



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 11:26 AM UTC

PDB ID : 4J9U / pdb_00004j9u
Title : Crystal Structure of the TrkH/TrkA potassium transport complex
Authors : Cao, Y.; Jin, X.; Huang, H.; Levin, E.J.; Zhou, M.; New York Consortium on Membrane Protein Structure (NYCOMPS)
Deposited on : 2013-02-17
Resolution : 3.80 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

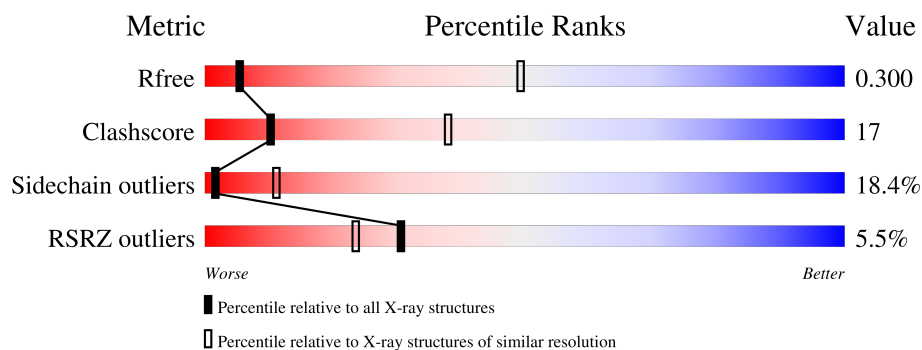
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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.



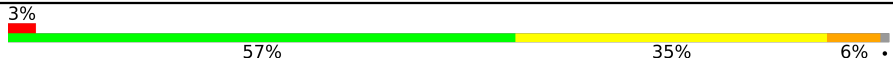
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

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	485	6% 49% 39% 7% 5%
1	B	485	6% 49% 39% 7% 5%
1	C	485	7% 50% 39% 6% 5%
1	D	485	6% 50% 39% 6% 5%
2	E	458	4% 57% 35% 7% .
2	F	458	5% 55% 35% 7% .

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Mol	Chain	Length	Quality of chain
2	G	458	
2	H	458	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	TBR	A	501	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 28567 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.

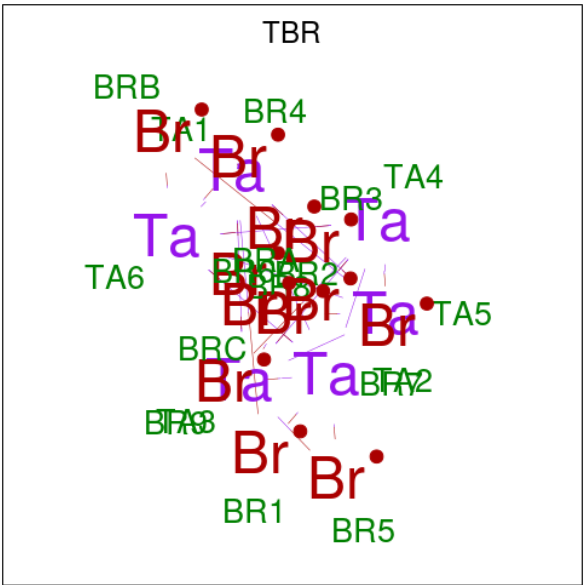
- Molecule 1 is a protein called Trk system potassium uptake protein TrkH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	462	Total	C	N	O	S	0	0	0
			3569	2389	564	598	18			
1	B	462	Total	C	N	O	S	0	0	0
			3569	2389	564	598	18			
1	C	462	Total	C	N	O	S	0	0	0
			3569	2389	564	598	18			
1	D	462	Total	C	N	O	S	0	0	0
			3569	2389	564	598	18			

- Molecule 2 is a protein called Potassium uptake protein TrkA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	451	Total	C	N	O	S	0	0	0
			3454	2162	611	669	12			
2	F	444	Total	C	N	O	S	0	0	0
			3410	2138	600	660	12			
2	G	452	Total	C	N	O	S	0	0	0
			3468	2174	612	670	12			
2	H	450	Total	C	N	O	S	0	0	0
			3455	2165	610	668	12			

- Molecule 3 is HEXATANTALUM DODECABROMIDE (CCD ID: TBR) (formula: Br₁₂Ta₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Br	Ta	0	0
			18	12	6		
3	A	1	Total	Br	Ta	0	0
			18	12	6		
3	A	1	Total	Br	Ta	0	0
			18	12	6		
3	B	1	Total	Br	Ta	0	0
			18	12	6		
3	B	1	Total	Br	Ta	0	0
			18	12	6		
3	C	1	Total	Br	Ta	0	0
			18	12	6		
3	C	1	Total	Br	Ta	0	0
			18	12	6		
3	D	1	Total	Br	Ta	0	0
			18	12	6		
3	D	1	Total	Br	Ta	0	0
			18	12	6		
3	D	1	Total	Br	Ta	0	0
			18	12	6		
3	E	1	Total	Br	Ta	0	0
			18	12	6		
3	E	1	Total	Br	Ta	0	0
			18	12	6		
3	F	1	Total	Br	Ta	0	0
			18	12	6		
3	F	1	Total	Br	Ta	0	0
			18	12	6		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	G	1	Total 18	Br 12	Ta 6	0	0
3	G	1	Total 18	Br 12	Ta 6	0	0
3	H	1	Total 18	Br 12	Ta 6	0	0
3	H	1	Total 18	Br 12	Ta 6	0	0

- | Mol | Chain | Residues | Atoms | ZeroOcc | AltConf |
|-----|-------|----------|----------------|---------|---------|
| 4 | A | 1 | Total K
1 1 | 0 | 0 |
| 4 | B | 1 | Total K
1 1 | 0 | 0 |
| 4 | C | 1 | Total K
1 1 | 0 | 0 |
| 4 | D | 1 | Total K
1 1 | 0 | 0 |

- # NAD

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

WORLDWIDE
PDB
PROTEIN DATA BANK

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
5	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
5	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

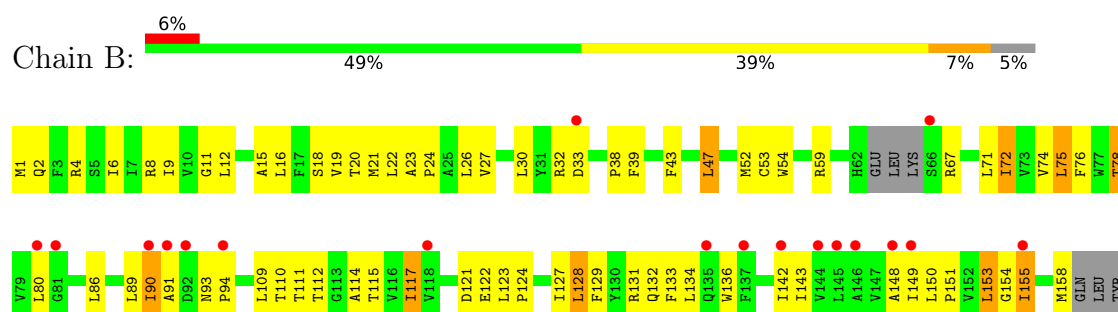
3 Residue-property plots [i](#)

