10	0.29	0
6	EDO	D	501	-	3,3,3	0.49	0	2,2,2	0.36	0
5	MRD	C	504	-	7,7,7	0.13	0	9,10,10	0.59	0
3	MPD	D	503	-	7,7,7	0.13	0	9,10,10	0.31	0
3	MPD	E	501	-	7,7,7	0.11	0	9,10,10	0.33	0
5	MRD	A	508	-	7,7,7	0.15	0	9,10,10	0.32	0
3	MPD	B	504	-	7,7,7	0.16	0	9,10,10	0.57	0
3	MPD	A	503	-	7,7,7	0.13	0	9,10,10	0.38	0
6	EDO	F	503	-	3,3,3	0.44	0	2,2,2	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAD	D	502	-	42,48,48	0.59	0	50,73,73	0.84	2 (4%)
5	MRD	E	505	-	7,7,7	0.17	0	9,10,10	0.30	0
5	MRD	B	505	-	7,7,7	0.15	0	9,10,10	0.40	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
3	MPD	A	505	-	-	0/5/5/5	-
2	NAD	F	501	-	-	7/26/62/62	0/5/5/5
3	MPD	E	503	-	-	2/5/5/5	-
3	MPD	C	503	-	-	2/5/5/5	-
3	MPD	A	502	-	-	1/5/5/5	-
2	NAD	A	501	-	-	1/26/62/62	0/5/5/5
2	NAD	C	501	-	-	6/26/62/62	0/5/5/5
3	MPD	A	504	-	-	1/5/5/5	-
3	MPD	D	504	-	-	0/5/5/5	-
2	NAD	B	501	-	-	1/26/62/62	0/5/5/5
3	MPD	C	502	-	-	1/5/5/5	-
7	AKG	F	502	-	-	2/3/9/9	-
3	MPD	B	503	-	-	0/5/5/5	-
3	MPD	D	505	-	-	1/5/5/5	-
3	MPD	D	506	-	-	0/5/5/5	-
2	NAD	E	502	-	-	6/26/62/62	0/5/5/5
3	MPD	B	502	-	-	2/5/5/5	-
5	MRD	D	508	-	-	1/5/5/5	-
6	EDO	D	501	-	-	1/1/1/1	-
5	MRD	C	504	-	-	2/5/5/5	-
3	MPD	D	503	-	-	0/5/5/5	-
3	MPD	E	501	-	-	0/5/5/5	-
5	MRD	A	508	-	-	3/5/5/5	-
3	MPD	B	504	-	-	3/5/5/5	-
3	MPD	A	503	-	-	0/5/5/5	-
6	EDO	F	503	-	-	0/1/1/1	-
2	NAD	D	502	-	-	3/26/62/62	0/5/5/5
5	MRD	E	505	-	-	1/5/5/5	-
5	MRD	B	505	-	-	0/5/5/5	-

There are no bond length outliers.

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	502	NAD	O4B-C1B-C2B	-2.48	103.30	106.93
2	F	501	NAD	C5A-C6A-N6A	2.42	124.03	120.35
7	F	502	AKG	C4-C3-C2	-2.40	107.96	113.14
2	D	502	NAD	C6N-N1N-C2N	-2.40	119.79	121.97
2	A	501	NAD	C6N-N1N-C2N	-2.35	119.83	121.97
2	E	502	NAD	C5A-C6A-N6A	2.32	123.88	120.35
2	C	501	NAD	C5A-C6A-N6A	2.24	123.75	120.35
2	B	501	NAD	C6N-N1N-C2N	-2.21	119.96	121.97
7	F	502	AKG	O5-C2-C3	-2.20	116.62	120.38
2	B	501	NAD	C5A-C6A-N6A	2.20	123.69	120.35
2	F	501	NAD	O4B-C1B-C2B	-2.19	103.73	106.93
2	E	502	NAD	C6N-N1N-C2N	-2.17	120.00	121.97
2	D	502	NAD	C5A-C6A-N6A	2.16	123.63	120.35
2	F	501	NAD	C6N-N1N-C2N	-2.05	120.11	121.97
2	A	501	NAD	C5A-C6A-N6A	2.03	123.43	120.35

There are no chirality outliers.

All (47) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	501	NAD	O4D-C1D-N1N-C2N
2	F	501	NAD	O4D-C1D-N1N-C6N
2	F	501	NAD	C2D-C1D-N1N-C2N
2	F	501	NAD	C2D-C1D-N1N-C6N
2	C	501	NAD	C5B-O5B-PA-O1A
2	C	501	NAD	C5B-O5B-PA-O2A
2	C	501	NAD	C5B-O5B-PA-O3
2	C	501	NAD	O4B-C4B-C5B-O5B
2	E	502	NAD	C5B-O5B-PA-O1A
2	E	502	NAD	C5B-O5B-PA-O3
3	B	502	MPD	C2-C3-C4-O4
5	A	508	MRD	O2-C2-C3-C4
5	A	508	MRD	CM-C2-C3-C4
2	C	501	NAD	C3B-C4B-C5B-O5B
7	F	502	AKG	C1-C2-C3-C4
7	F	502	AKG	O5-C2-C3-C4
6	D	501	EDO	O1-C1-C2-O2
2	D	502	NAD	O4D-C4D-C5D-O5D
3	A	502	MPD	O2-C2-C3-C4
3	C	502	MPD	O2-C2-C3-C4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	E	502	NAD	O4B-C4B-C5B-O5B
2	C	501	NAD	PN-O3-PA-O2A
3	C	503	MPD	C2-C3-C4-C5
3	B	502	MPD	C2-C3-C4-C5
5	C	504	MRD	C2-C3-C4-C5
2	E	502	NAD	C5B-O5B-PA-O2A
3	B	504	MPD	C2-C3-C4-O4
3	E	503	MPD	CM-C2-C3-C4
5	A	508	MRD	C1-C2-C3-C4
5	E	505	MRD	CM-C2-C3-C4
2	D	502	NAD	C3D-C4D-C5D-O5D
2	B	501	NAD	O4B-C4B-C5B-O5B
2	F	501	NAD	O4B-C4B-C5B-O5B
2	E	502	NAD	PN-O3-PA-O2A
3	E	503	MPD	O2-C2-C3-C4
3	A	504	MPD	O2-C2-C3-C4
3	B	504	MPD	O2-C2-C3-C4
2	D	502	NAD	O4B-C4B-C5B-O5B
2	F	501	NAD	C5D-O5D-PN-O3
2	A	501	NAD	O4B-C4B-C5B-O5B
2	E	502	NAD	PN-O3-PA-O1A
3	D	505	MPD	C2-C3-C4-C5
3	B	504	MPD	C2-C3-C4-C5
2	F	501	NAD	C5D-O5D-PN-O1N
3	C	503	MPD	C2-C3-C4-O4
5	D	508	MRD	C2-C3-C4-O4
5	C	504	MRD	C2-C3-C4-O4

There are no ring outliers.

13 monomers are involved in 18 short contacts:

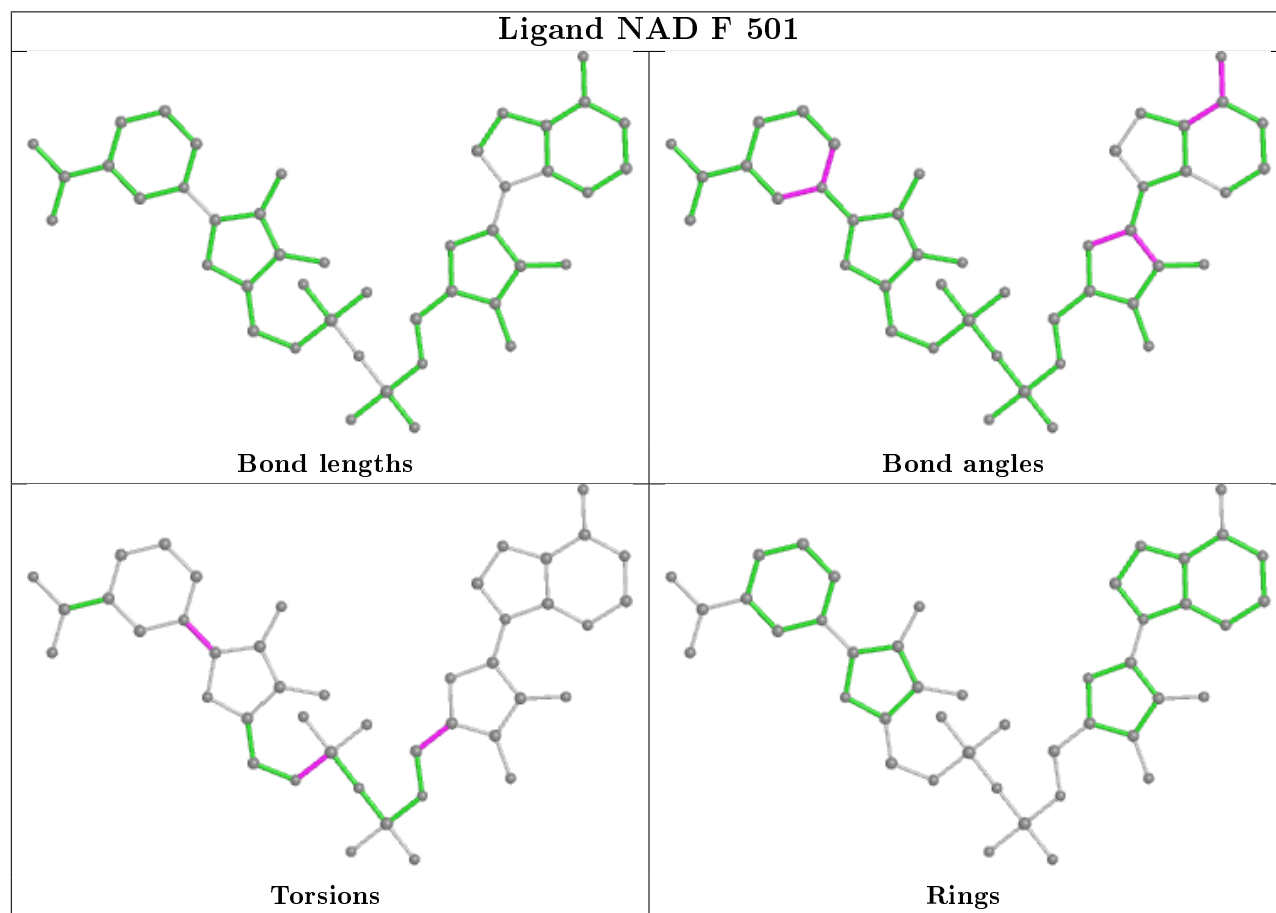
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	501	NAD	1	0
3	E	503	MPD	2	0
3	C	503	MPD	3	0
2	C	501	NAD	2	0
3	A	504	MPD	1	0
2	B	501	NAD	1	0
7	F	502	AKG	1	0
3	D	505	MPD	2	0
3	B	502	MPD	1	0
3	D	503	MPD	1	0

