



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 15, 2026 – 12:36 AM UTC

PDB ID : 1IB6 / pdb_00001ib6
Title : CRYSTAL STRUCTURE OF R153C E. COLI MALATE DEHYDROGENASE
Authors : Bell, J.K.; Yennawar, H.P.; Wright, S.K.; Thompson, J.R.; Viola, R.E.; Banaszak, L.J.
Deposited on : 2001-03-27
Resolution : 2.10 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

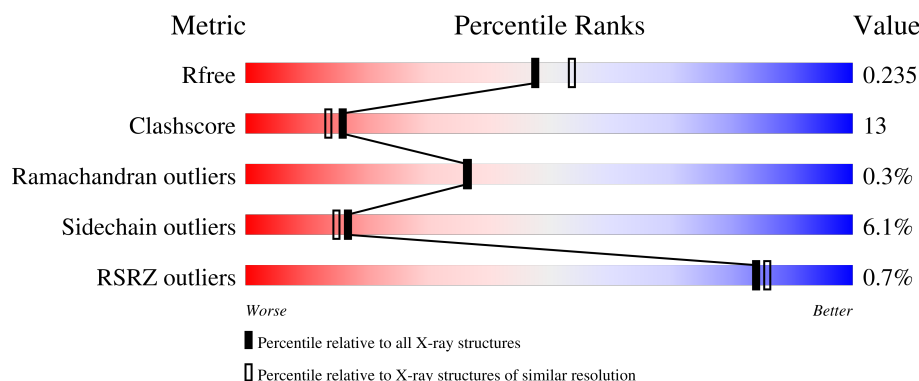
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	312	 65% 31% .
1	B	312	 3% 65% 30% .
1	C	312	 79% 19% .
1	D	312	 79% 19% .

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9508 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.

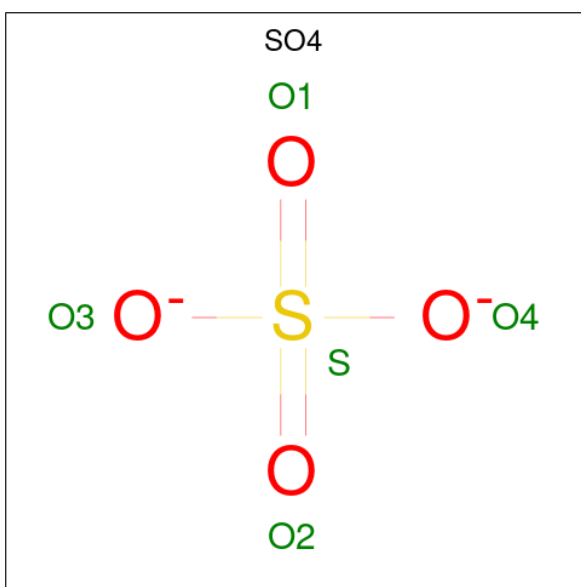
- Molecule 1 is a protein called MALATE DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	0	0
			2267	1435	384	440	8			
1	B	312	Total	C	N	O	S	0	0	0
			2267	1435	384	440	8			
1	C	312	Total	C	N	O	S	0	0	0
			2267	1435	384	440	8			
1	D	312	Total	C	N	O	S	0	0	0
			2267	1435	384	440	8			

There are 8 discrepancies between the modelled and reference sequences:

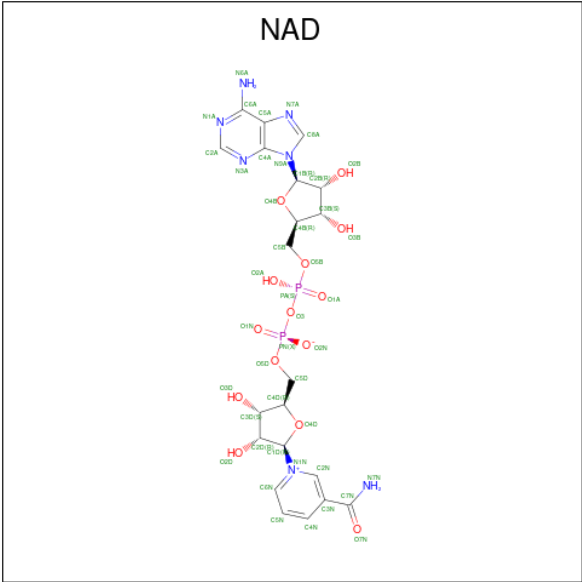
Chain	Residue	Modelled	Actual	Comment	Reference
A	153	CYS	ARG	engineered mutation	UNP P61889
A	307	GLN	GLU	SEE REMARK 999	UNP P61889
B	153	CYS	ARG	engineered mutation	UNP P61889
B	307	GLN	GLU	SEE REMARK 999	UNP P61889
C	153	CYS	ARG	engineered mutation	UNP P61889
C	307	GLN	GLU	SEE REMARK 999	UNP P61889
D	153	CYS	ARG	engineered mutation	UNP P61889
D	307	GLN	GLU	SEE REMARK 999	UNP P61889

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is water.

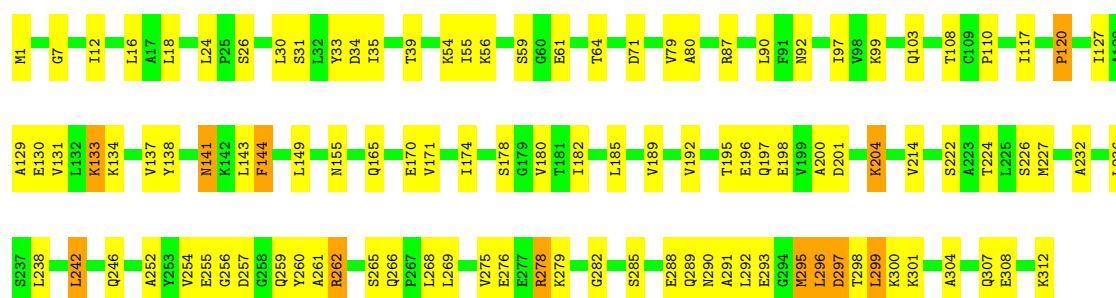
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	75	Total	O	0	0
			75	75		
4	B	54	Total	O	0	0
			54	54		
4	C	75	Total	O	0	0
			75	75		
4	D	74	Total	O	0	0
			74	74		

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.

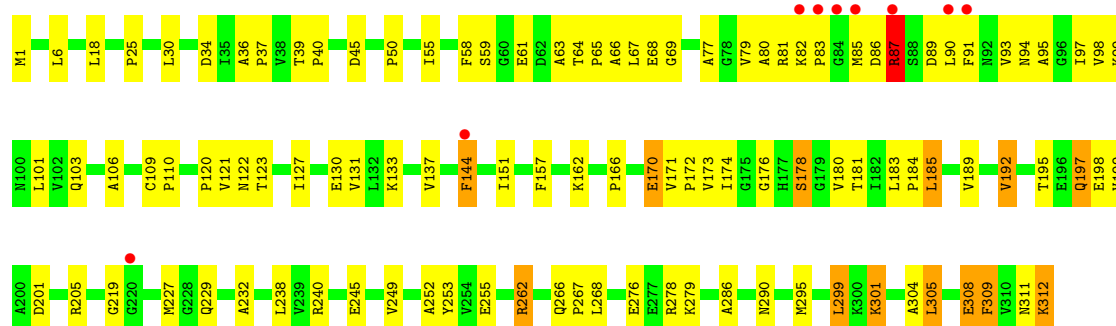
• Molecule 1: MALATE DEHYDROGENASE

Chain A: 



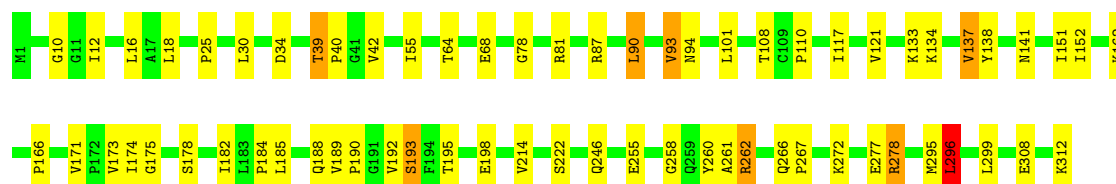
• Molecule 1: MALATE DEHYDROGENASE

Chain B: 