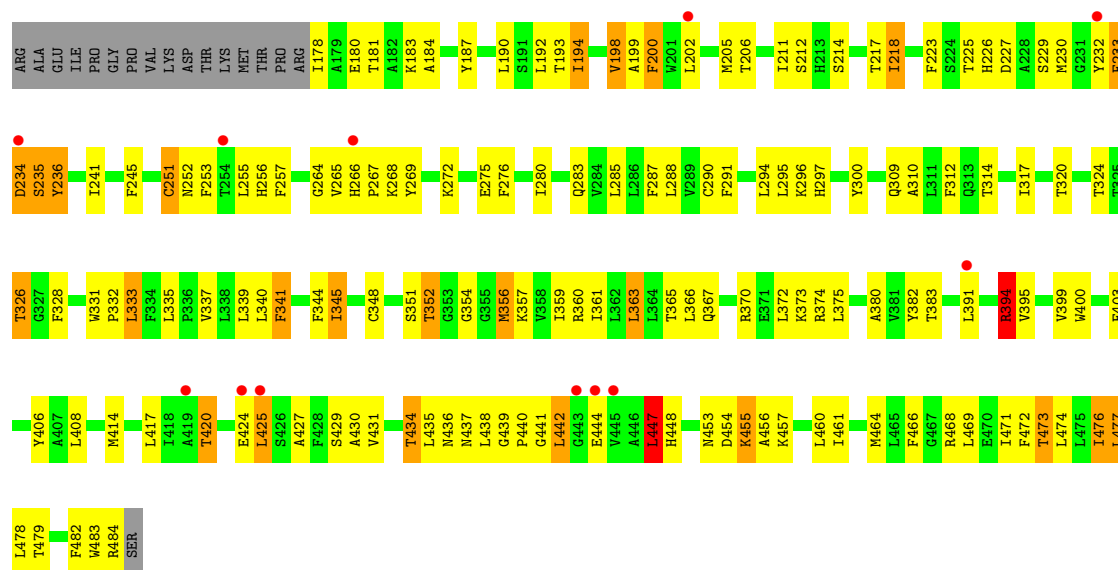
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Trk system potassium uptake protein TrkH