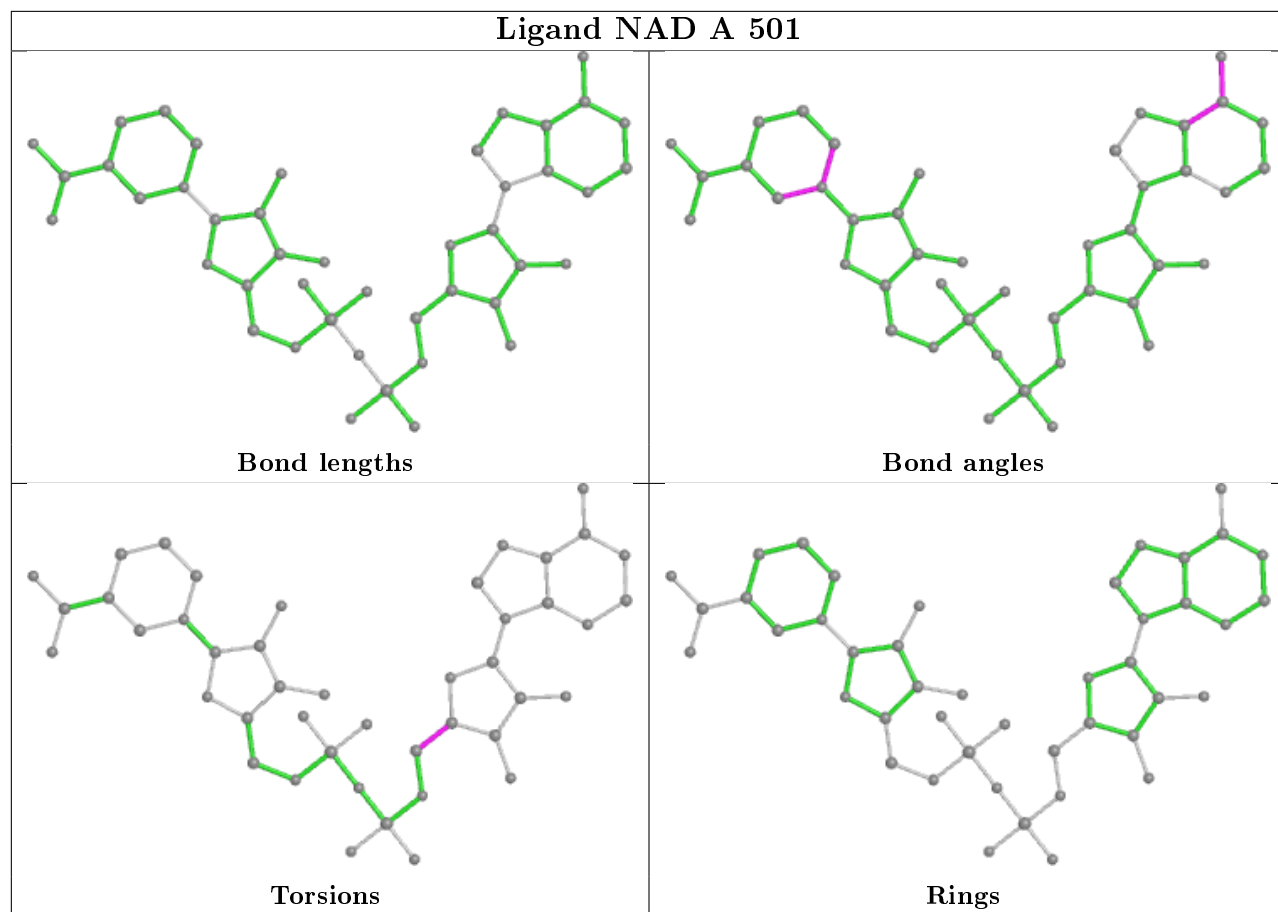
Continued on next page...

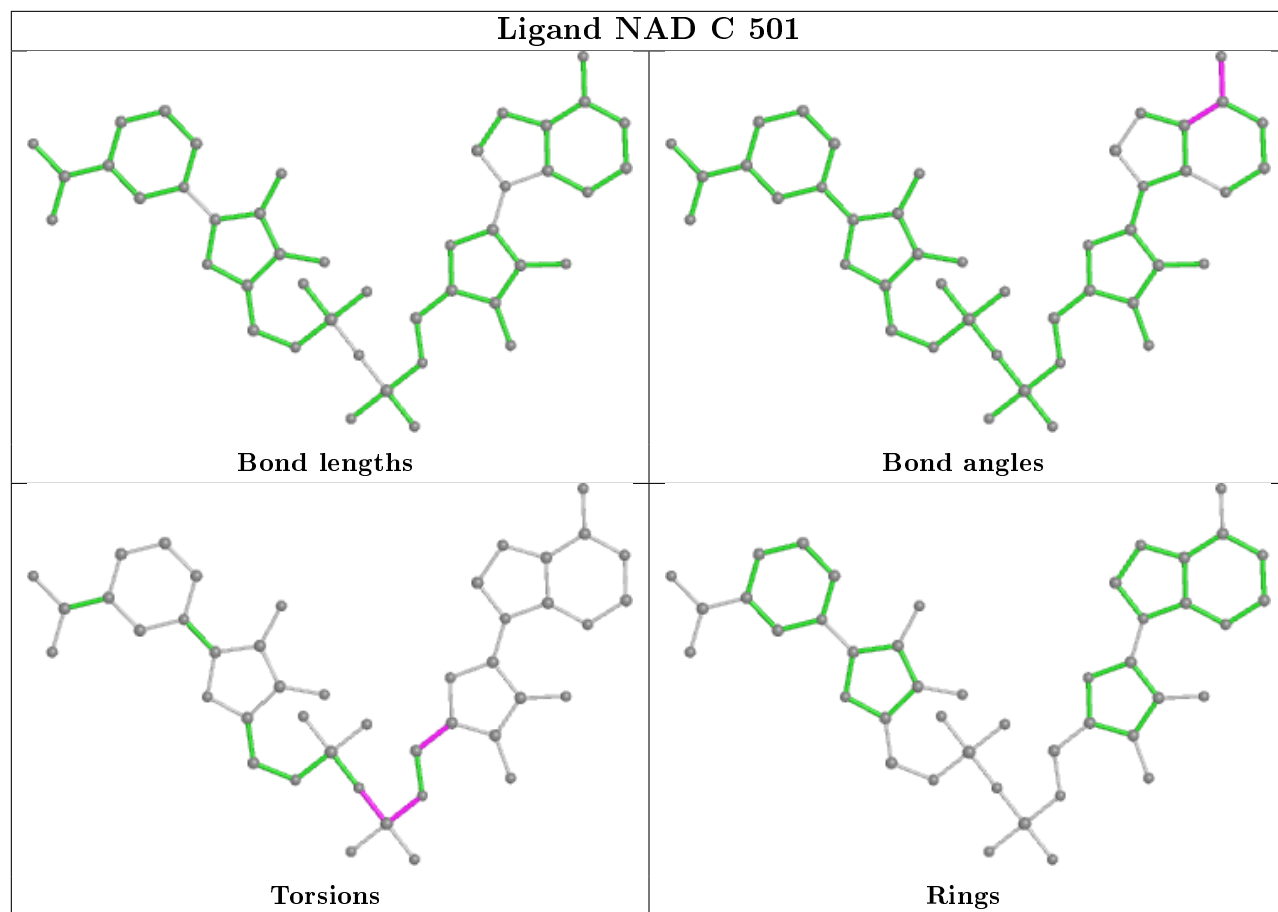
Continued from previous page...