• Molecule 1: MALATE DEHYDROGENASE

Chain C: 

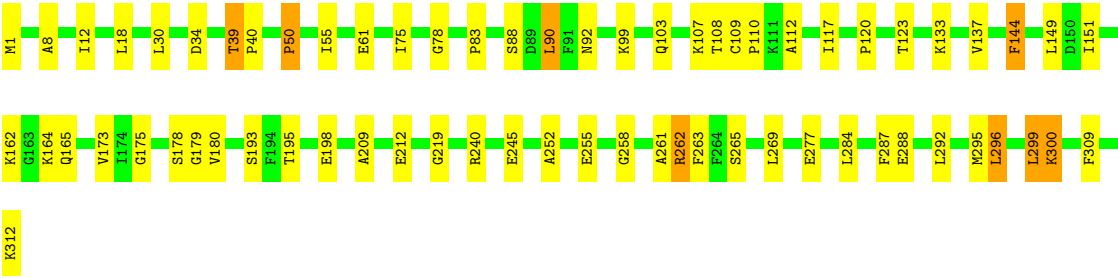


• Molecule 1: MALATE DEHYDROGENASE

Chain D:

79%

19%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	148.14Å 53.08Å 164.29Å 90.00° 95.26° 90.00°	Depositor
Resolution (Å)	37.42 – 2.10 37.42 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.4 (37.42-2.10) 98.4 (37.42-2.10)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.98 (at 2.00Å)	Xtriage
Refinement program	CNS 0.5	Depositor
R, R_{free}	0.192 , 0.244 0.183 , 0.235	Depositor DCC
R_{free} test set	7418 reflections (8.84%)	wwPDB-VP
Wilson B-factor (Å ²)	35.4	Xtriage
Anisotropy	0.110	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9508	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 5.30% 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: NAD, SO4

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	0.91	1/2295 (0.0%)	1.19	13/3108 (0.4%)
1	B	1.00	3/2295 (0.1%)	1.19	9/3108 (0.3%)
1	C	1.13	4/2295 (0.2%)	1.20	14/3108 (0.5%)
1	D	0.92	1/2295 (0.0%)	1.19	11/3108 (0.4%)
All	All	0.99	9/9180 (0.1%)	1.19	47/12432 (0.4%)

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	172	PRO	N-CD	-18.03	1.22	1.47
1	A	120	PRO	N-CD	-18.02	1.22	1.47
1	C	190	PRO	N-CD	-17.99	1.22	1.47
1	B	50	PRO	N-CD	-17.98	1.22	1.47
1	B	166	PRO	N-CD	-17.98	1.22	1.47
1	C	25	PRO	N-CD	-17.97	1.22	1.47
1	C	166	PRO	N-CD	-17.96	1.22	1.47
1	C	184	PRO	N-CD	-17.95	1.22	1.47
1	D	40	PRO	N-CD	-17.94	1.22	1.47

All (47) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	170	GLU	CA-C-N	-7.94	114.70	123.43
1	B	170	GLU	C-N-CA	-7.94	114.70	123.43
1	B	61	GLU	N-CA-C	-7.51	104.26	113.50
1	D	8	ALA	N-CA-C	7.00	121.08	112.54
1	C	138	TYR	N-CA-C	6.74	119.50	109.59
1	C	108	THR	N-CA-C	6.69	121.48	113.12
1	A	295	MET	N-CA-C	6.35	121.11	113.23
1	A	120	PRO	N-CD-CG	6.34	111.41	103.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	7	GLY	N-CA-C	-6.28	105.68	115.67
1	A	71	ASP	N-CA-C	-6.27	105.77	113.41
1	A	282	GLY	N-CA-C	6.24	122.21	111.47
1	B	121	VAL	N-CA-C	6.20	116.87	110.36
1	D	39	THR	CA-C-N	-6.11	113.39	119.56
1	D	39	THR	C-N-CA	-6.11	113.39	119.56
1	D	92	ASN	N-CA-C	6.10	117.93	111.28
1	C	42	VAL	N-CA-C	-6.08	104.58	110.72
1	C	78	GLY	N-CA-C	6.02	118.23	111.85
1	A	92	ASN	N-CA-C	5.98	117.80	111.28
1	D	112	ALA	N-CA-C	5.98	118.48	110.35
1	B	178	SER	N-CA-C	5.93	117.92	107.61
1	D	108	THR	N-CA-C	5.86	120.73	112.93
1	D	109	CYS	CA-C-N	5.79	127.07	119.84
1	D	109	CYS	C-N-CA	5.79	127.07	119.84
1	D	75	ILE	N-CA-C	5.74	116.07	107.51
1	A	108	THR	N-CA-C	5.70	120.37	112.45
1	C	296	LEU	N-CA-C	5.67	118.20	111.33
1	A	24	LEU	CA-C-N	5.65	125.60	119.78
1	A	24	LEU	C-N-CA	5.65	125.60	119.78
1	C	39	THR	N-CA-C	5.62	120.55	113.25
1	D	39	THR	N-CA-C	5.55	120.47	113.25
1	C	184	PRO	N-CD-CG	5.54	111.51	103.20
1	B	50	PRO	N-CD-CG	5.54	111.51	103.20
1	C	25	PRO	N-CD-CG	5.51	111.47	103.20
1	B	172	PRO	N-CD-CG	5.51	111.46	103.20
1	C	166	PRO	N-CD-CG	5.50	111.46	103.20
1	C	272	LYS	N-CA-C	5.50	119.09	112.38
1	C	190	PRO	N-CD-CG	5.50	111.45	103.20
1	D	40	PRO	N-CD-CG	5.49	111.44	103.20
1	B	166	PRO	N-CD-CG	5.49	111.44	103.20
1	C	121	VAL	N-CA-C	5.39	116.77	110.62
1	B	98	VAL	N-CA-C	-5.38	105.26	110.42
1	A	296	LEU	N-CA-C	5.36	117.82	111.33
1	C	277	GLU	N-CA-C	5.35	117.90	108.75
1	A	165	GLN	CA-C-N	5.27	126.42	119.84
1	A	165	GLN	C-N-CA	5.27	126.42	119.84
1	A	141	ASN	N-CA-C	-5.07	107.14	113.38
1	C	93	VAL	N-CA-C	5.04	116.92	111.58

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	2267	0	2351	82	0
1	B	2267	0	2351	77	0
1	C	2267	0	2351	45	0
1	D	2267	0	2351	44	0
2	A	10	0	0	0	0
2	C	10	0	0	1	0
2	D	10	0	0	0	0
3	A	44	0	26	5	0
3	C	44	0	26	5	0
3	D	44	0	26	5	0
4	A	75	0	0	8	0
4	B	54	0	0	4	0
4	C	75	0	0	2	0
4	D	74	0	0	1	0
All	All	9508	0	9482	246	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 13.