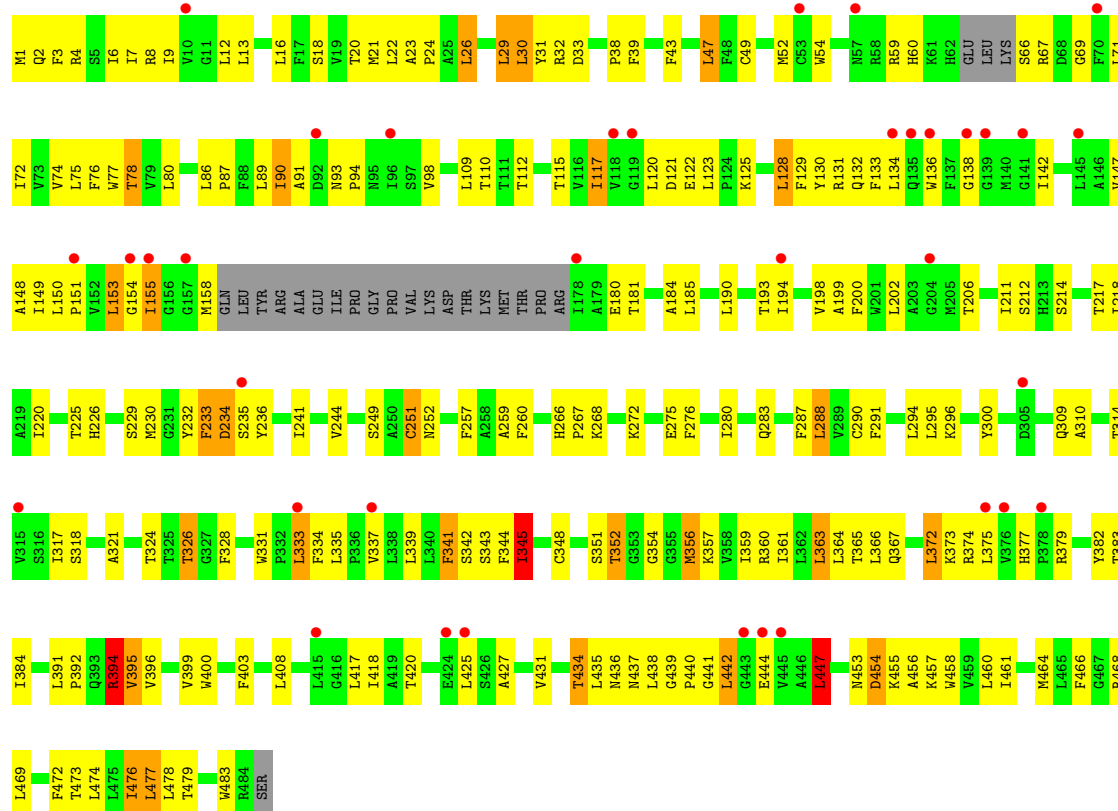


- Molecule 1: Trk system potassium uptake protein TrkH



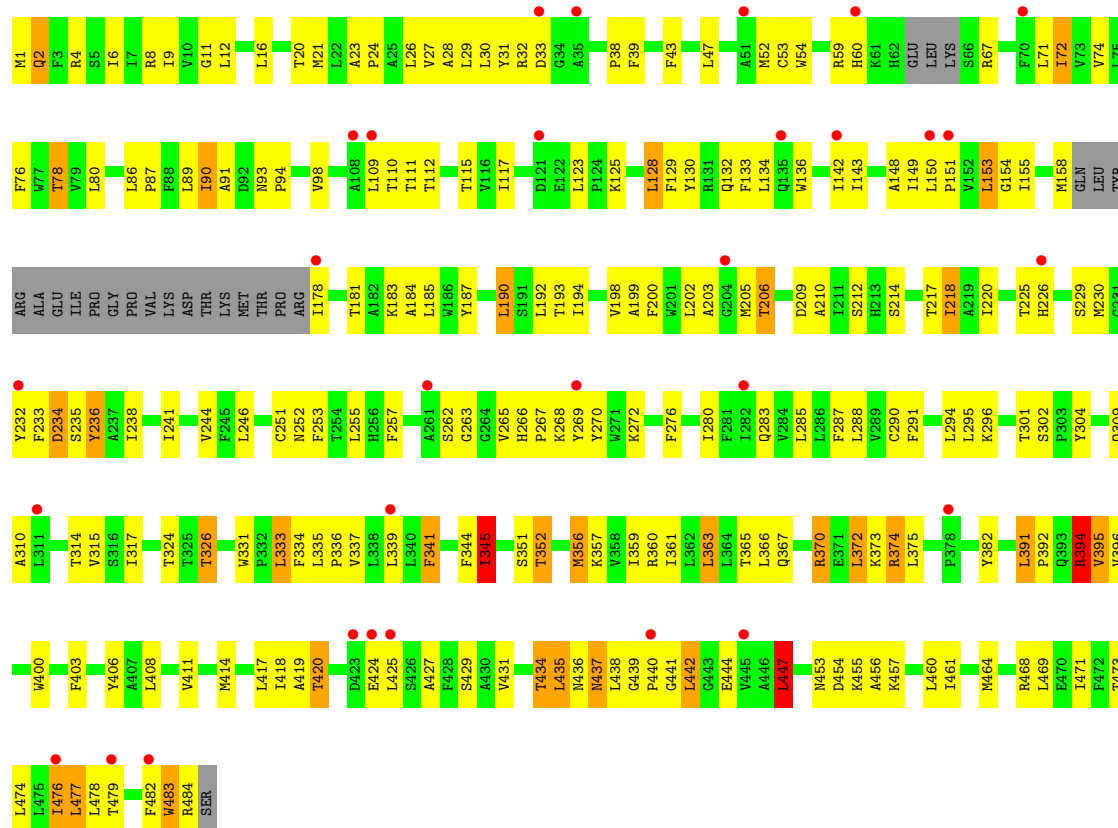


• Molecule 1: Trk system potassium uptake protein TrkH

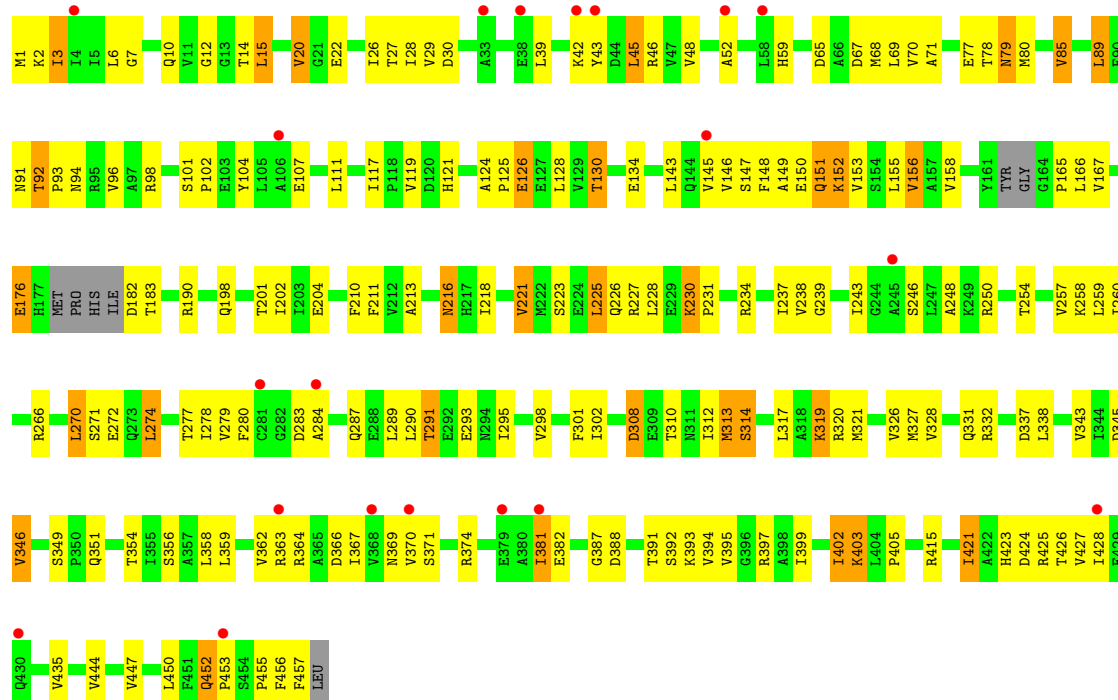


• Molecule 1: Trk system potassium uptake protein TrkH

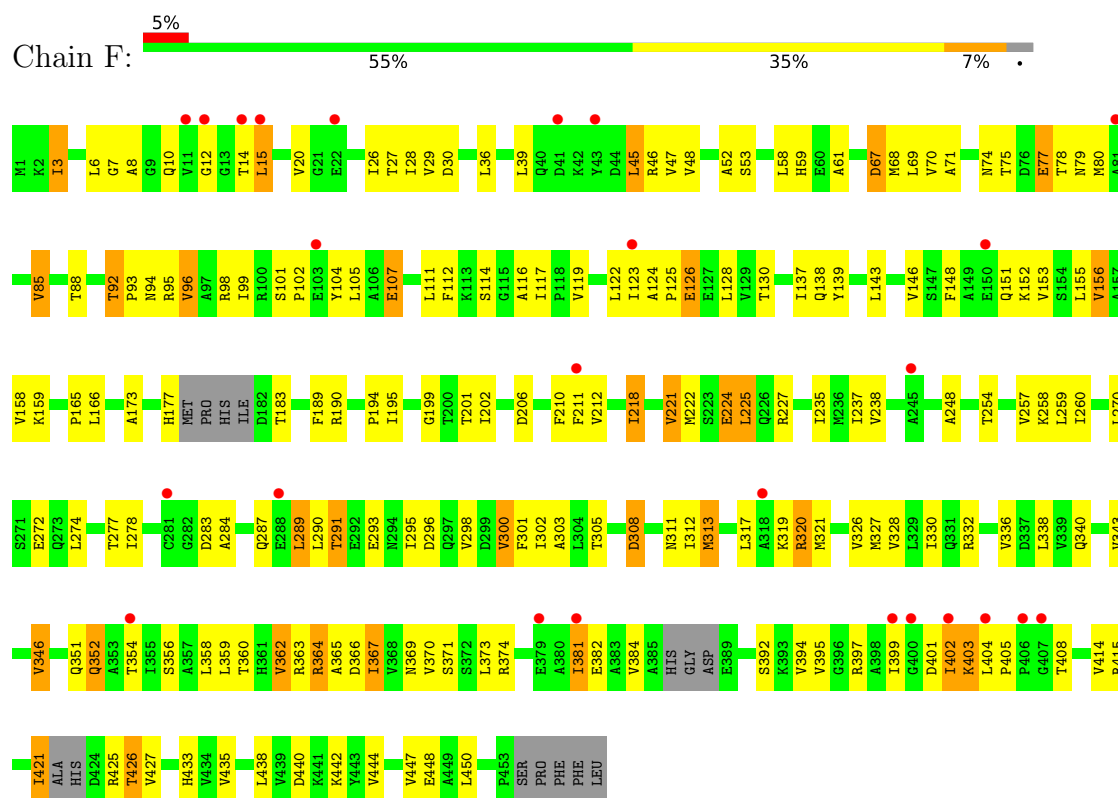




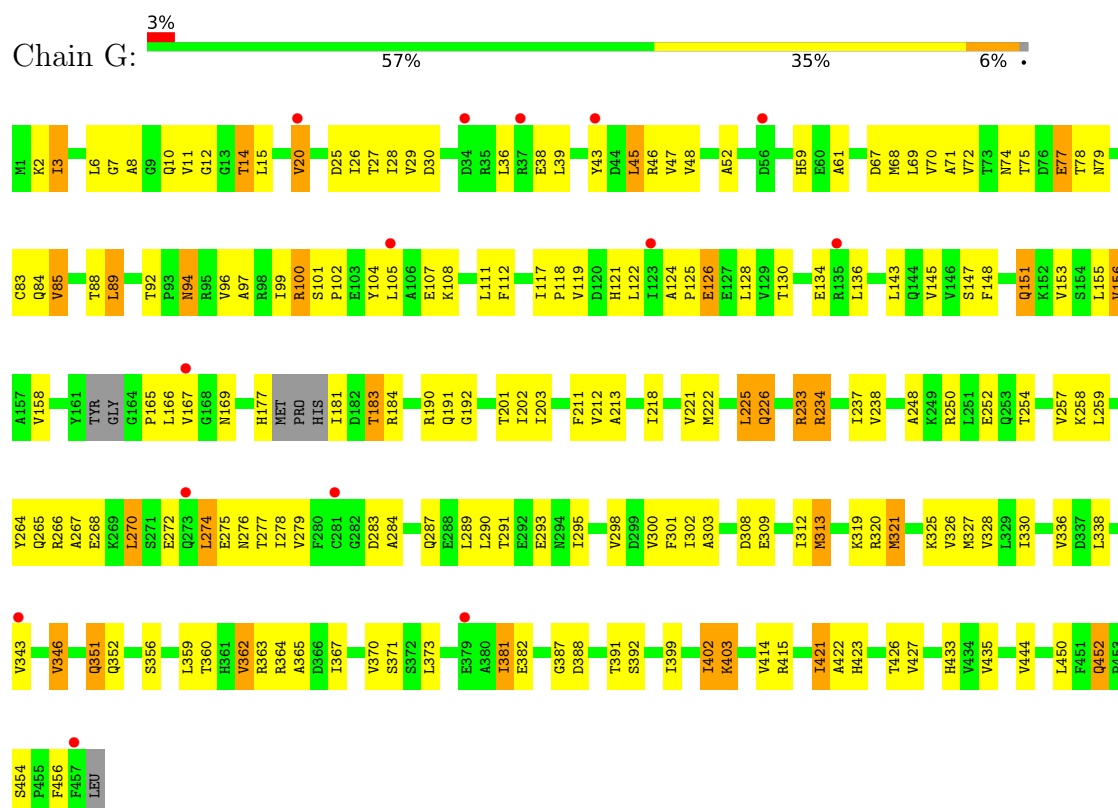
• Molecule 2: Potassium uptake protein TrkA