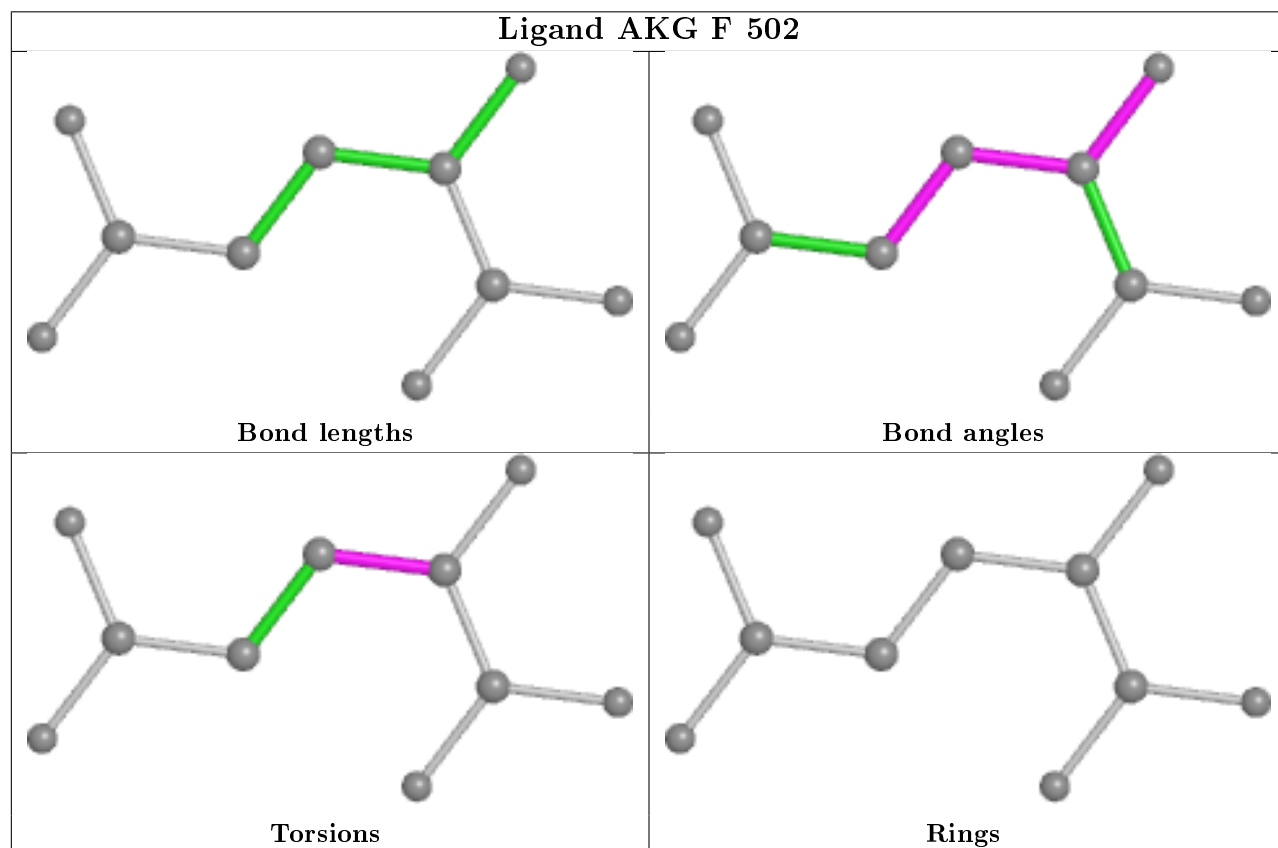
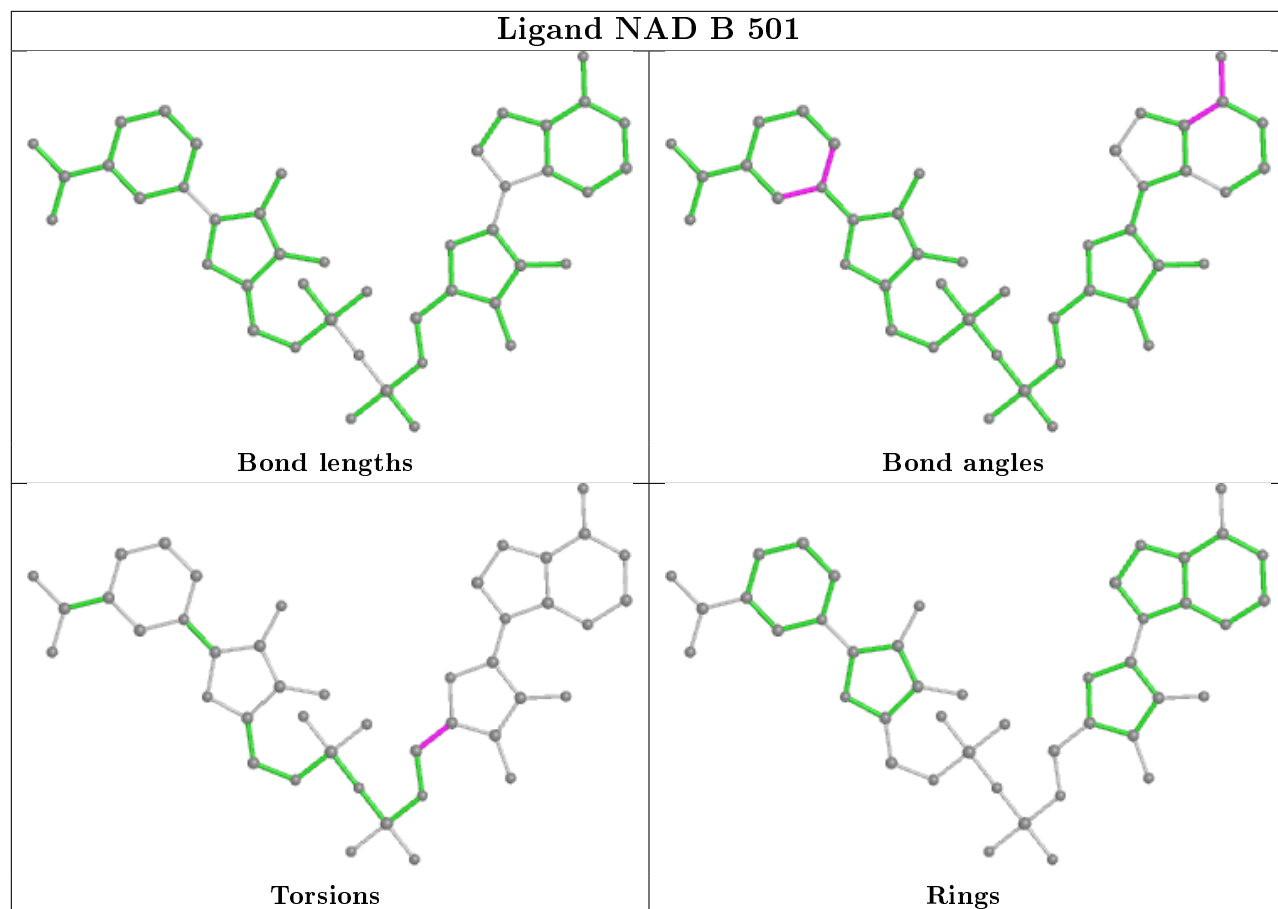
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	508	MRD	1	0
3	B	504	MPD	1	0
2	D	502	NAD	1	0