All (246) 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:110:PRO:HB3	1:B:137:VAL:HG21	1.44	0.99
1:A:289:GLN:HE21	1:A:289:GLN:HA	1.37	0.90
1:B:106:ALA:O	1:B:110:PRO:HG3	1.72	0.90
1:C:30:LEU:HD23	1:C:55:ILE:HD12	1.55	0.88
1:A:174:ILE:HG22	1:A:266:GLN:HA	1.58	0.84
1:C:81:ARG:HB3	1:C:90:LEU:HD21	1.58	0.83
1:B:266:GLN:NE2	1:B:278:ARG:HB3	1.94	0.83
1:A:129:ALA:O	1:A:133:LYS:HG3	1.80	0.82
1:B:83:PRO:HD3	1:B:219:GLY:HA2	1.62	0.81
1:C:12:ILE:HD12	3:C:314:NAD:H51N	1.63	0.79
1:A:238:LEU:O	1:A:242:LEU:HD22	1.83	0.79
1:D:12:ILE:HD12	3:D:315:NAD:H51N	1.62	0.78
1:A:224:THR:HG21	4:B:351:HOH:O	1.84	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:TYR:CE1	1:A:292:LEU:HD21	2.19	0.77
1:A:255:GLU:CD	1:A:262:ARG:HH11	1.92	0.77
1:A:296:LEU:O	1:A:300:LYS:HG3	1.86	0.75
1:B:81:ARG:HD3	1:B:86:ASP:O	1.86	0.75
1:B:286:ALA:HB3	4:B:446:HOH:O	1.85	0.74
1:A:295:MET:CE	1:A:299:LEU:HD12	2.18	0.72
1:B:311:ASN:O	1:B:312:LYS:HB3	1.88	0.71
1:C:134:LYS:NZ	1:C:134:LYS:HB3	2.04	0.71
1:A:289:GLN:HA	1:A:289:GLN:NE2	2.04	0.71
1:A:97:ILE:HG23	3:A:313:NAD:N6A	2.06	0.70
1:A:197:GLN:HG3	4:A:376:HOH:O	1.89	0.70
1:B:266:GLN:HE21	1:B:278:ARG:HB3	1.55	0.70
1:A:110:PRO:HB2	1:A:137:VAL:HG21	1.74	0.69
1:C:110:PRO:CB	1:C:137:VAL:HG21	2.23	0.69
1:C:175:GLY:CA	1:C:295:MET:HE1	2.23	0.69
1:B:99:LYS:O	1:B:103:GLN:HG3	1.93	0.69
1:C:110:PRO:HB2	1:C:137:VAL:HG21	1.75	0.69
1:B:127:ILE:O	1:B:131:VAL:HG23	1.92	0.68
1:D:195:THR:OG1	1:D:198:GLU:HG3	1.93	0.67
1:A:130:GLU:OE2	1:A:262:ARG:NH2	2.28	0.67
1:A:222:SER:HB2	4:A:353:HOH:O	1.94	0.67
1:D:110:PRO:HB2	1:D:137:VAL:HG21	1.77	0.66
1:B:90:LEU:O	1:B:93:VAL:HB	1.97	0.65
1:A:35:ILE:HD11	4:A:396:HOH:O	1.96	0.65
1:B:77:ALA:HB1	1:B:97:ILE:CD1	2.27	0.65
1:A:285:SER:OG	1:A:288:GLU:HG3	1.98	0.64
1:A:143:LEU:O	1:A:254:VAL:HG12	1.97	0.64
1:C:117:ILE:O	3:C:314:NAD:H2N	1.97	0.63
1:D:255:GLU:OE2	1:D:262:ARG:HD3	1.98	0.63
1:A:12:ILE:HD12	3:A:313:NAD:H51N	1.81	0.63
1:B:151:ILE:HD13	1:B:173:VAL:HB	1.81	0.63
1:A:297:ASP:HB2	4:A:371:HOH:O	1.99	0.62
1:B:137:VAL:O	1:B:137:VAL:HG22	2.00	0.62
1:A:269:LEU:HD23	1:A:276:GLU:HG2	1.81	0.61
1:B:37:PRO:HD2	4:B:406:HOH:O	1.99	0.61
1:C:195:THR:OG1	1:C:198:GLU:HG3	2.01	0.61
1:A:127:ILE:O	1:A:131:VAL:HG23	2.01	0.60
1:A:87:ARG:O	1:A:120:PRO:HG3	2.01	0.60
1:A:134:LYS:HG3	4:A:365:HOH:O	2.01	0.60
1:C:260:TYR:HB3	1:C:296:LEU:HD11	1.82	0.60
1:B:6:LEU:HD13	1:B:101:LEU:HD22	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:ILE:CD1	1:B:173:VAL:HB	2.31	0.60
1:B:162:LYS:HG3	1:B:192:VAL:CG1	2.32	0.59
1:A:133:LYS:NZ	1:A:133:LYS:HB3	2.17	0.59
1:D:30:LEU:O	1:D:55:ILE:HA	2.02	0.59
1:B:34:ASP:HB3	1:B:39:THR:OG1	2.03	0.59
1:A:259:GLN:O	1:A:259:GLN:HG2	2.02	0.59
1:B:58:PHE:CD1	1:B:66:ALA:HB2	2.38	0.59
1:A:30:LEU:HD23	1:A:55:ILE:HD12	1.85	0.58
1:A:149:LEU:HD22	1:A:227:MET:SD	2.43	0.58
1:B:83:PRO:HD3	1:B:219:GLY:CA	2.33	0.58
1:B:110:PRO:CB	1:B:137:VAL:HG21	2.25	0.58
1:D:99:LYS:HE2	1:D:103:GLN:NE2	2.18	0.58
1:D:309:PHE:HA	1:D:312:LYS:HE3	1.85	0.58
1:B:94:ASN:O	1:B:97:ILE:HG22	2.03	0.58
1:A:255:GLU:CD	1:A:262:ARG:NH1	2.61	0.57
1:A:232:ALA:O	1:A:236:LEU:HG	2.05	0.57
1:B:195:THR:O	1:B:199:VAL:HG23	2.05	0.57
1:B:255:GLU:OE2	1:B:262:ARG:HD3	2.05	0.57
1:C:64:THR:O	1:C:68:GLU:HG3	2.05	0.57
1:A:26:SER:OG	1:C:246:GLN:HG3	2.05	0.56
1:C:185:LEU:HD23	1:C:188:GLN:NE2	2.19	0.56
1:D:255:GLU:HB2	1:D:263:PHE:CE1	2.41	0.56
1:B:39:THR:HB	1:B:40:PRO:HD3	1.86	0.56
1:B:77:ALA:HB1	1:B:97:ILE:HD13	1.86	0.56
1:C:222:SER:HB2	4:C:472:HOH:O	2.06	0.56
1:B:240:ARG:CZ	1:B:245:GLU:OE1	2.54	0.56
1:B:151:ILE:HD13	1:B:173:VAL:CG2	2.36	0.55
1:B:89:ASP:C	1:B:91:PHE:H	2.15	0.55
1:B:109:CYS:N	1:B:110:PRO:HD3	2.22	0.55
1:B:144:PHE:CD1	1:B:144:PHE:N	2.74	0.55
1:A:214:VAL:HG22	1:A:222:SER:HB3	1.87	0.55
1:C:110:PRO:HB2	1:C:137:VAL:CG2	2.37	0.55
1:C:175:GLY:HA2	1:C:295:MET:HE1	1.87	0.54
1:A:266:GLN:NE2	1:A:278:ARG:HB2	2.23	0.54
1:B:106:ALA:O	1:B:110:PRO:CG	2.53	0.54
1:C:255:GLU:CD	1:C:262:ARG:HH11	2.16	0.54
1:C:87:ARG:HD3	2:C:318:SO4:O1	2.08	0.53
1:A:79:VAL:HG12	1:A:80:ALA:O	2.07	0.53
1:A:97:ILE:HG23	3:A:313:NAD:H61A	1.73	0.53
1:A:226:SER:HB3	1:B:45:ASP:O	2.09	0.52
1:B:276:GLU:HA	1:B:276:GLU:OE1	2.08	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:83:PRO:HD2	1:D:219:GLY:HA2	1.91	0.52
1:A:99:LYS:O	1:A:103:GLN:HG3	2.09	0.52
1:A:201:ASP:HB3	4:A:377:HOH:O	2.10	0.52
1:B:162:LYS:HG3	1:B:192:VAL:HG11	1.91	0.52
1:D:110:PRO:HB2	1:D:137:VAL:CG2	2.38	0.52
1:B:67:LEU:O	1:B:68:GLU:C	2.52	0.52
1:B:94:ASN:HA	1:B:97:ILE:HG22	1.92	0.52
1:A:252:ALA:O	1:A:265:SER:HA	2.10	0.51
1:C:178:SER:O	1:C:182:ILE:HG13	2.10	0.51
1:A:30:LEU:O	1:A:55:ILE:HA	2.09	0.51
1:A:110:PRO:CB	1:A:137:VAL:HG21	2.40	0.51
1:B:197:GLN:NE2	1:B:201:ASP:OD2	2.44	0.51
1:A:295:MET:HE1	1:A:299:LEU:HD12	1.92	0.51
1:B:122:ASN:HA	1:B:253:TYR:CZ	2.46	0.51
1:C:110:PRO:HB3	1:C:137:VAL:HG21	1.93	0.51
1:A:189:VAL:CG1	1:A:192:VAL:HG22	2.41	0.51
1:B:63:ALA:C	1:B:65:PRO:HD2	2.35	0.51
1:C:87:ARG:HA	1:C:90:LEU:HD23	1.93	0.51
1:C:152:ILE:HB	1:D:50:PRO:HD3	1.93	0.50
1:D:120:PRO:HG2	1:D:123:THR:HB	1.93	0.50
1:D:175:GLY:CA	1:D:295:MET:HE1	2.41	0.50
1:B:189:VAL:HG12	1:B:192:VAL:HG23	1.92	0.50
1:B:85:MET:CE	1:B:89:ASP:HB3	2.41	0.50
1:C:30:LEU:CD2	1:C:55:ILE:HD12	2.34	0.50
1:B:77:ALA:HB1	1:B:97:ILE:HD11	1.92	0.50
1:C:133:LYS:HE3	1:C:262:ARG:HH12	1.77	0.49
1:C:189:VAL:HB	1:C:192:VAL:CG2	2.42	0.49
1:B:189:VAL:HG12	1:B:192:VAL:CG2	2.42	0.49
1:D:240:ARG:NH1	1:D:245:GLU:OE2	2.45	0.49
1:B:130:GLU:OE1	1:B:130:GLU:HA	2.11	0.49