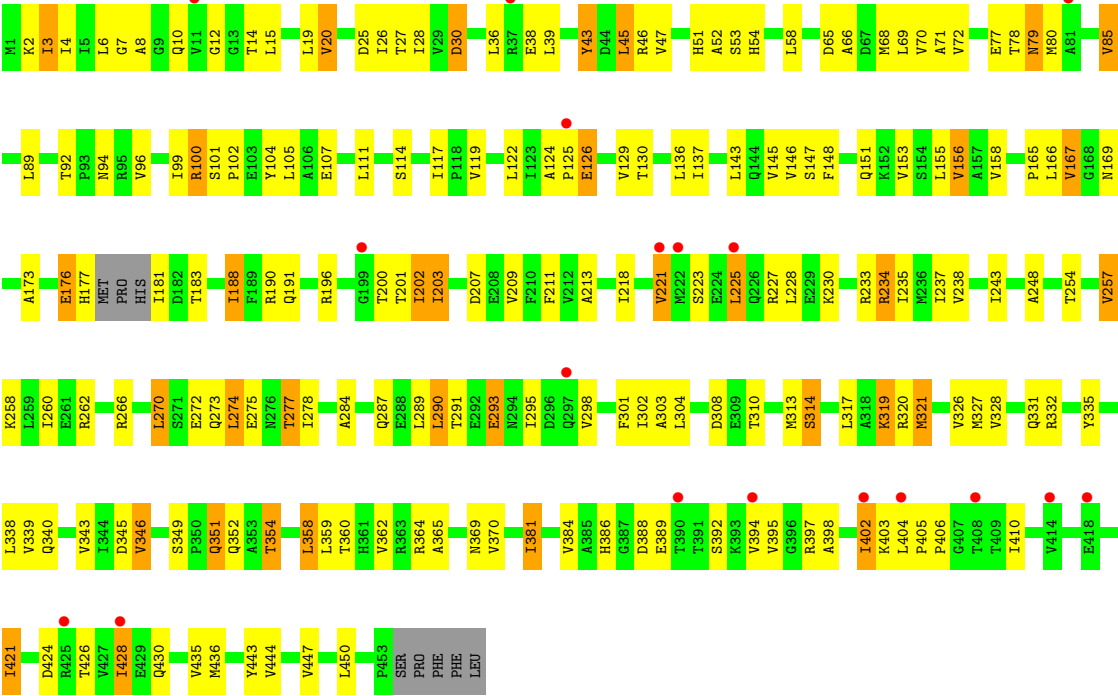
• Molecule 2: Potassium uptake protein TrkA



• Molecule 2: Potassium uptake protein TrkA



• Molecule 2: Potassium uptake protein TrkA



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	133.72Å 146.63Å 163.67Å 90.00° 99.32° 90.00°	Depositor
Resolution (Å)	49.79 – 3.80 49.79 – 3.80	Depositor EDS
% Data completeness (in resolution range)	99.5 (49.79-3.80) 99.5 (49.79-3.80)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.52 (at 3.77Å)	Xtriage
Refinement program	PHENIX 1.8.1_1168	Depositor
R, R_{free}	0.232 , 0.280 0.258 , 0.300	Depositor DCC
R_{free} test set	3130 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	118.3	Xtriage
Anisotropy	0.337	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 85.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	28567	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.89 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 7.8858e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: NAD, TBR, K

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	0.40	0/3670	0.90	6/5000 (0.1%)
1	B	0.39	0/3670	0.94	12/5000 (0.2%)
1	C	0.39	0/3670	0.91	9/5000 (0.2%)
1	D	0.38	0/3670	0.90	8/5000 (0.2%)
2	E	0.36	0/3498	0.91	8/4743 (0.2%)
2	F	0.36	0/3451	0.91	5/4676 (0.1%)
2	G	0.36	0/3513	0.89	5/4763 (0.1%)
2	H	0.38	0/3500	0.94	14/4746 (0.3%)
All	All	0.38	0/28642	0.91	67/38928 (0.2%)

There are no bond length outliers.

The worst 5 of 67 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	27	VAL	N-CA-C	-9.37	104.20	113.20
1	A	447	LEU	N-CA-C	8.19	121.32	111.82
1	D	394	ARG	N-CA-C	-7.65	104.85	114.56
1	A	155	ILE	N-CA-C	-7.64	105.24	111.81
1	D	27	VAL	N-CA-C	-7.58	105.93	113.20

There are no chirality outliers.

There are no planarity outliers.

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	3569	0	3638	149	0
1	B	3569	0	3638	136	0
1	C	3569	0	3638	136	0
1	D	3569	0	3638	135	0
2	E	3454	0	3489	110	0
2	F	3410	0	3458	118	0
2	G	3468	0	3507	119	0
2	H	3455	0	3497	112	0
3	A	54	0	0	0	0
3	B	36	0	0	0	0
3	C	36	0	0	1	0
3	D	54	0	0	2	0
3	E	36	0	0	3	0
3	F	36	0	0	2	0
3	G	36	0	0	3	0
3	H	36	0	0	3	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
5	E	44	0	26	6	0
5	F	44	0	26	3	0
5	G	44	0	26	5	0
5	H	44	0	26	5	0
All	All	28567	0	28607	980	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 17.

The worst 5 of 980 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:B:420:THR:HG21	1:B:456:ALA:HB2	1.50	0.94
2:F:3:ILE:HG22	2:F:68:MET:HB3	1.59	0.85
1:A:420:THR:HG21	1:A:456:ALA:HB2	1.58	0.85
1:B:132:GLN:HG3	1:B:212:SER:HB2	1.57	0.84
1:D:420:THR:HG21	1:D:456:ALA:HB2	1.60	0.83

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

There are no protein backbone outliers to report in this entry.

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	374/395 (95%)	296 (79%)	78 (21%)	1	7
1	B	374/395 (95%)	296 (79%)	78 (21%)	1	7
1	C	374/395 (95%)	302 (81%)	72 (19%)	1	9
1	D	374/395 (95%)	302 (81%)	72 (19%)	1	9
2	E	370/378 (98%)	307 (83%)	63 (17%)	2	13
2	F	366/378 (97%)	305 (83%)	61 (17%)	2	13
2	G	372/378 (98%)	319 (86%)	53 (14%)	3	17
2	H	370/378 (98%)	299 (81%)	71 (19%)	1	9
All	All	2974/3092 (96%)	2426 (82%)	548 (18%)	1	11

5 of 548 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	343	VAL
2	G	452	GLN
2	G	338	LEU
2	H	320	ARG
1	C	283	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
2	F	294	ASN
2	H	51	HIS
2	G	40	GLN

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Mol	Chain	Res	Type
2	G	297	GLN
2	H	191	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 26 ligands modelled in this entry, 4 are monoatomic - leaving 22 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	TBR	C	502	-	0,36,36	-	-	-		
3	TBR	C	501	-	0,36,36	-	-	-		
3	TBR	H	502	-	0,36,36	-	-	-		
3	TBR	G	503	-	0,36,36	-	-	-		
5	NAD	H	501	-	46,48,48	1.23	4 (8%)	64,73,73	1.66	11 (17%)
3	TBR	E	502	-	0,36,36	-	-	-		
3	TBR	D	501	-	0,36,36	-	-	-		
3	TBR	E	503	-	0,36,36	-	-	-		
5	NAD	G	501	-	46,48,48	1.22	5 (10%)	64,73,73	1.63	11 (17%)
3	TBR	B	501	-	0,36,36	-	-	-		
5	NAD	F	501	-	46,48,48	1.29	6 (13%)	64,73,73	1.64	8 (12%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	TBR	A	501	-	0,36,36	-	-	-		
3	TBR	F	503	-	0,36,36	-	-	-		
3	TBR	A	502	-	0,36,36	-	-	-		
3	TBR	G	502	-	0,36,36	-	-	-		
3	TBR	D	502	-	0,36,36	-	-	-		
3	TBR	A	503	-	0,36,36	-	-	-		
3	TBR	D	503	-	0,36,36	-	-	-		
3	TBR	B	502	-	0,36,36	-	-	-		
3	TBR	H	503	-	0,36,36	-	-	-		
5	NAD	E	501	-	46,48,48	1.22	4 (8%)	64,73,73	1.71	13 (20%)
3	TBR	F	502	-	0,36,36	-	-	-		

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	NAD	H	501	-	-	8/30/62/62	0/5/5/5
5	NAD	E	501	-	-	5/30/62/62	0/5/5/5
5	NAD	G	501	-	-	8/30/62/62	0/5/5/5
5	NAD	F	501	-	-	9/30/62/62	0/5/5/5

The worst 5 of 19 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	F	501	NAD	C5A-C4A	5.11	1.48	1.39
5	E	501	NAD	C5A-C4A	5.08	1.48	1.39
5	G	501	NAD	C5A-C4A	4.96	1.47	1.39
5	H	501	NAD	C5A-C4A	4.94	1.47	1.39
5	H	501	NAD	C5A-N7A	-2.97	1.33	1.39