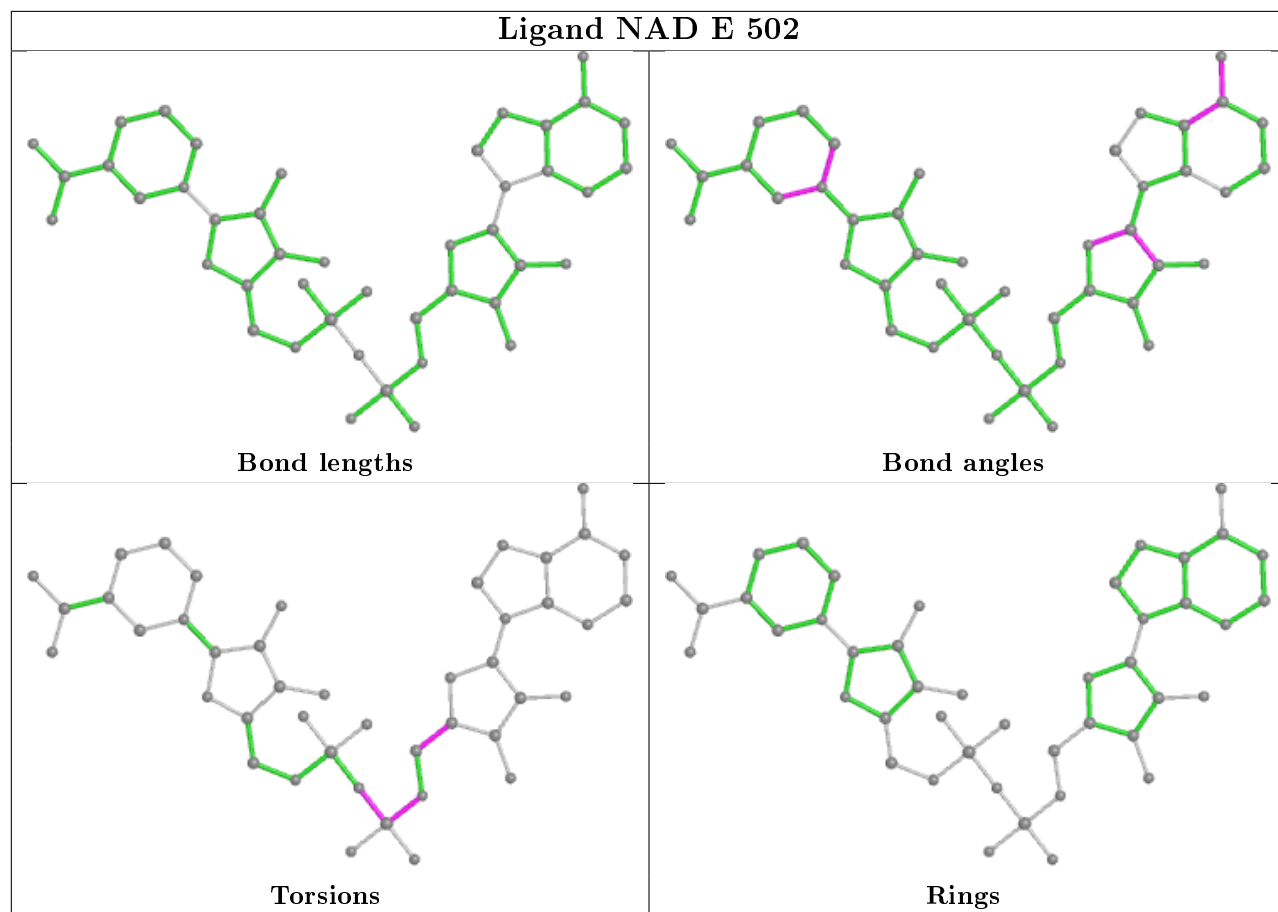
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

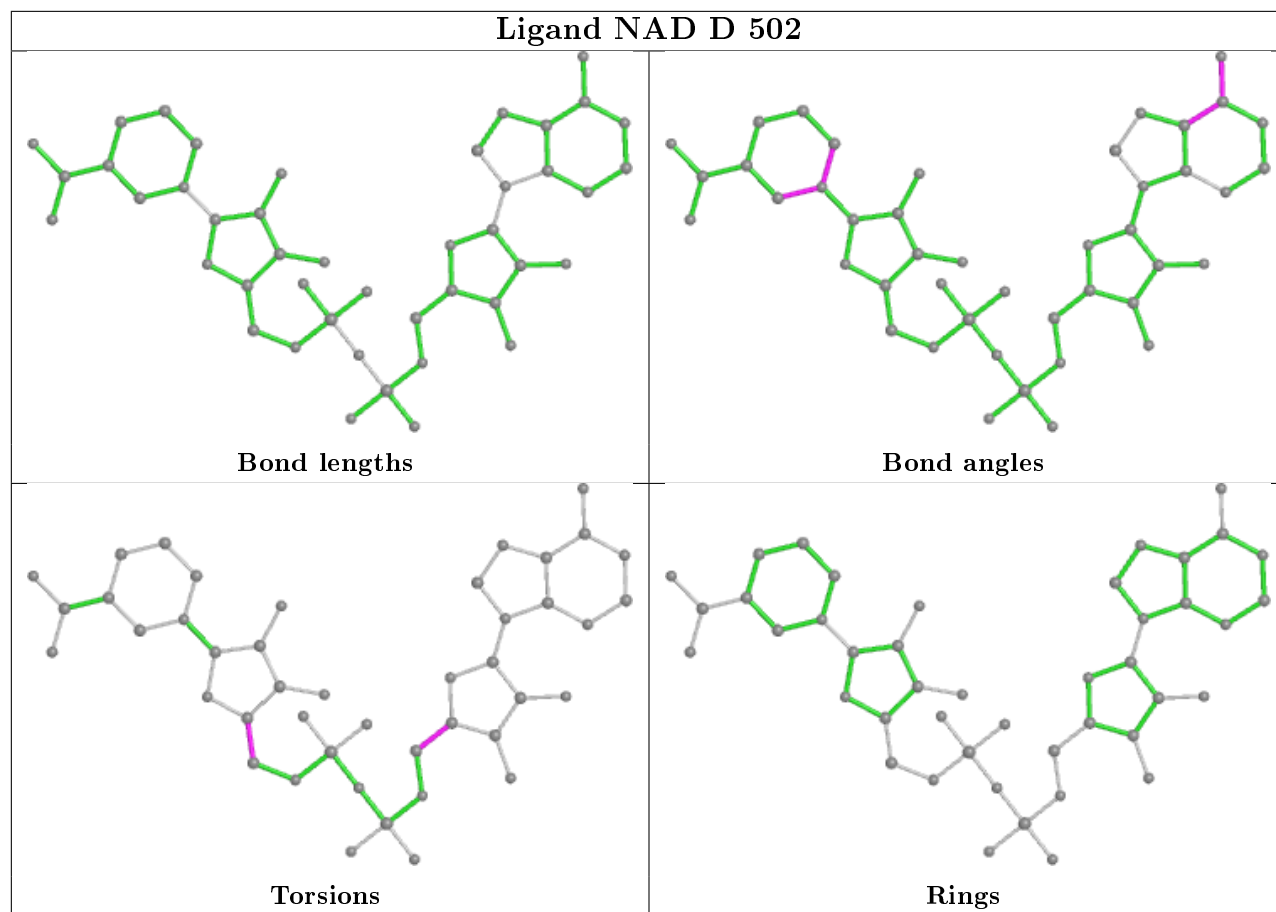












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	409/414 (98%)	-0.02	0 100 100	23, 36, 62, 95	0
1	B	406/414 (98%)	-0.08	3 (0%) 87 87	24, 42, 85, 127	0
1	C	407/414 (98%)	0.44	33 (8%) 12 11	25, 54, 120, 150	0
1	D	407/414 (98%)	0.25	18 (4%) 34 33	25, 45, 94, 128	0
1	E	406/414 (98%)	0.88	79 (19%) 1 0	28, 57, 158, 202	0
1	F	410/414 (99%)	-0.08	2 (0%) 91 91	26, 43, 69, 103	0
All	All	2445/2484 (98%)	0.23	135 (5%) 25 24	23, 44, 114, 202	0

All (135) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	295	ASN	6.1
1	E	328	VAL	6.1
1	E	246	ASP	6.1
1	E	296	ARG	6.0
1	E	318	ASP	6.0
1	E	322	ILE	5.9
1	C	267	ASP	5.7
1	E	250	ILE	5.2
1	E	294	ILE	4.9
1	E	325	LYS	4.8
1	E	283	ASP	4.8
1	E	278	LEU	4.7
1	C	296	ARG	4.7
1	E	316	ASP	4.6
1	E	241	ALA	4.5
1	E	327	GLY	4.5
1	C	274	PRO	4.5
1	D	325	LYS	4.5
1	E	301	GLU	4.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	301	GLU	4.4
1	D	296	ARG	4.4
1	D	297	GLU	4.3
1	E	267	ASP	4.3
1	E	300	ASN	4.3
1	D	298	ASN	4.3
1	C	277	ILE	4.2
1	E	303	LYS	4.2
1	E	272	ILE	4.1
1	E	271	PRO	4.1
1	C	293	VAL	4.0
1	D	8	ASN	4.0
1	E	269	ALA	3.9
1	E	317	PRO	3.9
1	C	258	LYS	3.9
1	E	307	ILE	3.9
1	E	291	GLY	3.8
1	C	321	GLU	3.8
1	C	247	GLY	3.7
1	E	320	ASP	3.7
1	E	329	VAL	3.7
1	E	290	LEU	3.7
1	E	321	GLU	3.7
1	E	279	VAL	3.7
1	D	322	ILE	3.6
1	D	318	ASP	3.6
1	E	314	PRO	3.5
1	D	301	GLU	3.5
1	E	297	GLU	3.4
1	E	242	ILE	3.4
1	E	276	SER	3.4
1	E	311	ALA	3.4
1	C	261	ARG	3.4
1	E	238	ILE	3.4
1	E	274	PRO	3.4
1	C	206	GLY	3.3
1	E	302	ILE	3.3
1	E	200	HIS	3.3
1	C	249	ASP	3.2
1	E	326	LYS	3.2
1	D	261	ARG	3.2
1	D	7	THR	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	E	258	LYS	3.2
1	E	266	PHE	3.2
1	E	292	GLY	3.2
1	E	263	VAL	3.1
1	E	252	ALA	3.1
1	C	318	ASP	3.1
1	E	265	GLY	3.0
1	C	316	ASP	3.0
1	E	324	SER	3.0
1	E	247	GLY	3.0
1	C	304	ALA	3.0
1	E	284	ILE	3.0
1	C	272	ILE	2.9
1	E	330	ILE	2.9
1	E	323	LEU	2.9
1	C	242	ILE	2.9
1	E	225	ILE	2.8
1	E	260	HIS	2.8
1	C	298	ASN	2.8
1	E	289	ALA	2.8
1	E	304	ALA	2.8
1	E	281	ASP	2.8
1	E	299	ALA	2.7
1	E	282	CYS	2.7
1	C	205	SER	2.7
1	C	322	ILE	2.6
1	C	16	ARG	2.6
1	E	285	LEU	2.6
1	D	319	ALA	2.6
1	C	323	LEU	2.6
1	C	284	ILE	2.6
1	D	302	ILE	2.5
1	D	9	ARG	2.5
1	C	297	GLU	2.5
1	E	298	ASN	2.5
1	E	270	ASP	2.5
1	E	9	ARG	2.5
1	E	205	SER	2.5
1	E	268	GLY	2.5
1	C	300	ASN	2.4
1	D	295	ASN	2.4
1	E	248	ILE	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	262	GLY	2.4
1	D	299	ALA	2.4
1	E	235	VAL	2.4
1	C	214	PHE	2.4
1	C	235	VAL	2.4
1	E	203	THR	2.4
1	F	261	ARG	2.4
1	E	237	ASP	2.4
1	E	293	VAL	2.3
1	C	4	LEU	2.3
1	E	201	GLY	2.3
1	E	8	ASN	2.3
1	E	315	THR	2.3
1	E	305	LYS	2.3
1	D	327	GLY	2.3
1	C	227	GLU	2.2
1	B	6	ALA	2.2
1	E	206	GLY	2.2
1	D	324	SER	2.2
1	C	290	LEU	2.2
1	D	12	LYS	2.2
1	E	199	GLU	2.2
1	E	229	GLY	2.1
1	E	286	VAL	2.1
1	E	239	THR	2.1
1	F	245	LYS	2.1
1	B	267	ASP	2.1
1	C	269	ALA	2.0
1	E	309	GLU	2.0
1	B	261	ARG	2.0
1	E	387	ASP	2.0
1	C	204	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates ⓘ