1:B:130:GLU:OE1	1:B:133:LYS:HE3	2.12	0.49
1:D:133:LYS:HE2	4:D:576:HOH:O	2.12	0.49
1:A:141:ASN:OD1	1:A:278:ARG:NH2	2.46	0.49
1:B:301:LYS:O	1:B:304:ALA:HB3	2.13	0.48
1:A:34:ASP:O	1:A:59:SER:HA	2.13	0.48
1:C:134:LYS:HB3	1:C:134:LYS:HZ2	1.76	0.48
1:D:292:LEU:O	1:D:295:MET:HG2	2.14	0.48
1:A:227:MET:HE3	1:A:227:MET:O	2.13	0.48
1:A:304:ALA:HA	1:A:307:GLN:NE2	2.29	0.48
1:B:64:THR:N	1:B:65:PRO:HD2	2.29	0.48
1:A:34:ASP:HB3	1:A:39:THR:OG1	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:SER:H	1:A:182:ILE:HG13	1.79	0.48
1:C:34:ASP:OD2	3:C:314:NAD:H1B	2.14	0.48
1:D:295:MET:CE	1:D:299:LEU:HD12	2.44	0.48
1:C:308:GLU:O	1:C:312:LYS:HB3	2.13	0.48
1:A:261:ALA:O	1:A:262:ARG:C	2.56	0.47
3:C:314:NAD:H6N	4:C:474:HOH:O	2.13	0.47
1:A:144:PHE:CE2	1:A:275:VAL:HG23	2.50	0.47
1:B:267:PRO:HB2	1:B:279:LYS:HB2	1.94	0.47
1:B:151:ILE:HD13	1:B:173:VAL:CB	2.44	0.47
1:B:252:ALA:HB3	1:B:268:LEU:CD1	2.45	0.47
1:A:54:LYS:NZ	1:A:56:LYS:HE3	2.30	0.47
1:A:174:ILE:HG22	1:A:265:SER:O	2.14	0.47
1:A:133:LYS:HB3	1:A:133:LYS:HZ3	1.79	0.47
1:A:33:TYR:CD1	1:A:33:TYR:C	2.93	0.46
1:B:91:PHE:CE1	1:B:305:LEU:HD23	2.50	0.46
1:D:103:GLN:O	1:D:107:LYS:HG2	2.15	0.46
1:C:39:THR:HB	1:C:40:PRO:HD3	1.97	0.46
1:A:298:THR:O	1:A:301:LYS:HB3	2.16	0.46
1:A:308:GLU:O	1:A:312:LYS:HB3	2.15	0.46
1:B:227:MET:HE3	1:B:227:MET:O	2.15	0.46
1:D:110:PRO:CB	1:D:137:VAL:HG21	2.42	0.46
1:D:252:ALA:O	1:D:265:SER:HA	2.16	0.46
1:A:54:LYS:HZ3	1:A:56:LYS:HE3	1.81	0.46
1:A:304:ALA:HA	1:A:307:GLN:HE21	1.81	0.46
1:D:34:ASP:HB3	1:D:39:THR:OG1	2.15	0.45
1:B:308:GLU:OE1	1:B:312:LYS:HG2	2.16	0.45
1:D:269:LEU:HB3	1:D:277:GLU:HG2	1.98	0.45
1:B:130:GLU:CD	1:B:133:LYS:HE3	2.41	0.45
1:A:204:LYS:HB2	1:A:204:LYS:HE3	1.84	0.45
1:A:224:THR:CG2	4:B:351:HOH:O	2.54	0.45
1:B:94:ASN:O	1:B:95:ALA:C	2.60	0.45
1:A:144:PHE:CD1	1:A:144:PHE:N	2.84	0.45
1:A:246:GLN:OE1	1:D:165:GLN:HG2	2.17	0.45
1:D:144:PHE:N	1:D:144:PHE:CD1	2.85	0.45
1:C:10:GLY:HA3	3:C:314:NAD:O5B	2.17	0.44
1:D:284:LEU:HB3	1:D:288:GLU:HB2	1.99	0.44
1:A:189:VAL:HG12	1:A:192:VAL:HG22	2.00	0.44
1:C:174:ILE:HG22	1:C:266:GLN:HA	2.00	0.44
1:D:295:MET:HG2	1:D:296:LEU:HD23	1.99	0.44
1:A:97:ILE:HD13	3:A:313:NAD:N7A	2.33	0.44
1:C:134:LYS:HB3	1:C:134:LYS:HZ3	1.78	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:266:GLN:HB2	1:C:267:PRO:HD2	2.00	0.44
1:A:260:TYR:O	1:A:261:ALA:HB2	2.18	0.44
1:B:240:ARG:NH1	1:B:245:GLU:OE1	2.51	0.44
1:D:78:GLY:O	3:D:315:NAD:H51A	2.18	0.44
1:D:287:PHE:CD1	1:D:287:PHE:C	2.95	0.44
1:C:101:LEU:HD23	1:C:101:LEU:HA	1.79	0.44
1:C:214:VAL:HG22	1:C:222:SER:HB3	1.99	0.44
1:D:162:LYS:NZ	1:D:193:SER:O	2.47	0.44
1:B:176:GLY:HA3	1:B:181:THR:HB	1.99	0.44
1:B:249:VAL:HA	1:B:268:LEU:O	2.17	0.43
1:D:88:SER:C	1:D:90:LEU:H	2.26	0.43
1:A:257:ASP:OD1	1:A:257:ASP:N	2.47	0.43
1:B:87:ARG:O	1:B:120:PRO:HB3	2.18	0.43
1:B:110:PRO:HB3	1:B:137:VAL:CG2	2.31	0.43
1:A:268:LEU:HD13	1:A:275:VAL:CG2	2.49	0.43
1:A:103:GLN:HG2	1:A:131:VAL:CG1	2.49	0.43
1:C:141:ASN:OD1	1:C:278:ARG:NH2	2.49	0.43
1:A:195:THR:O	1:A:196:GLU:C	2.60	0.43
1:D:258:GLY:HA2	1:D:261:ALA:O	2.19	0.43
1:B:36:ALA:HA	1:B:37:PRO:HD3	1.83	0.43
1:B:174:ILE:HD13	1:B:185:LEU:HD21	2.01	0.43
1:B:183:LEU:HA	1:B:184:PRO:HD3	1.87	0.43
1:C:30:LEU:O	1:C:55:ILE:HA	2.18	0.43
1:C:93:VAL:HG23	1:C:94:ASN:N	2.34	0.43
1:D:99:LYS:HG2	1:D:103:GLN:HE21	1.84	0.43
1:B:229:GLN:O	1:B:232:ALA:HB3	2.17	0.42
1:D:300:LYS:HE2	1:D:300:LYS:HB3	1.59	0.42
1:B:90:LEU:O	1:B:93:VAL:CB	2.65	0.42
1:B:295:MET:CE	1:B:299:LEU:HD12	2.49	0.42
1:C:258:GLY:HA2	1:C:261:ALA:O	2.19	0.42
1:A:138:TYR:CE2	1:A:255:GLU:OE1	2.73	0.42
1:D:83:PRO:CD	1:D:219:GLY:HA2	2.49	0.42
1:D:209:ALA:O	1:D:212:GLU:HB3	2.20	0.42
1:A:260:TYR:N	4:A:361:HOH:O	2.49	0.42
1:C:162:LYS:HE3	1:C:193:SER:O	2.19	0.42
1:C:255:GLU:O	1:C:278:ARG:NH1	2.53	0.42
1:D:295:MET:HE3	1:D:299:LEU:HD12	2.02	0.42
1:A:291:ALA:O	1:A:292:LEU:C	2.63	0.41
1:B:30:LEU:HD23	1:B:55:ILE:HD12	2.02	0.41
1:B:79:VAL:HG12	1:B:80:ALA:N	2.35	0.41
1:D:99:LYS:HE2	1:D:103:GLN:HE21	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:LEU:HD13	1:A:275:VAL:HG22	2.02	0.41
1:B:290:ASN:HD22	1:B:290:ASN:HA	1.66	0.41
1:D:61:GLU:CD	1:D:61:GLU:N	2.78	0.41
1:A:117:ILE:O	3:A:313:NAD:H2N	2.19	0.41
1:D:292:LEU:O	1:D:296:LEU:HD23	2.21	0.41
1:A:155:ASN:ND2	1:A:170:GLU:OE2	2.54	0.41
1:A:195:THR:OG1	1:A:198:GLU:HG3	2.20	0.41
1:B:157:PHE:CE1	1:B:205:ARG:CZ	3.04	0.41
1:B:91:PHE:CE1	1:B:123:THR:HG21	2.56	0.41
1:C:151:ILE:HD13	1:C:173:VAL:HG23	2.02	0.41
1:C:255:GLU:CD	1:C:262:ARG:HD3	2.45	0.41
1:A:289:GLN:O	1:A:293:GLU:HG2	2.20	0.41
3:D:315:NAD:H6N	3:D:315:NAD:H2D	1.86	0.41
1:B:309:PHE:CD1	1:B:309:PHE:C	2.99	0.41
1:D:117:ILE:O	3:D:315:NAD:H2N	2.20	0.41
1:D:151:ILE:CD1	1:D:173:VAL:HB	2.51	0.41
1:D:178:SER:O	1:D:180:VAL:N	2.54	0.41
1:A:256:GLY:HA3	4:A:359:HOH:O	2.20	0.41
1:C:175:GLY:HA3	1:C:295:MET:HE1	1.99	0.40
1:A:90:LEU:HB2	1:A:120:PRO:HD3	2.03	0.40
1:B:34:ASP:O	1:B:59:SER:HA	2.19	0.40
1:B:133:LYS:NZ	1:B:262:ARG:NH2	2.70	0.40
1:C:151:ILE:HD13	1:C:173:VAL:CG2	2.51	0.40
1:D:12:ILE:HD12	3:D:315:NAD:C5D	2.42	0.40
1:A:197:GLN:O	1:A:200:ALA:HB3	2.21	0.40
1:A:289:GLN:HE21	1:A:289:GLN:CA	2.10	0.40
1:D:149:LEU:HD12	1:D:149:LEU:HA	1.93	0.40
1:B:195:THR:OG1	1:B:198:GLU:HG3	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	310/312 (99%)	291 (94%)	19 (6%)	0	100	100
1	B	310/312 (99%)	280 (90%)	27 (9%)	3 (1%)	12	9
1	C	310/312 (99%)	303 (98%)	7 (2%)	0	100	100
1	D	310/312 (99%)	299 (96%)	10 (3%)	1 (0%)	36	36
All	All	1240/1248 (99%)	1173 (95%)	63 (5%)	4 (0%)	36	36