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	501	NAD	C5A-C4A-N3A	-6.35	117.97	126.72
5	H	501	NAD	C5A-C4A-N3A	-6.26	118.10	126.72
5	G	501	NAD	C5A-C4A-N3A	-6.16	118.23	126.72
5	E	501	NAD	C5A-C4A-N3A	-6.10	118.32	126.72
5	H	501	NAD	N3A-C4A-N9A	5.37	136.31	127.17

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

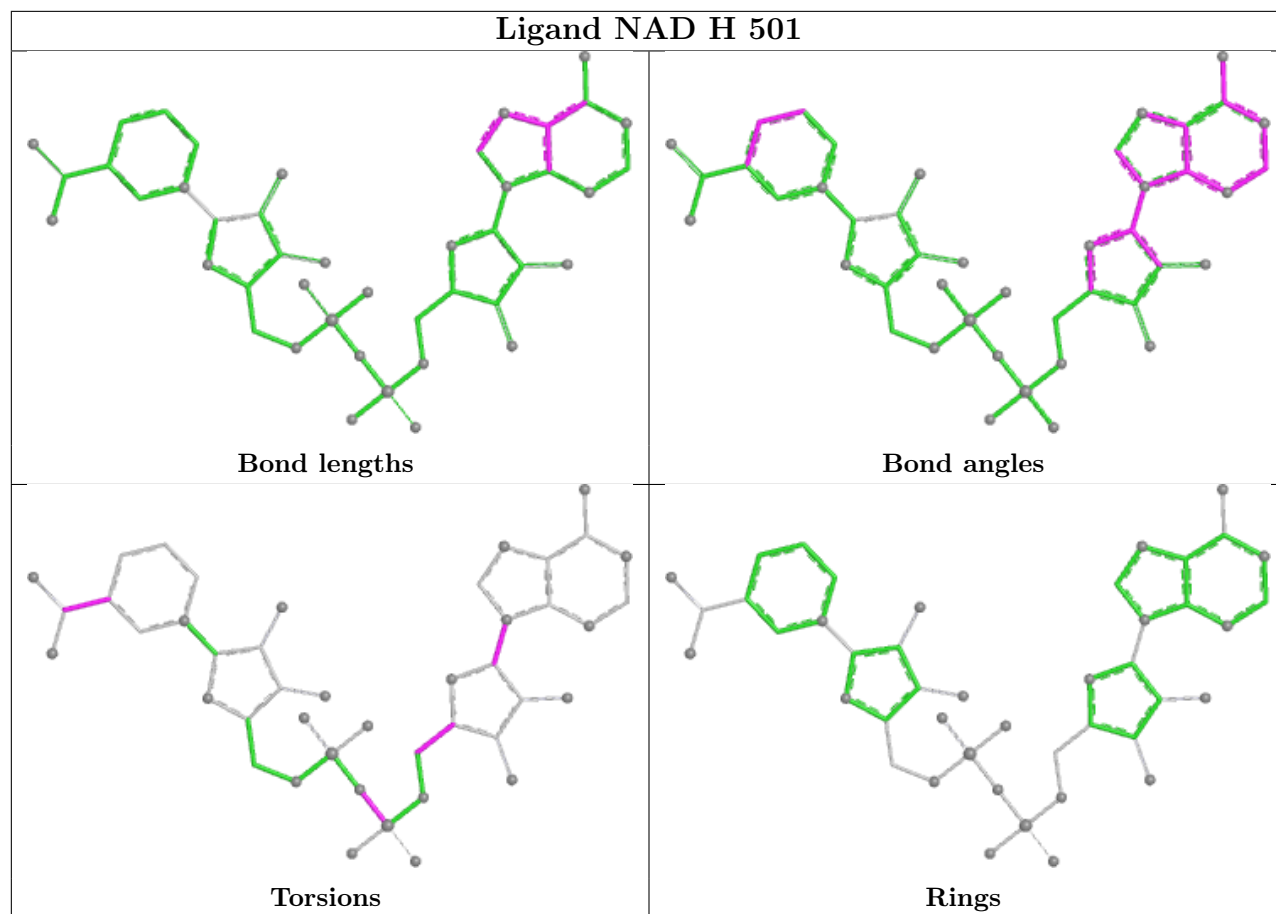
Mol	Chain	Res	Type	Atoms
5	G	501	NAD	C2N-C3N-C7N-O7N
5	G	501	NAD	C2N-C3N-C7N-N7N
5	E	501	NAD	O4B-C4B-C5B-O5B
5	G	501	NAD	C4N-C3N-C7N-N7N
5	G	501	NAD	C4N-C3N-C7N-O7N

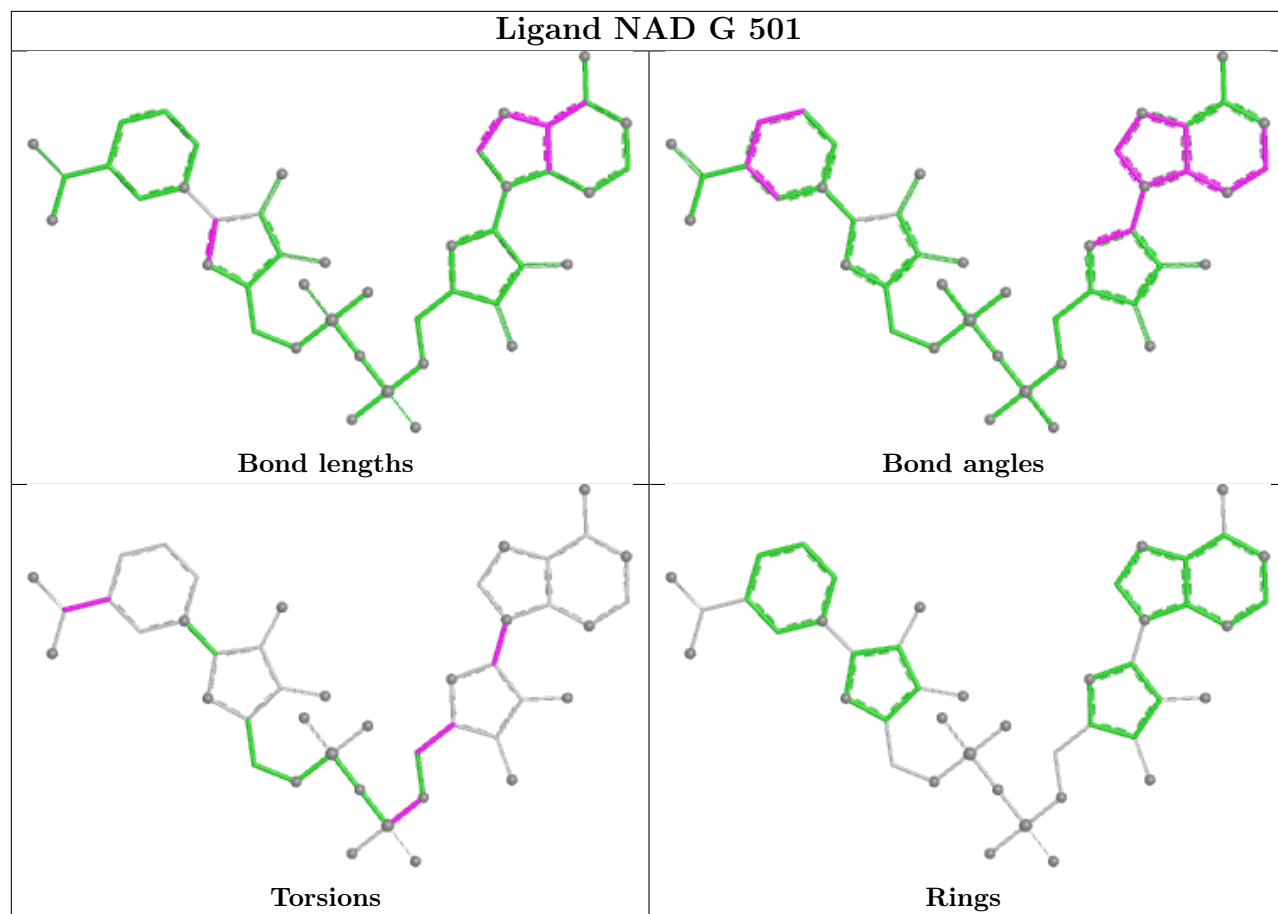
There are no ring outliers.