There are no monosaccharides 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.

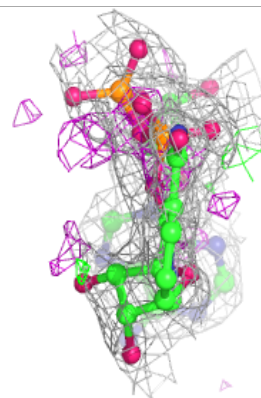
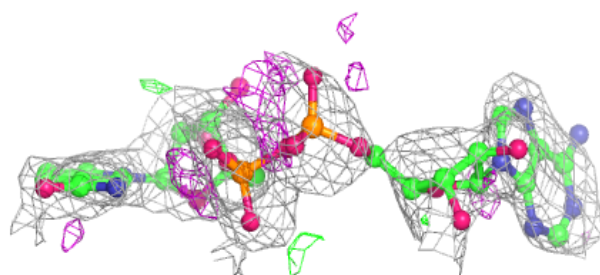
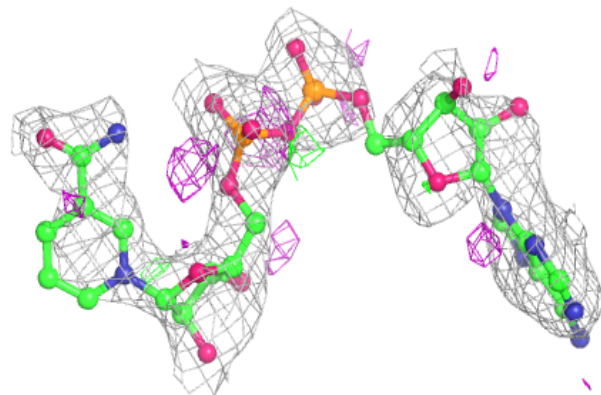
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MRD	C	504	8/8	0.78	0.23	70,91,93,95	0
6	EDO	D	501	4/4	0.80	0.23	71,74,78,80	0
2	NAD	E	502	44/44	0.84	0.21	88,110,115,116	0
7	AKG	F	502	10/10	0.84	0.23	58,68,76,82	0
3	MPD	D	506	8/8	0.84	0.31	58,73,80,85	0
3	MPD	B	504	8/8	0.84	0.20	73,78,82,85	0
3	MPD	C	503	8/8	0.85	0.30	74,79,84,85	0
3	MPD	D	505	8/8	0.86	0.39	69,79,87,88	0
3	MPD	A	505	8/8	0.86	0.19	46,64,71,78	0
5	MRD	B	505	8/8	0.86	0.19	66,83,92,95	0
5	MRD	A	508	8/8	0.87	0.28	84,91,98,101	0
3	MPD	C	502	8/8	0.87	0.16	54,60,69,72	0
5	MRD	E	505	8/8	0.87	0.26	92,95,99,104	0
3	MPD	B	502	8/8	0.87	0.25	50,63,78,80	0
5	MRD	D	508	8/8	0.89	0.24	67,77,81,90	0
3	MPD	A	503	8/8	0.89	0.21	59,66,70,70	0
3	MPD	A	504	8/8	0.90	0.15	57,61,64,74	0
3	MPD	E	501	8/8	0.91	0.22	74,79,81,82	0
6	EDO	F	503	4/4	0.91	0.19	64,64,67,67	0
3	MPD	B	503	8/8	0.91	0.14	50,59,62,68	0
2	NAD	C	501	44/44	0.91	0.17	62,98,109,110	0
3	MPD	A	502	8/8	0.92	0.20	60,65,70,76	0
3	MPD	D	504	8/8	0.93	0.19	36,48,59,65	0
2	NAD	B	501	44/44	0.94	0.14	39,63,75,81	0
3	MPD	D	503	8/8	0.94	0.14	52,61,65,66	0
3	MPD	E	503	8/8	0.94	0.19	54,62,65,66	0
2	NAD	D	502	44/44	0.96	0.14	41,62,71,72	0
2	NAD	A	501	44/44	0.97	0.11	32,42,54,64	0
2	NAD	F	501	44/44	0.97	0.12	35,44,55,61	0
4	K	E	504	1/1	0.98	0.10	43,43,43,43	0
4	K	E	506	1/1	0.98	0.11	40,40,40,40	0
4	K	A	506	1/1	0.99	0.15	31,31,31,31	0
4	K	C	505	1/1	0.99	0.09	45,45,45,45	0
4	K	D	507	1/1	0.99	0.10	38,38,38,38	0
4	K	A	507	1/1	0.99	0.13	37,37,37,37	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.

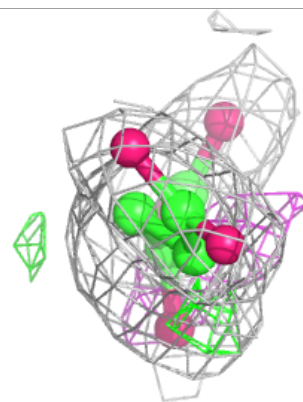
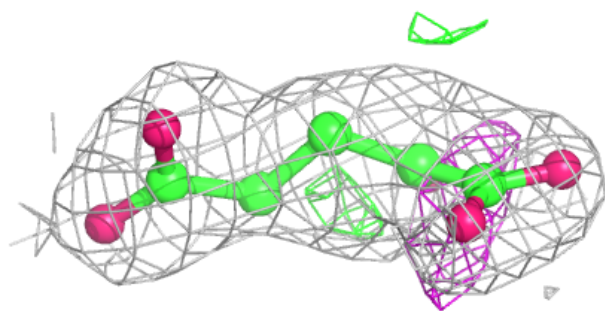
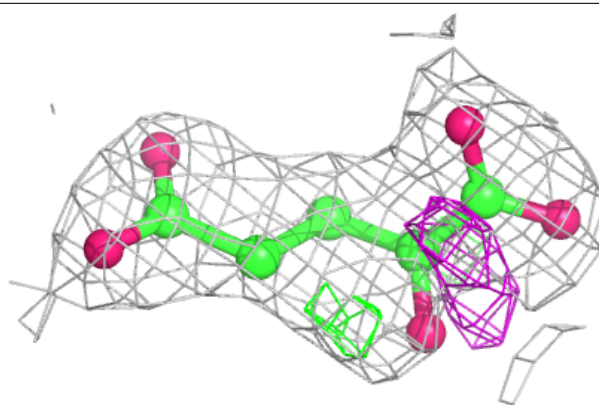
Electron density around NAD E 502:

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

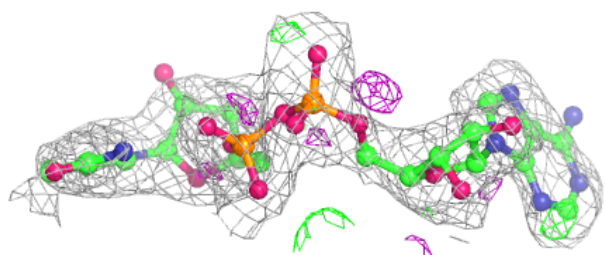
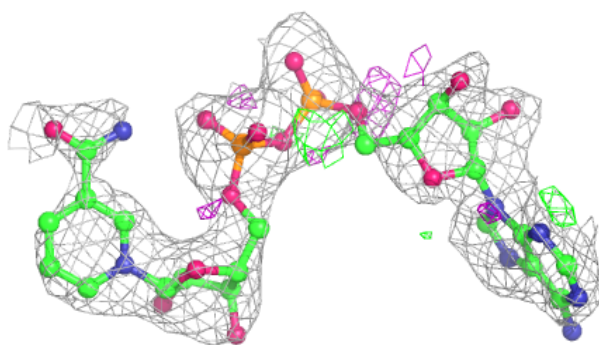


Electron density around AKG F 502:

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

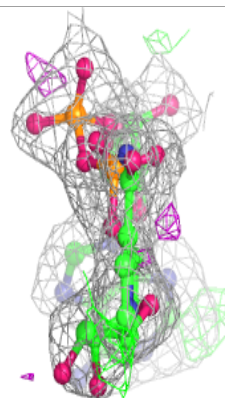
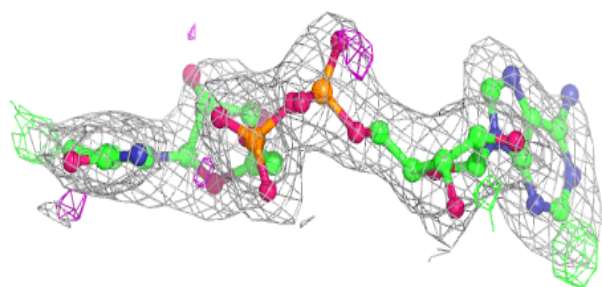
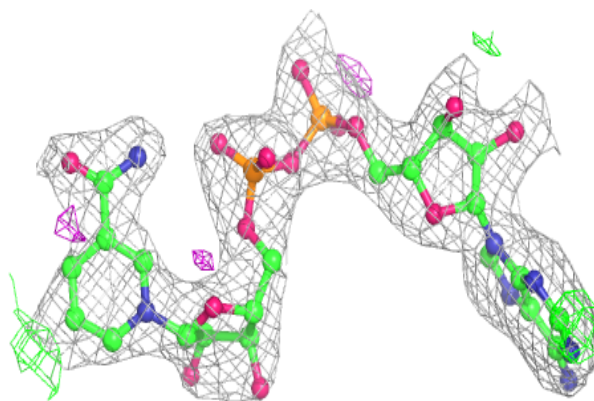
**Electron density around NAD C 501:**

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

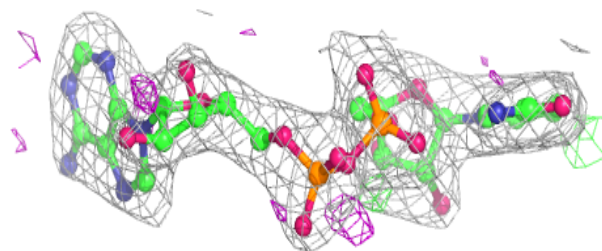
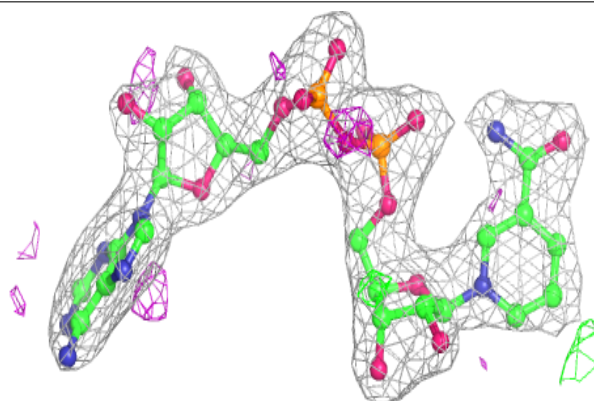


Electron density around NAD B 501:

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

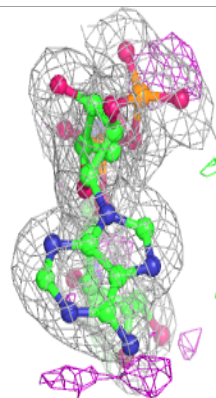
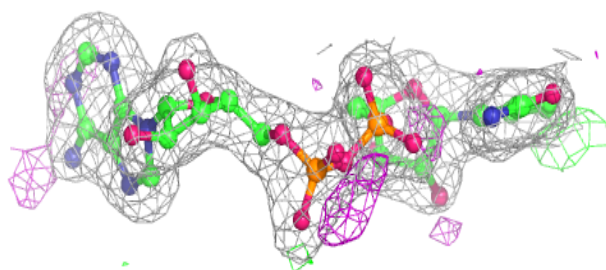
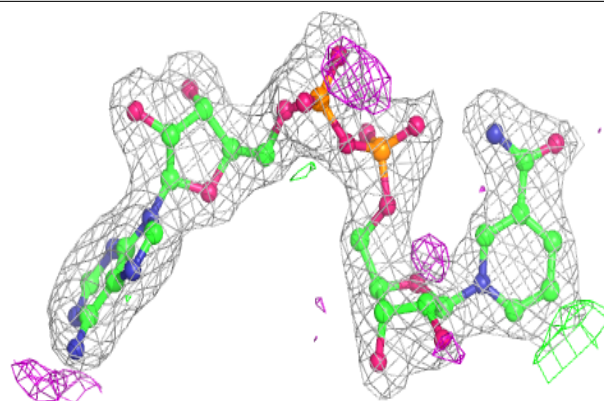
**Electron density around NAD D 502:**

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

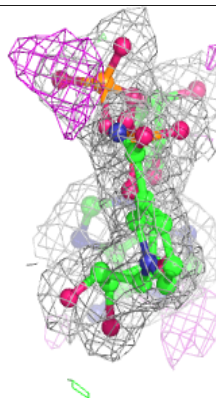
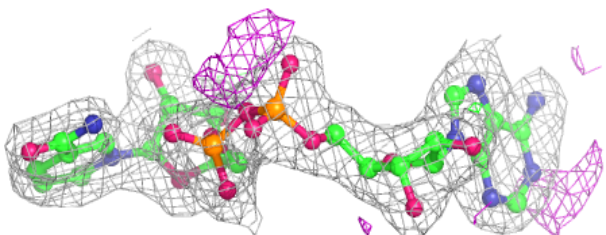
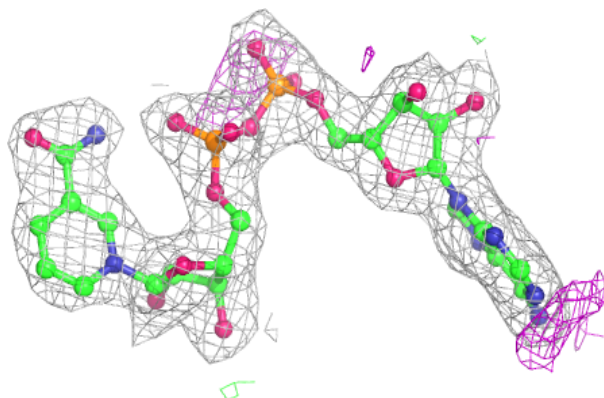


Electron density around NAD A 501:

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

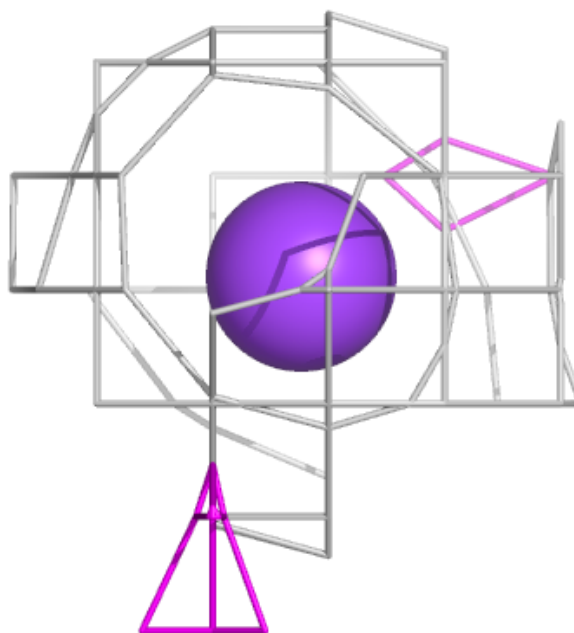
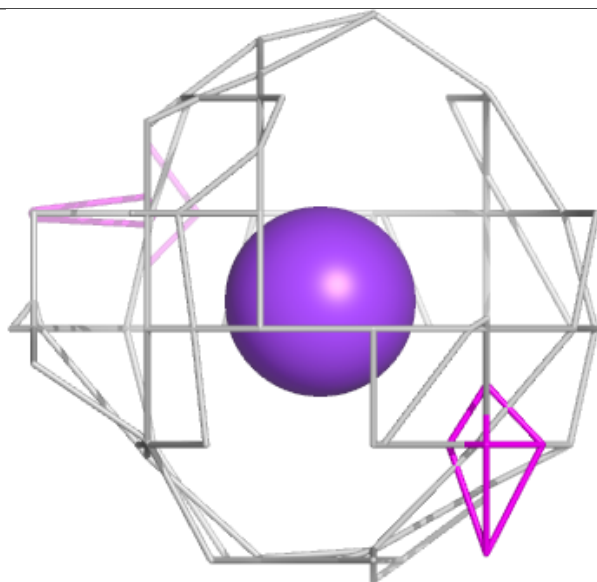
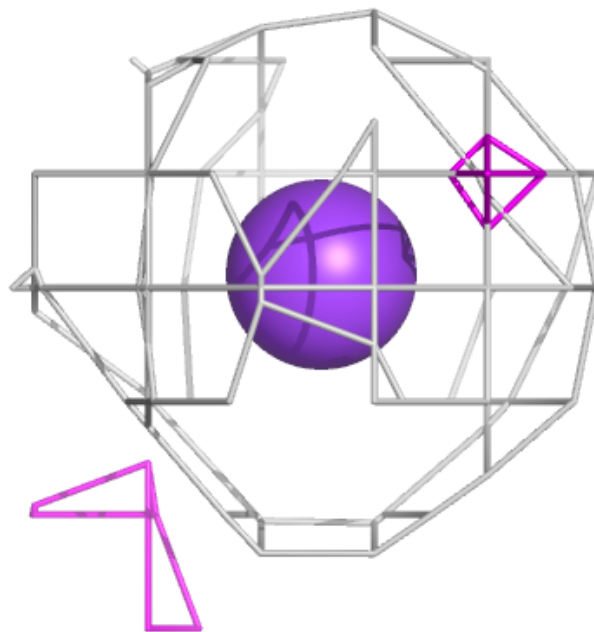
**Electron density around NAD F 501:**