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	179	GLY
1	B	69	GLY
1	B	87	ARG
1	B	309	PHE

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	241/241 (100%)	222 (92%)	19 (8%)	11	9
1	B	241/241 (100%)	221 (92%)	20 (8%)	10	8
1	C	241/241 (100%)	231 (96%)	10 (4%)	27	29
1	D	241/241 (100%)	231 (96%)	10 (4%)	27	29
All	All	964/964 (100%)	905 (94%)	59 (6%)	17	15

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	16	LEU
1	A	18	LEU
1	A	31	SER
1	A	61	GLU
1	A	64	THR
1	A	133	LYS

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Mol	Chain	Res	Type
1	A	144	PHE
1	A	171	VAL
1	A	180	VAL
1	A	185	LEU
1	A	204	LYS
1	A	242	LEU
1	A	262	ARG
1	A	278	ARG
1	A	279	LYS
1	A	290	ASN
1	A	297	ASP
1	A	299	LEU
1	B	1	MET
1	B	18	LEU
1	B	25	PRO
1	B	82	LYS
1	B	87	ARG
1	B	144	PHE
1	B	170	GLU
1	B	171	VAL
1	B	178	SER
1	B	180	VAL
1	B	185	LEU
1	B	192	VAL
1	B	197	GLN
1	B	238	LEU
1	B	262	ARG
1	B	299	LEU
1	B	301	LYS
1	B	305	LEU
1	B	308	GLU
1	B	312	LYS
1	C	16	LEU
1	C	18	LEU
1	C	90	LEU
1	C	137	VAL
1	C	171	VAL
1	C	193	SER
1	C	262	ARG
1	C	278	ARG
1	C	296	LEU
1	C	299	LEU

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Mol	Chain	Res	Type
1	D	1	MET
1	D	18	LEU
1	D	50	PRO
1	D	90	LEU
1	D	144	PHE
1	D	164	LYS
1	D	262	ARG
1	D	296	LEU
1	D	299	LEU
1	D	300	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	GLN
1	A	23	GLN
1	A	208	ASN
1	A	259	GLN
1	A	289	GLN
1	A	307	GLN
1	A	311	ASN
1	B	103	GLN
1	B	197	GLN
1	B	266	GLN
1	B	290	ASN
1	B	307	GLN
1	C	165	GLN
1	C	208	ASN
1	D	92	ASN
1	D	103	GLN
1	D	259	GLN
1	D	307	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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	317	-	4,4,4	1.91	2 (50%)	6,6,6	0.86	0
3	NAD	A	313	-	46,48,48	2.40	10 (21%)	64,73,73	1.65	7 (10%)
2	SO4	C	318	-	4,4,4	1.87	2 (50%)	6,6,6	0.87	0
2	SO4	D	321	-	4,4,4	1.92	2 (50%)	6,6,6	0.79	0
2	SO4	D	320	-	4,4,4	1.91	1 (25%)	6,6,6	0.74	0
3	NAD	C	314	-	46,48,48	2.63	10 (21%)	64,73,73	1.63	8 (12%)
2	SO4	A	316	-	4,4,4	1.90	1 (25%)	6,6,6	0.81	0
3	NAD	D	315	-	46,48,48	2.75	10 (21%)	64,73,73	1.58	6 (9%)
2	SO4	C	319	-	4,4,4	1.88	2 (50%)	6,6,6	0.82	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	NAD	C	314	-	-	10/30/62/62	0/5/5/5
3	NAD	D	315	-	-	10/30/62/62	0/5/5/5
3	NAD	A	313	-	-	10/30/62/62	0/5/5/5