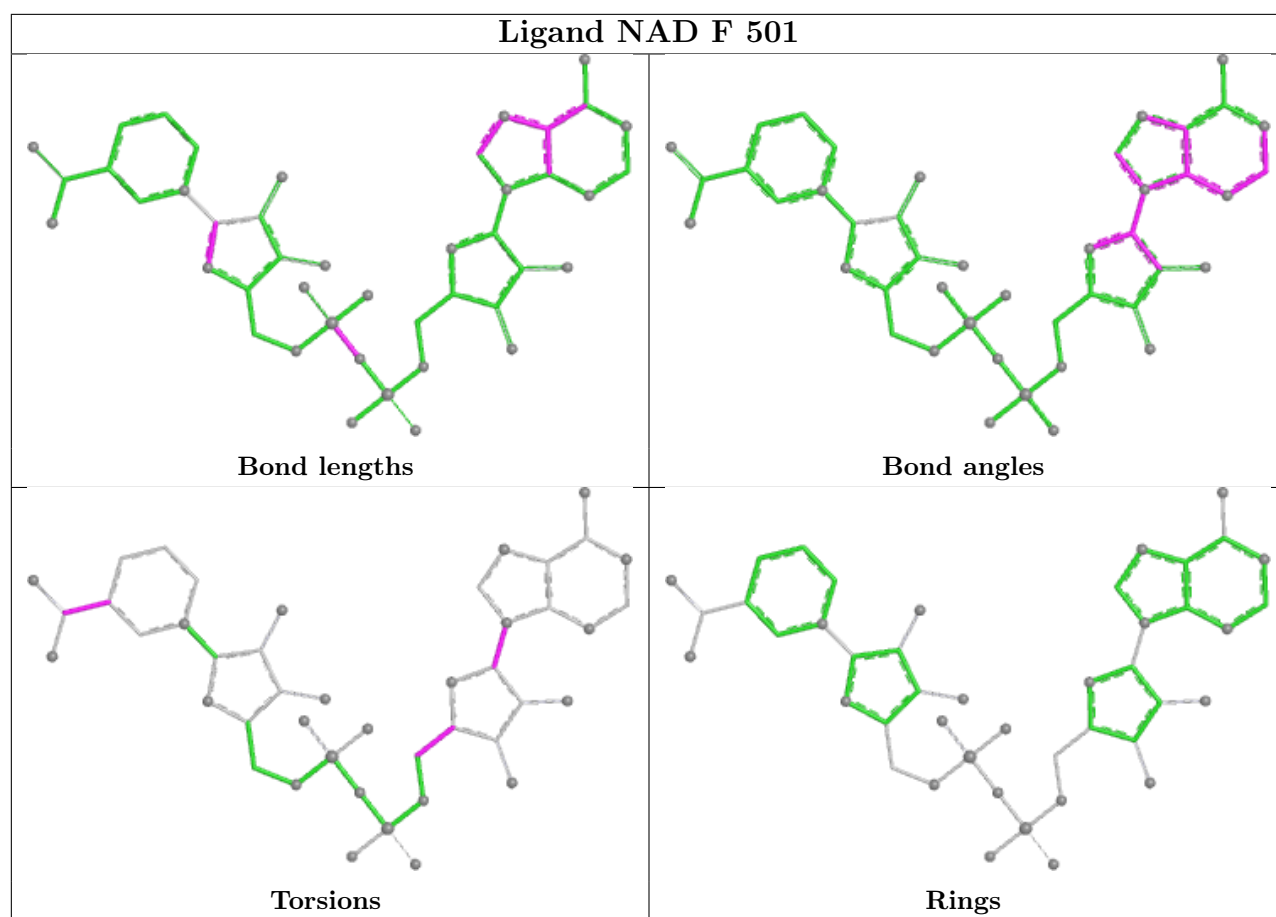
14 monomers are involved in 33 short contacts:

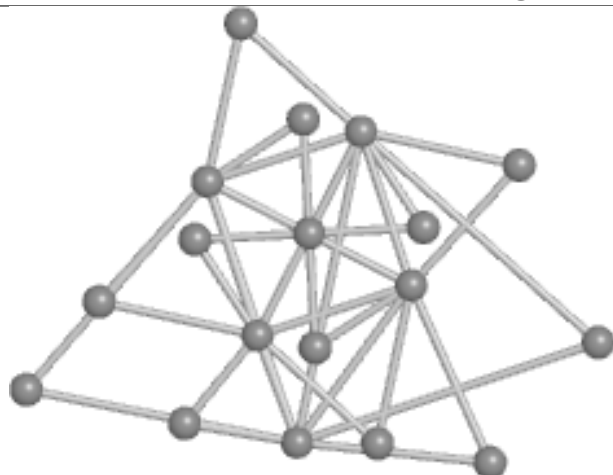
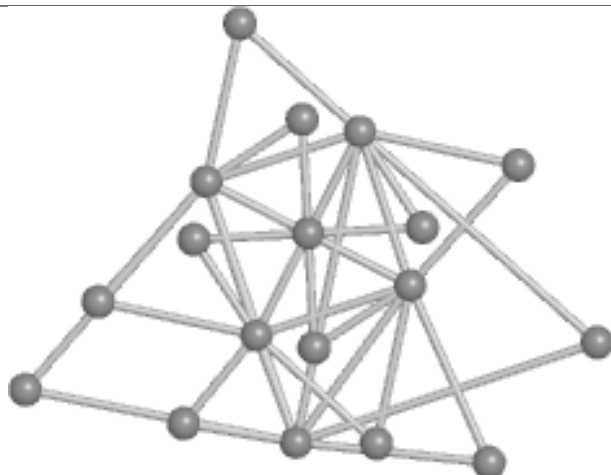
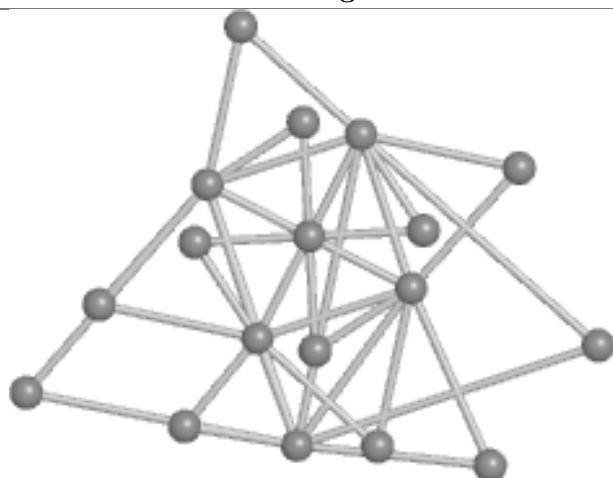
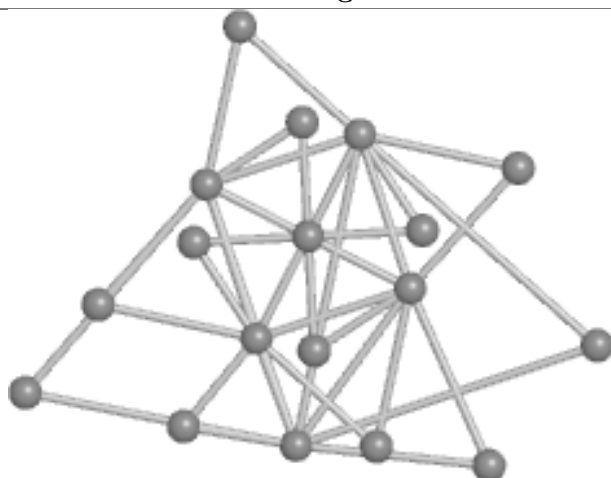
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	502	TBR	1	0
3	H	502	TBR	1	0
3	G	503	TBR	2	0
5	H	501	NAD	5	0
3	D	501	TBR	1	0
3	E	503	TBR	3	0
5	G	501	NAD	5	0
5	F	501	NAD	3	0
3	F	503	TBR	1	0
3	G	502	TBR	1	0
3	D	502	TBR	1	0
3	H	503	TBR	2	0
5	E	501	NAD	6	0
3	F	502	TBR	1	0