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



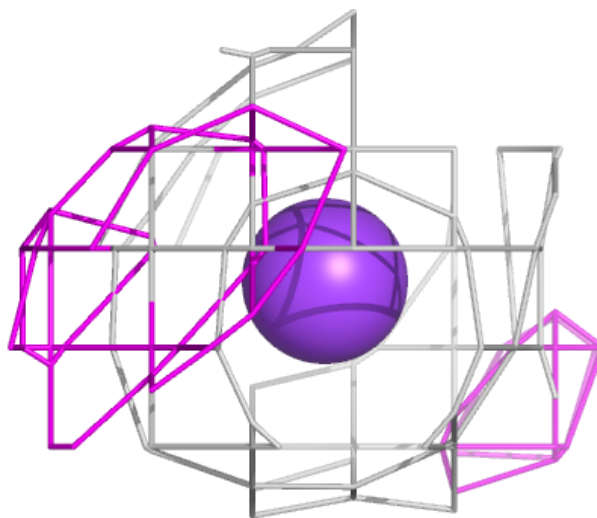
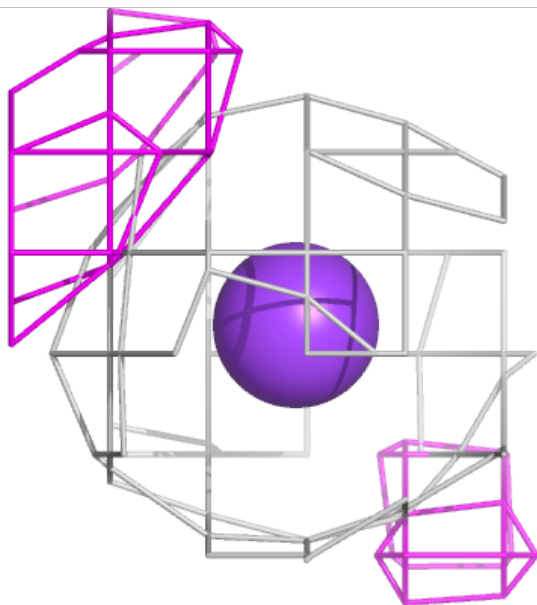
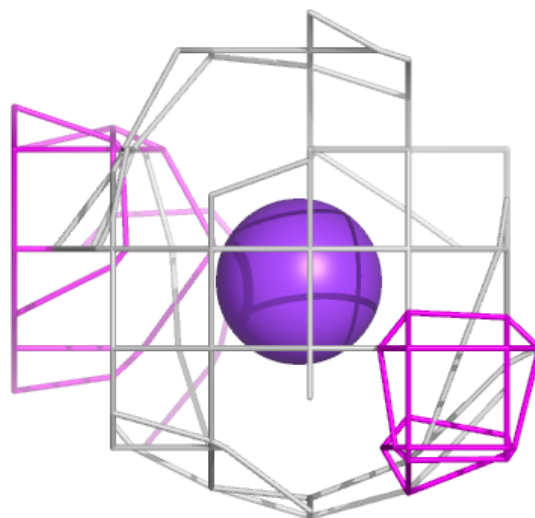
Electron density around K E 504:

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



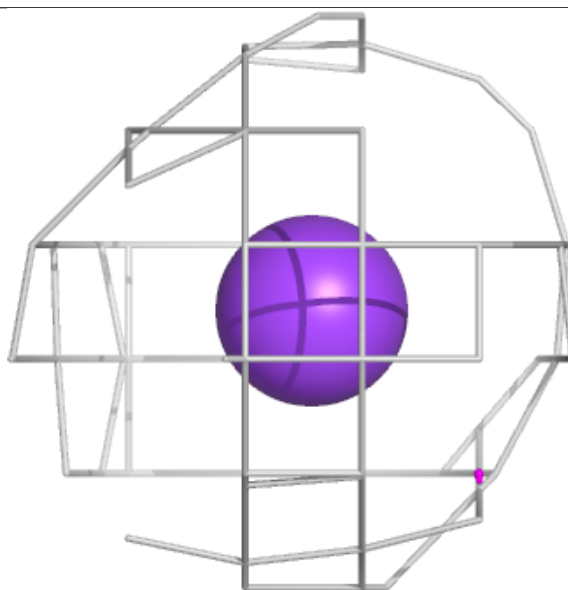
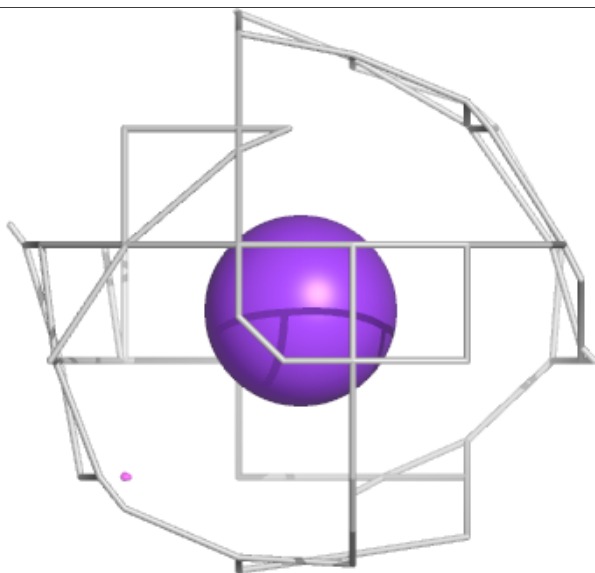
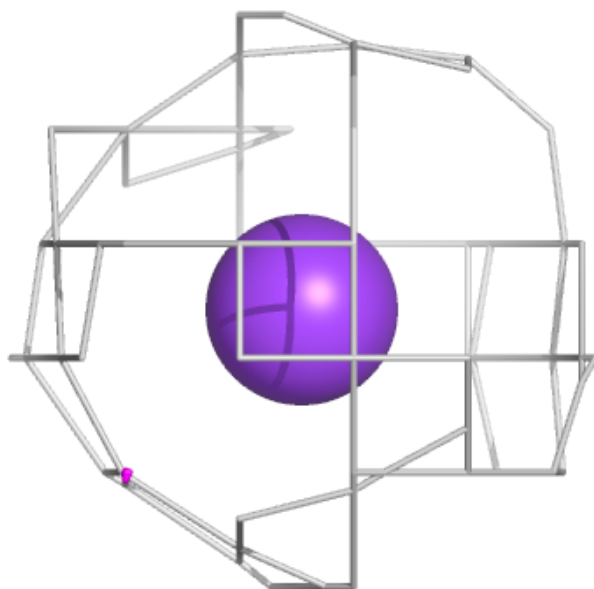
Electron density around K E 506:

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



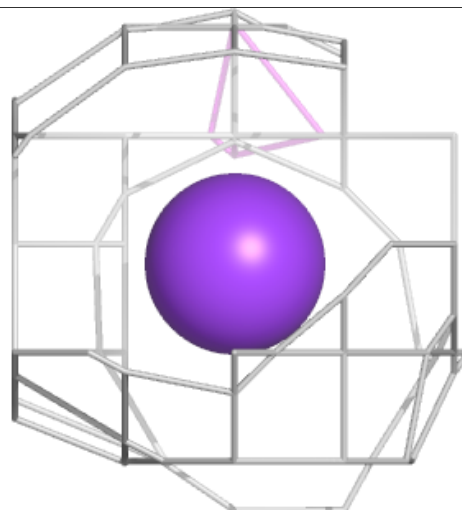
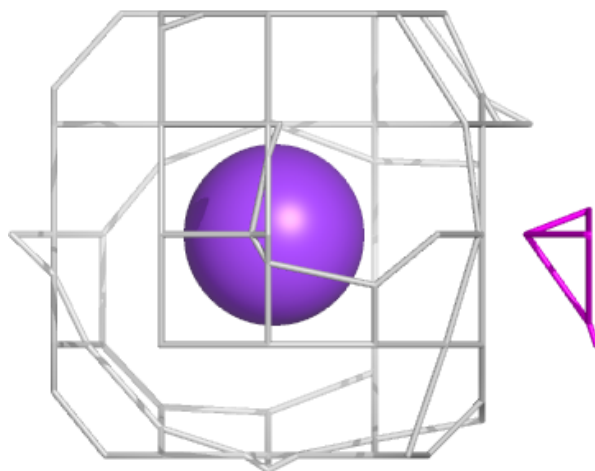
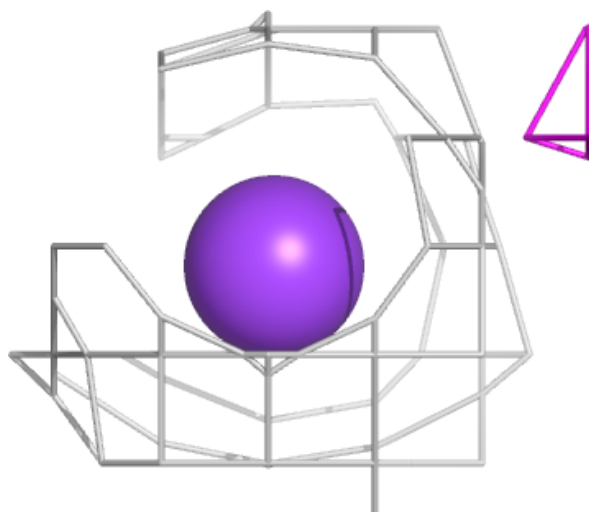
Electron density around K A 506:

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



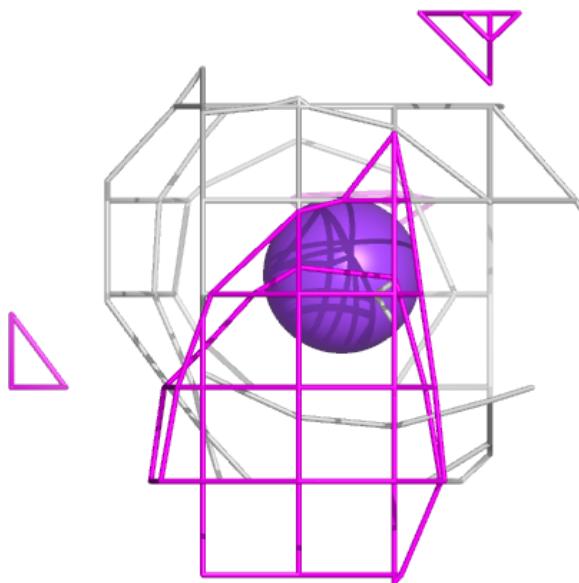
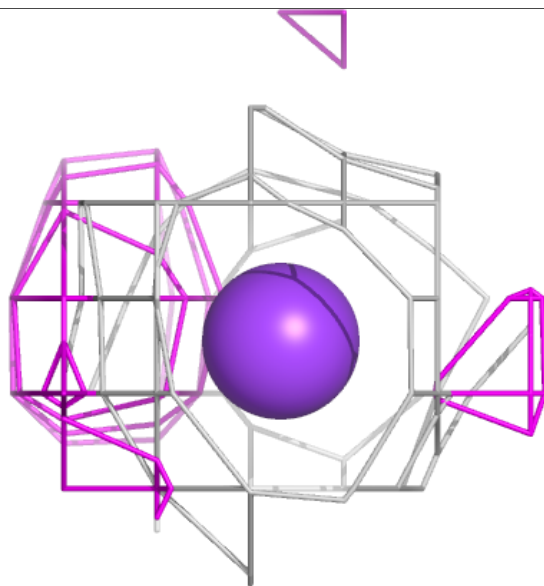
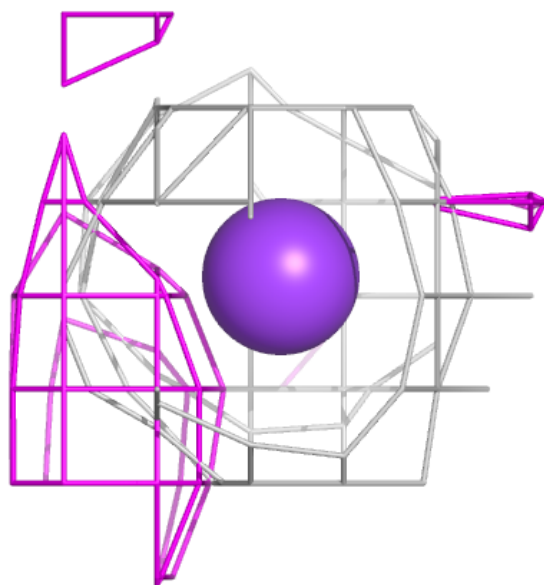
Electron density around K C 505:

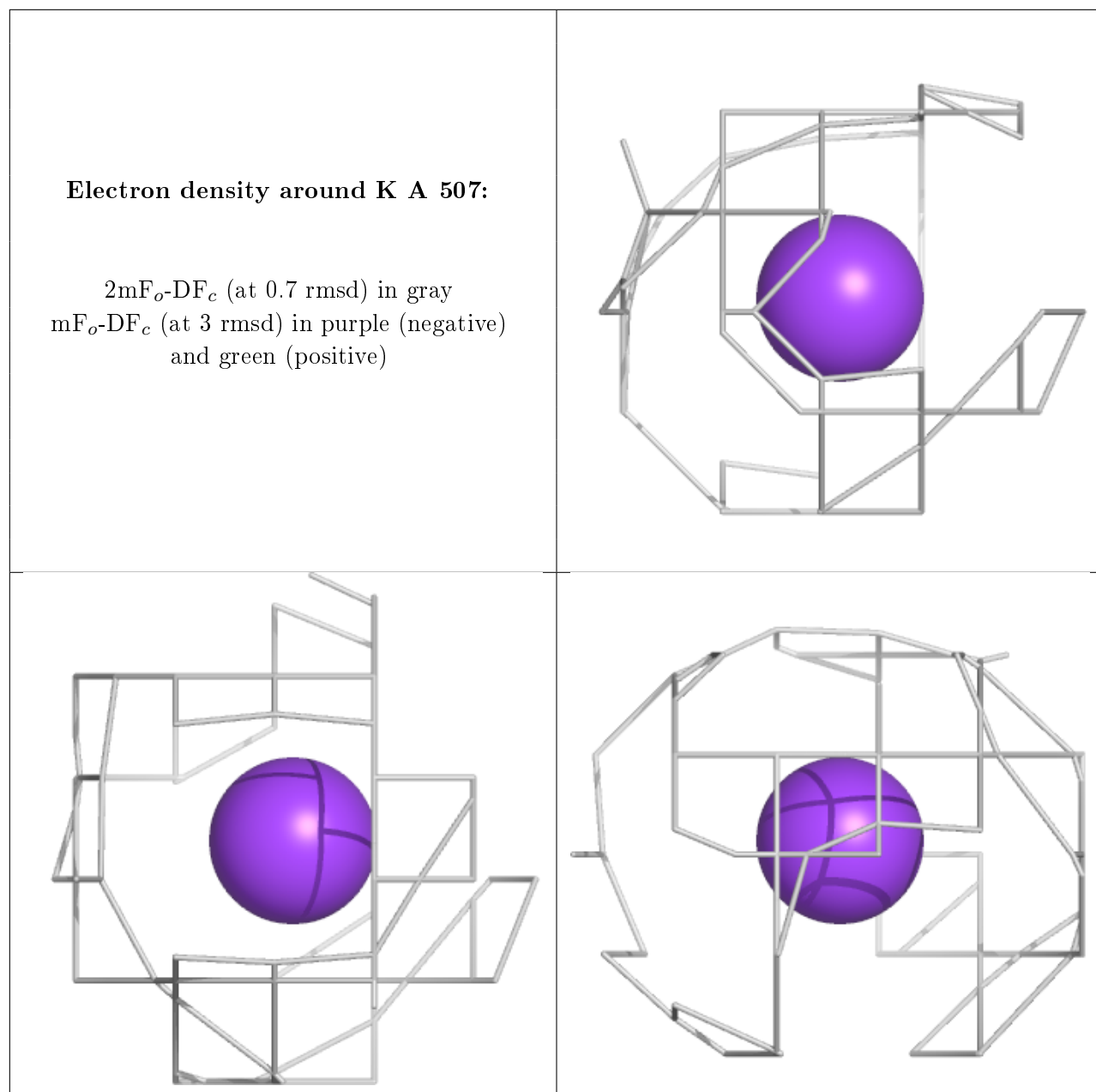
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around K D 507:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.