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	315	NAD	C4N-C3N	8.96	1.53	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	314	NAD	C4N-C3N	8.84	1.52	1.39
3	A	313	NAD	C4N-C3N	8.55	1.52	1.39
3	D	315	NAD	PN-O3	8.44	1.68	1.59
3	C	314	NAD	C5N-C4N	6.89	1.50	1.38
3	C	314	NAD	C2N-C3N	6.82	1.49	1.39
3	D	315	NAD	C5N-C4N	6.70	1.50	1.38
3	A	313	NAD	C5N-C4N	6.32	1.49	1.38
3	D	315	NAD	C2N-C3N	6.30	1.49	1.39
3	A	313	NAD	C2N-C3N	5.95	1.48	1.39
3	C	314	NAD	PN-O3	5.92	1.65	1.59
3	A	313	NAD	PN-O3	5.21	1.65	1.59
3	C	314	NAD	C2N-N1N	5.05	1.40	1.35
3	C	314	NAD	PA-O3	-4.96	1.54	1.59
3	D	315	NAD	PA-O3	-4.61	1.54	1.59
3	A	313	NAD	C2N-N1N	4.39	1.39	1.35
3	D	315	NAD	C6N-N1N	4.35	1.45	1.35
3	C	314	NAD	C6N-N1N	4.23	1.45	1.35
3	D	315	NAD	C2N-N1N	4.14	1.39	1.35
3	A	313	NAD	C6N-N1N	3.90	1.44	1.35
2	D	320	SO4	O1-S	3.24	1.64	1.44
2	A	316	SO4	O1-S	3.22	1.64	1.44
2	D	321	SO4	O1-S	3.18	1.63	1.44
2	A	317	SO4	O1-S	3.16	1.63	1.44
3	A	313	NAD	C6N-C5N	-3.12	1.32	1.38
2	C	318	SO4	O1-S	3.11	1.63	1.44
2	C	319	SO4	O1-S	3.09	1.63	1.44
3	D	315	NAD	C3N-C7N	-3.03	1.46	1.50
3	A	313	NAD	PA-O3	-3.00	1.56	1.59
3	C	314	NAD	C6N-C5N	-2.82	1.32	1.38
3	D	315	NAD	C6N-C5N	-2.68	1.33	1.38
3	D	315	NAD	C2A-N1A	2.55	1.38	1.33
3	A	313	NAD	O2B-C2B	2.39	1.48	1.43
3	A	313	NAD	C2A-N1A	2.35	1.38	1.33
3	C	314	NAD	C2A-N1A	2.19	1.37	1.33
3	C	314	NAD	O4D-C4D	2.12	1.49	1.45
2	D	321	SO4	O3-S	-2.10	1.30	1.48
2	A	317	SO4	O3-S	-2.10	1.30	1.48
2	C	319	SO4	O3-S	-2.06	1.31	1.48
2	C	318	SO4	O3-S	-2.03	1.31	1.48

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	313	NAD	C5N-C4N-C3N	-7.75	112.75	120.36
3	D	315	NAD	C5N-C4N-C3N	-7.43	113.06	120.36
3	C	314	NAD	C5N-C4N-C3N	-7.39	113.10	120.36
3	A	313	NAD	C3N-C7N-N7N	5.47	124.47	117.74
3	C	314	NAD	C3N-C7N-N7N	5.07	123.98	117.74
3	D	315	NAD	C3N-C7N-N7N	4.91	123.79	117.74
3	A	313	NAD	C6N-C5N-C4N	4.19	125.48	119.45
3	C	314	NAD	C6N-C5N-C4N	3.95	125.14	119.45
3	C	314	NAD	C6N-N1N-C2N	-3.90	118.56	121.88
3	D	315	NAD	C6N-C5N-C4N	3.54	124.55	119.45
3	A	313	NAD	C6N-N1N-C2N	-3.49	118.91	121.88
3	D	315	NAD	C6N-N1N-C2N	-3.31	119.06	121.88
3	A	313	NAD	O7N-C7N-C3N	-3.19	115.70	119.60
3	D	315	NAD	O7N-C7N-C3N	-2.92	116.03	119.60
3	C	314	NAD	O7N-C7N-C3N	-2.51	116.53	119.60
3	C	314	NAD	O2N-PN-O5D	2.43	118.58	107.57
3	A	313	NAD	O2N-PN-O5D	2.43	118.57	107.57
3	D	315	NAD	O2N-PN-O5D	2.34	118.16	107.57
3	C	314	NAD	O4B-C1B-C2B	-2.18	101.95	106.62
3	C	314	NAD	O7N-C7N-N7N	-2.16	119.49	122.62
3	A	313	NAD	O4D-C4D-C5D	-2.04	102.80	109.33

There are no chirality outliers.

All (30) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	313	NAD	C5D-O5D-PN-O3
3	A	313	NAD	C5D-O5D-PN-O2N
3	A	313	NAD	O4D-C1D-N1N-C2N
3	A	313	NAD	O4D-C1D-N1N-C6N
3	A	313	NAD	C2D-C1D-N1N-C2N
3	A	313	NAD	C2D-C1D-N1N-C6N
3	C	314	NAD	C5D-O5D-PN-O3
3	C	314	NAD	C5D-O5D-PN-O2N
3	C	314	NAD	O4D-C1D-N1N-C2N
3	C	314	NAD	O4D-C1D-N1N-C6N
3	C	314	NAD	C2D-C1D-N1N-C2N
3	C	314	NAD	C2D-C1D-N1N-C6N
3	D	315	NAD	C5D-O5D-PN-O3
3	D	315	NAD	C5D-O5D-PN-O2N
3	D	315	NAD	O4D-C1D-N1N-C2N
3	D	315	NAD	O4D-C1D-N1N-C6N
3	D	315	NAD	C2D-C1D-N1N-C2N

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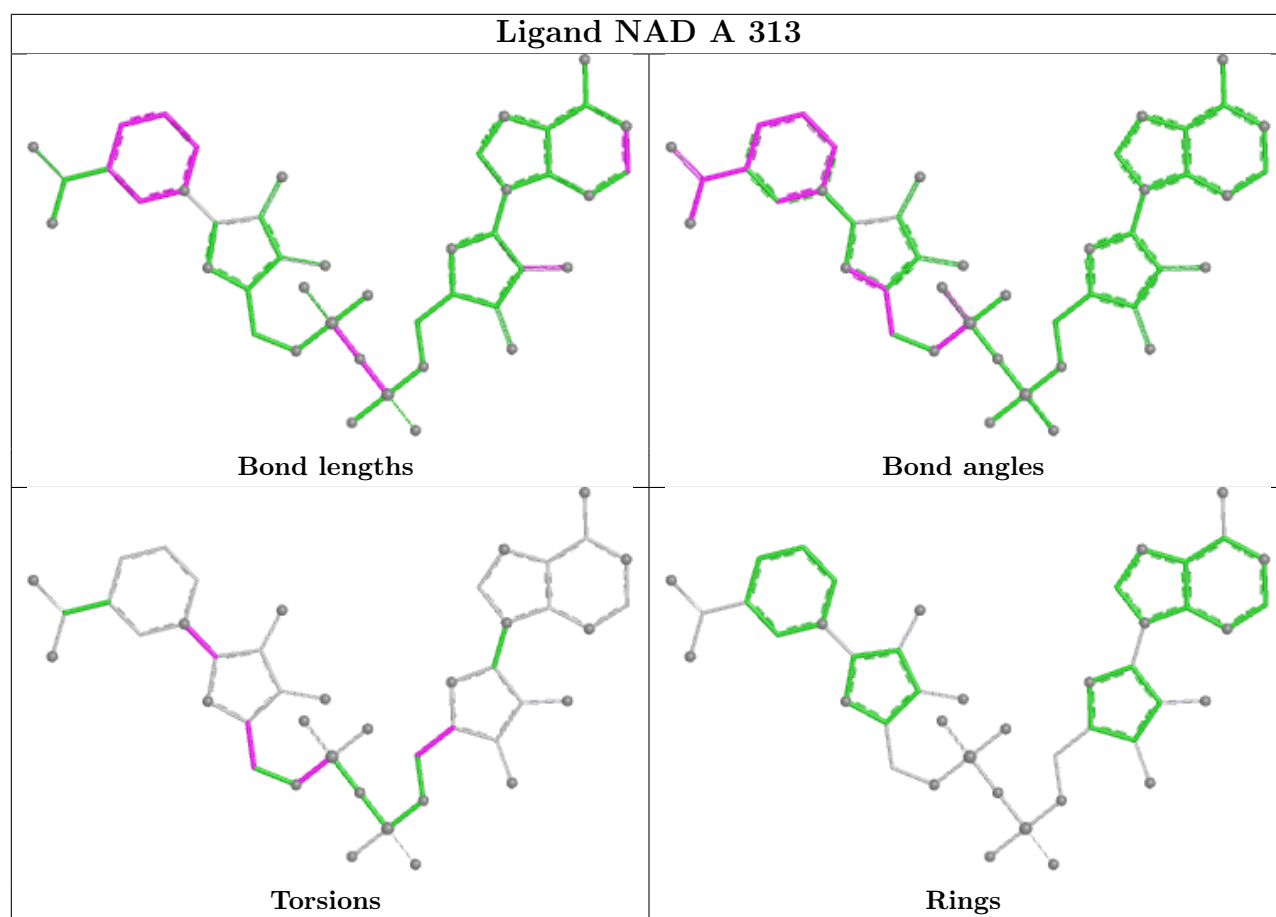
Mol	Chain	Res	Type	Atoms
3	D	315	NAD	C2D-C1D-N1N-C6N
3	C	314	NAD	C3D-C4D-C5D-O5D
3	D	315	NAD	C3D-C4D-C5D-O5D
3	C	314	NAD	O4D-C4D-C5D-O5D
3	D	315	NAD	O4D-C4D-C5D-O5D
3	A	313	NAD	O4D-C4D-C5D-O5D
3	A	313	NAD	C3D-C4D-C5D-O5D
3	A	313	NAD	C5D-O5D-PN-O1N
3	C	314	NAD	C5D-O5D-PN-O1N
3	D	315	NAD	C5D-O5D-PN-O1N
3	A	313	NAD	O4B-C4B-C5B-O5B
3	C	314	NAD	O4B-C4B-C5B-O5B
3	D	315	NAD	O4B-C4B-C5B-O5B