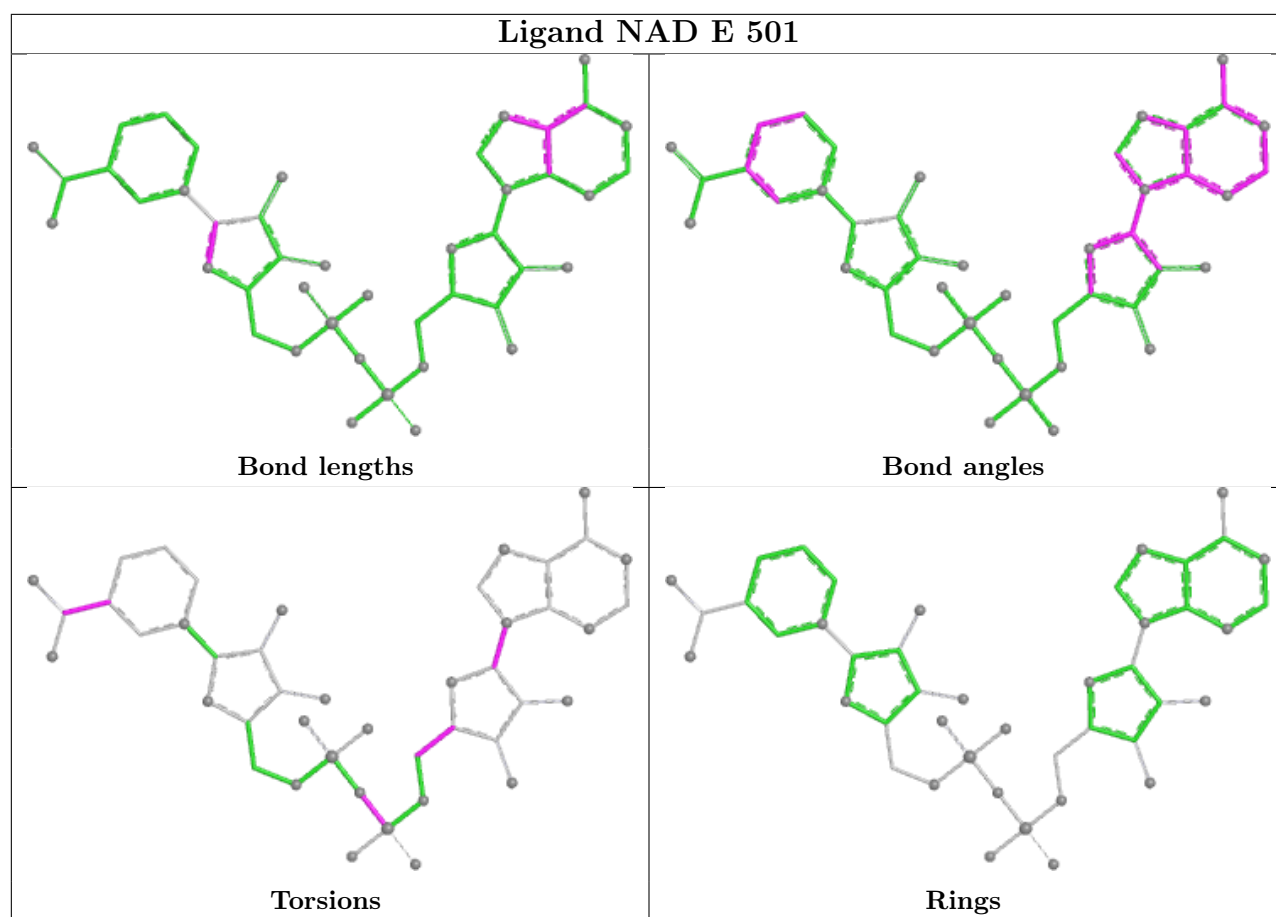
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.







Ligand TBR A 501**Bond lengths****Bond angles****Torsions****Rings**



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	462/485 (95%)	0.17	28 (6%) 27 22	31, 70, 118, 155	0
1	B	462/485 (95%)	0.19	30 (6%) 25 21	29, 75, 127, 165	0
1	C	462/485 (95%)	0.43	36 (7%) 19 17	39, 94, 142, 173	0
1	D	462/485 (95%)	0.30	30 (6%) 25 21	41, 87, 139, 163	0
2	E	451/458 (98%)	0.21	20 (4%) 39 28	39, 84, 158, 186	0
2	F	444/458 (96%)	0.27	25 (5%) 30 23	43, 80, 132, 161	0
2	G	452/458 (98%)	0.16	14 (3%) 51 35	43, 89, 158, 181	0
2	H	450/458 (98%)	0.19	18 (4%) 42 30	43, 88, 158, 183	0
All	All	3645/3772 (96%)	0.24	201 (5%) 30 23	29, 83, 146, 186	0

The worst 5 of 201 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	443	GLY	7.4
1	B	118	VAL	7.2
2	F	11	VAL	6.1
1	D	424	GLU	5.9
1	C	118	VAL	5.8

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 ⓘ

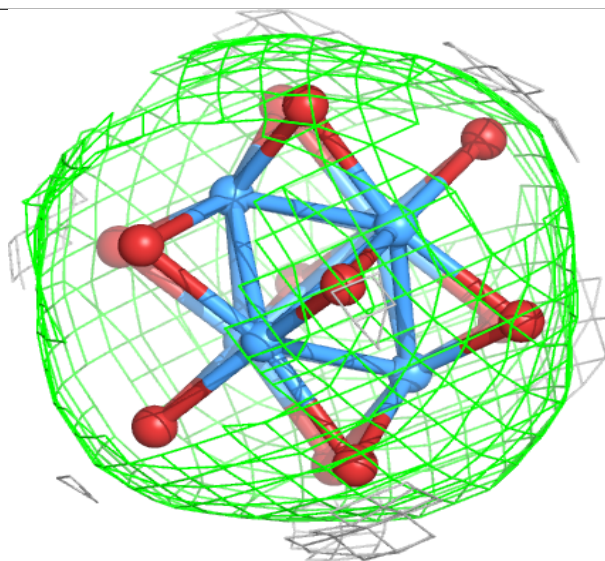
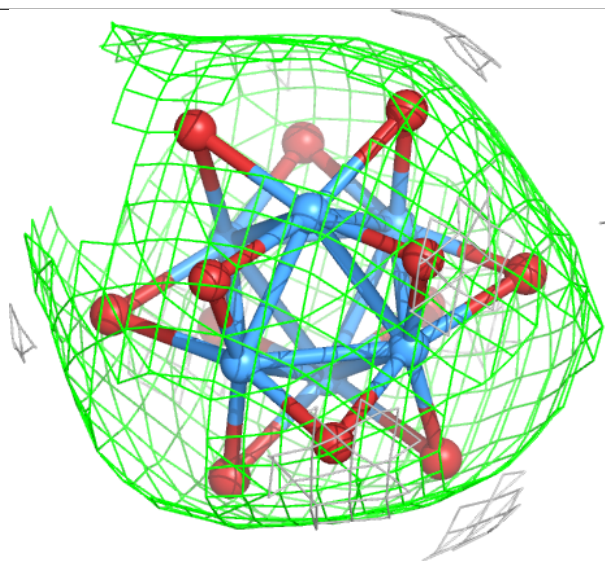
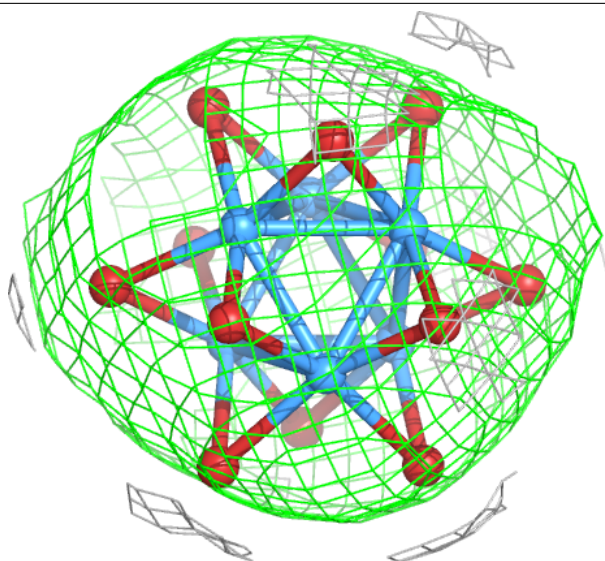
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	TBR	D	503	18/18	0.53	0.24	73,128,323,367	18
3	TBR	A	503	18/18	0.64	0.13	99,160,345,346	18
3	TBR	E	502	18/18	0.69	0.12	59,128,282,314	18
3	TBR	G	502	18/18	0.69	0.12	70,139,259,285	18
3	TBR	H	502	18/18	0.70	0.12	83,180,334,361	18
3	TBR	F	502	18/18	0.75	0.15	81,118,256,309	18
3	TBR	C	501	18/18	0.77	0.36	50,93,125,189	18
3	TBR	A	501	18/18	0.77	0.53	86,145,324,330	18
3	TBR	B	501	18/18	0.81	0.40	41,95,161,539	18
3	TBR	B	502	18/18	0.82	0.23	74,116,217,295	18
3	TBR	A	502	18/18	0.83	0.28	86,125,275,297	18
3	TBR	F	503	18/18	0.84	0.44	49,80,197,198	18
3	TBR	D	502	18/18	0.84	0.37	45,104,211,261	18
3	TBR	C	502	18/18	0.84	0.23	81,131,298,309	18
3	TBR	E	503	18/18	0.85	0.38	48,100,209,232	18
3	TBR	G	503	18/18	0.86	0.43	53,122,192,197	18
3	TBR	D	501	18/18	0.89	0.26	31,77,99,170	18
3	TBR	H	503	18/18	0.90	0.41	52,92,184,211	18
5	NAD	E	501	44/44	0.92	0.10	33,54,84,122	0
5	NAD	G	501	44/44	0.93	0.10	36,58,82,115	0
4	K	B	503	1/1	0.94	0.05	73,73,73,73	0
5	NAD	H	501	44/44	0.94	0.11	41,62,102,117	0
4	K	C	503	1/1	0.95	0.04	103,103,103,103	0
5	NAD	F	501	44/44	0.95	0.09	40,70,92,125	0
4	K	A	504	1/1	0.97	0.06	66,66,66,66	0
4	K	D	504	1/1	0.98	0.03	119,119,119,119	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.