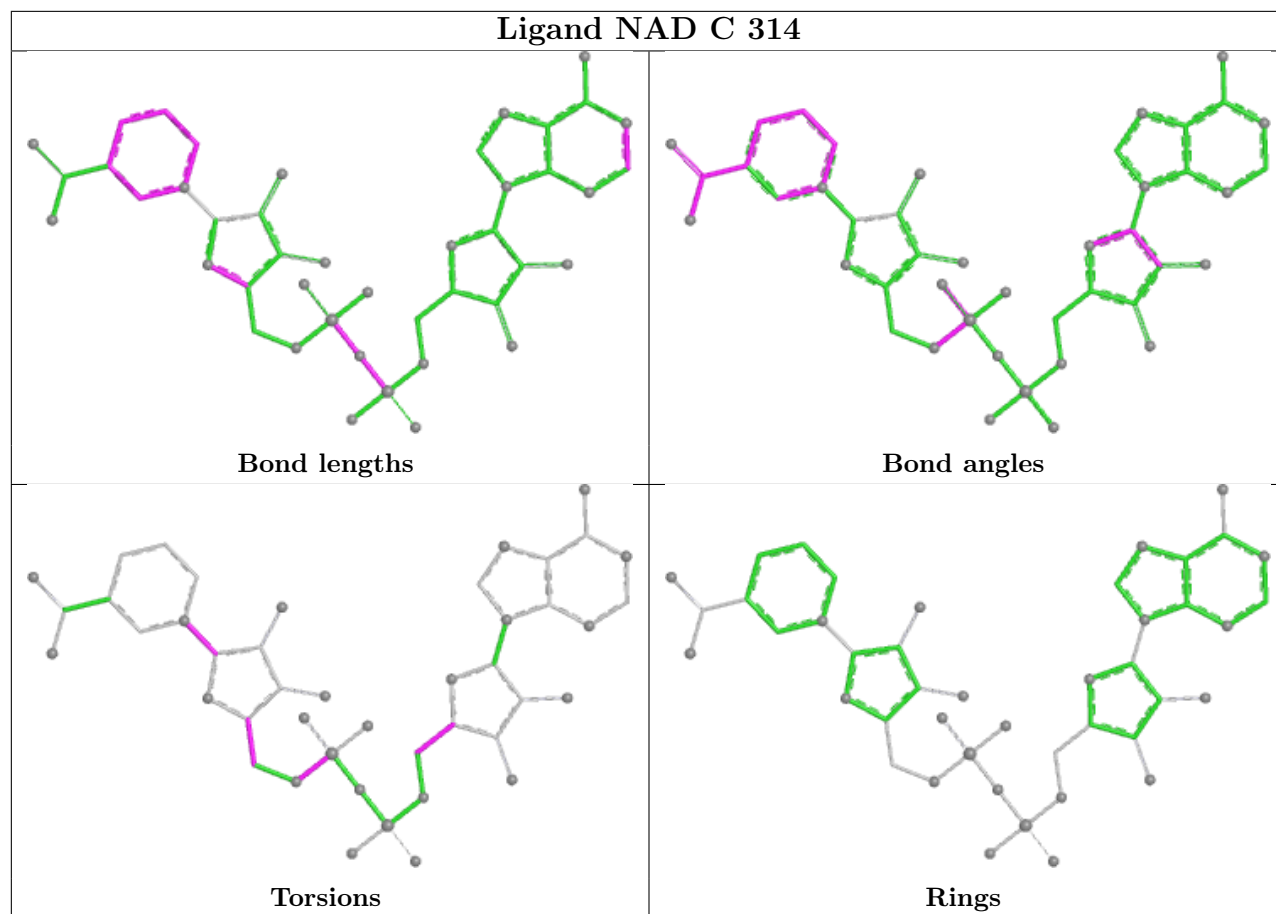
There are no ring outliers.

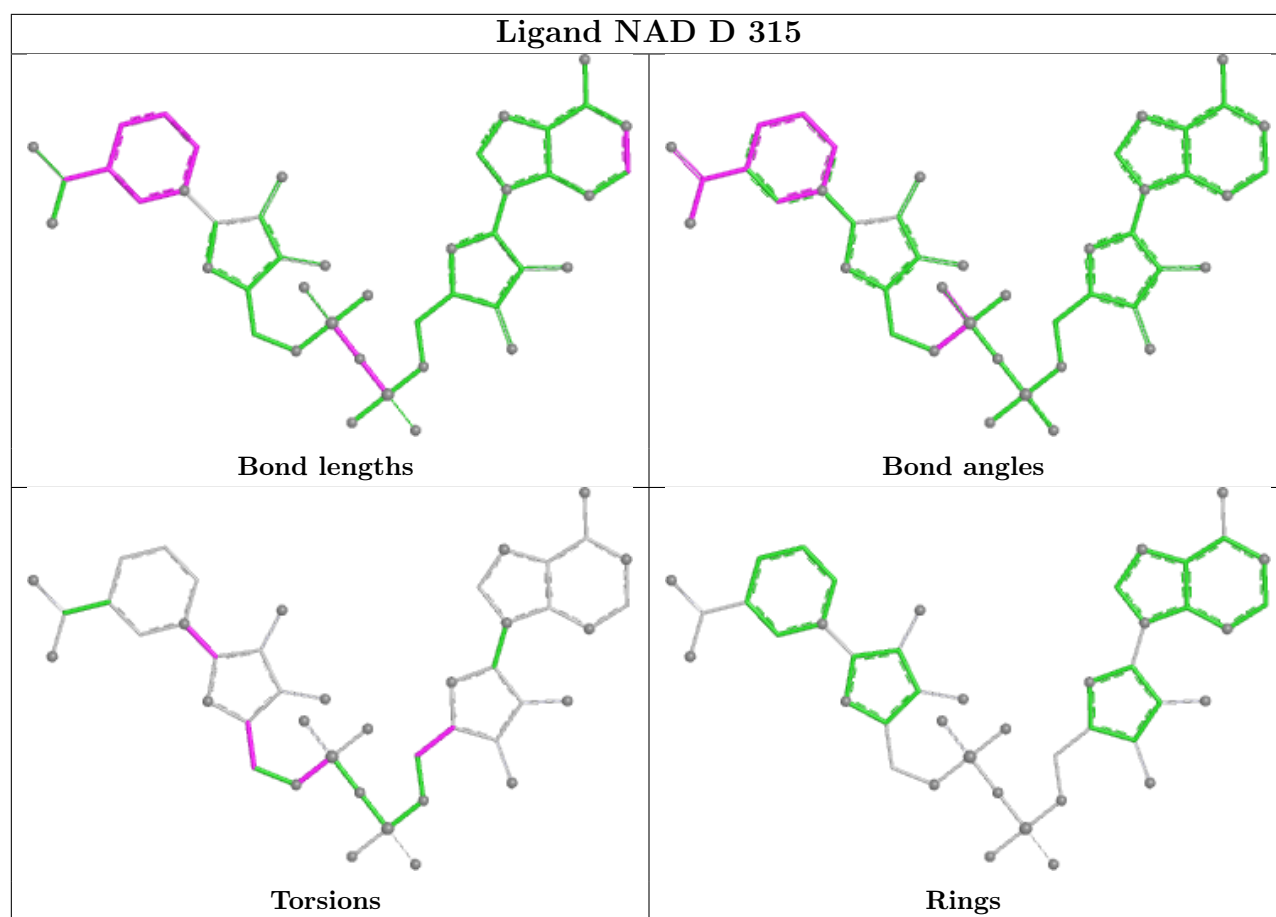
4 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	313	NAD	5	0
2	C	318	SO4	1	0
3	C	314	NAD	5	0
3	D	315	NAD	5	0