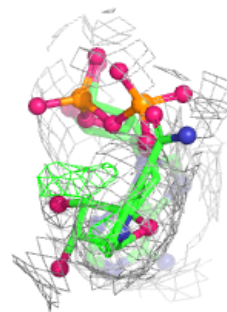
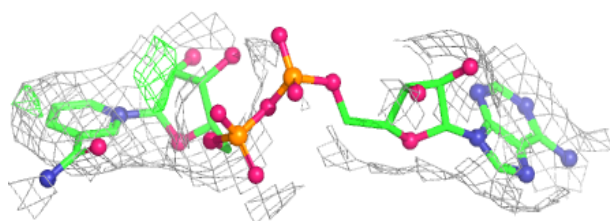
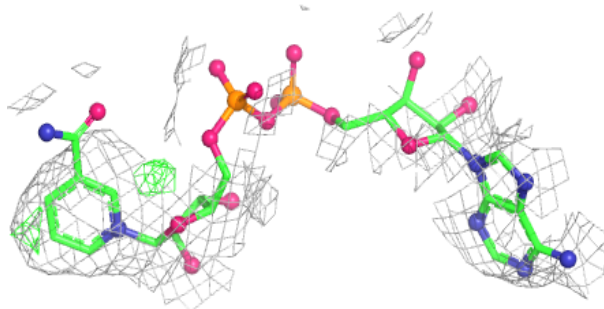
Electron density around TBR A 501:

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

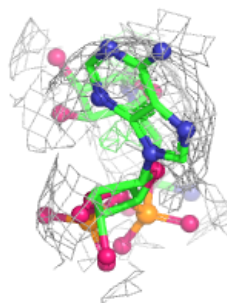
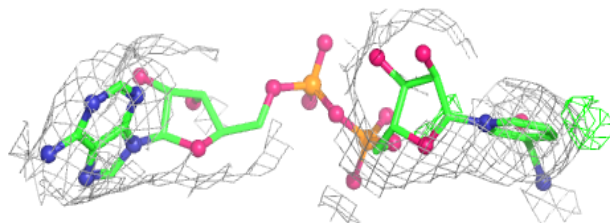
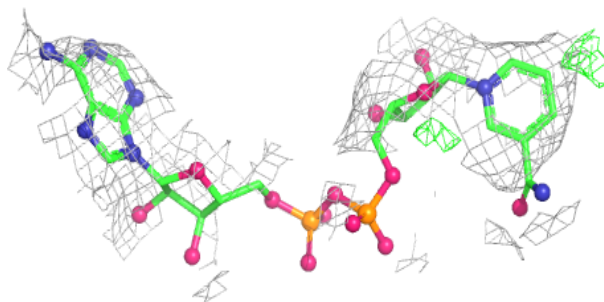


Electron density around NAD E 501:

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

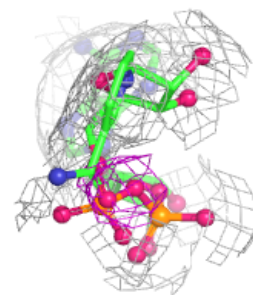
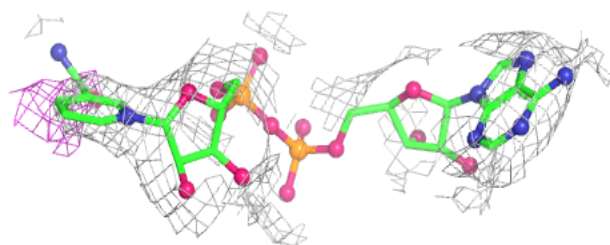
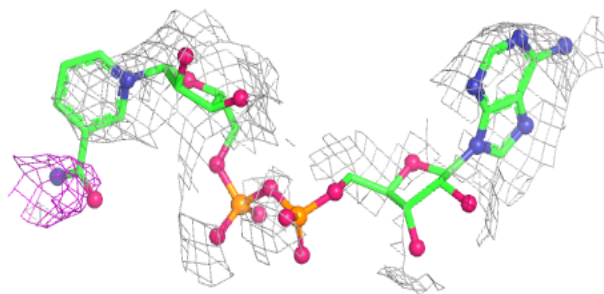
**Electron density around NAD G 501:**

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

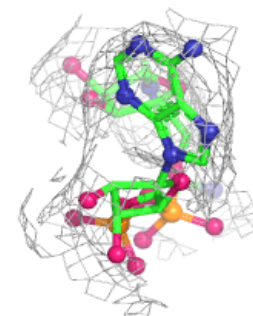
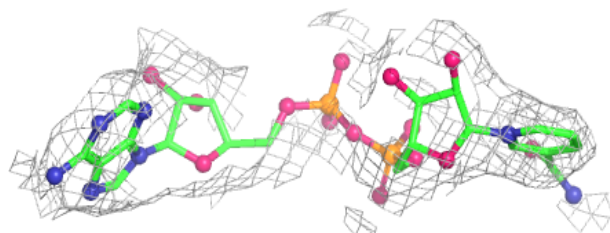
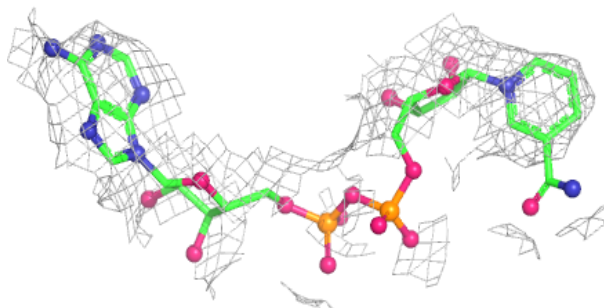


Electron density around NAD H 501:

$2mF_o-DF_c$ (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)



6.5 Other polymers [i](#)

There are no such residues in this entry.