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







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	312/312 (100%)	-0.19	0 100 100	29, 45, 76, 93	0
1	B	312/312 (100%)	0.02	9 (2%) 53 56	27, 49, 79, 100	7 (2%)
1	C	312/312 (100%)	-0.44	0 100 100	25, 39, 62, 94	0
1	D	312/312 (100%)	-0.42	0 100 100	25, 41, 61, 92	0
All	All	1248/1248 (100%)	-0.26	9 (0%) 84 86	25, 44, 72, 100	7 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	85	MET	4.5
1	B	83	PRO	4.5
1	B	87	ARG	3.6
1	B	82	LYS	3.3
1	B	84	GLY	3.0
1	B	220	GLY	2.8
1	B	144	PHE	2.6
1	B	91	PHE	2.2
1	B	90	LEU	2.2

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

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

6.3 Carbohydrates [i](#)

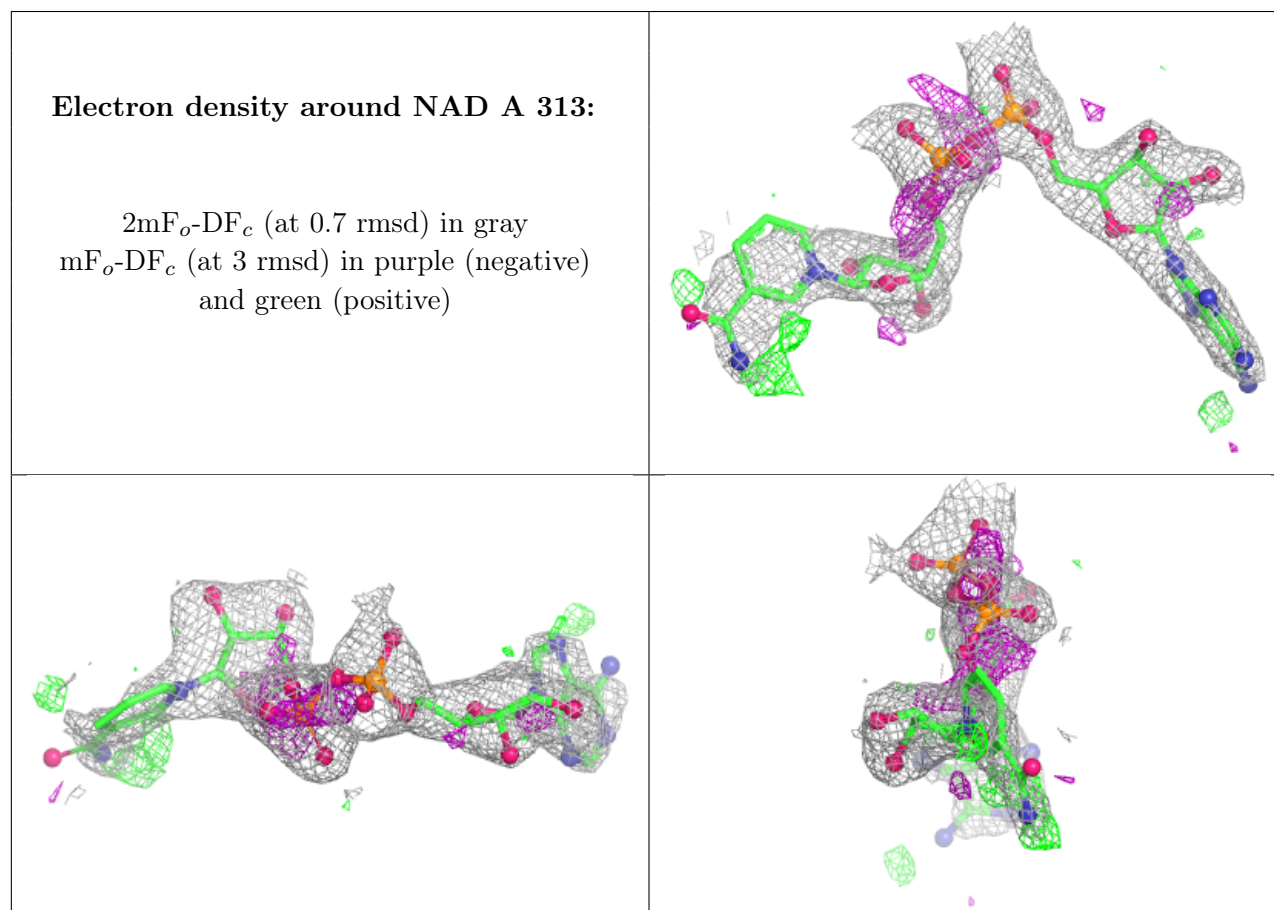
There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

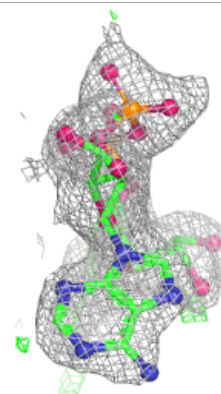
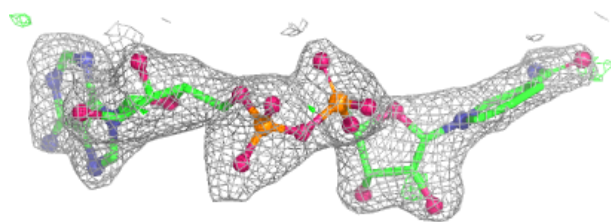
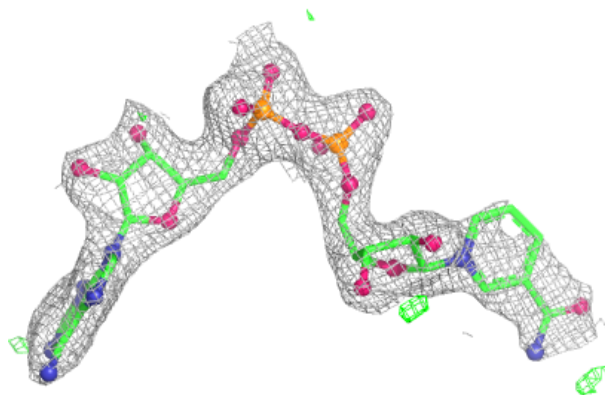
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SO4	A	316	5/5	0.84	0.13	97,100,100,100	0
3	NAD	A	313	44/44	0.86	0.16	37,61,74,80	20
2	SO4	A	317	5/5	0.88	0.11	46,48,54,57	5
2	SO4	D	321	5/5	0.89	0.09	55,61,66,69	5
2	SO4	C	318	5/5	0.91	0.12	56,58,62,67	5
2	SO4	C	319	5/5	0.93	0.08	27,39,45,47	5
3	NAD	C	314	44/44	0.94	0.09	35,44,54,56	44
2	SO4	D	320	5/5	0.95	0.08	52,55,67,67	0
3	NAD	D	315	44/44	0.97	0.08	22,34,49,56	43

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.

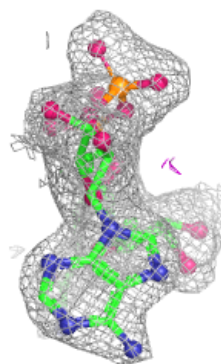
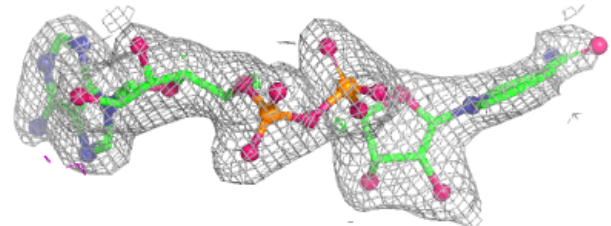
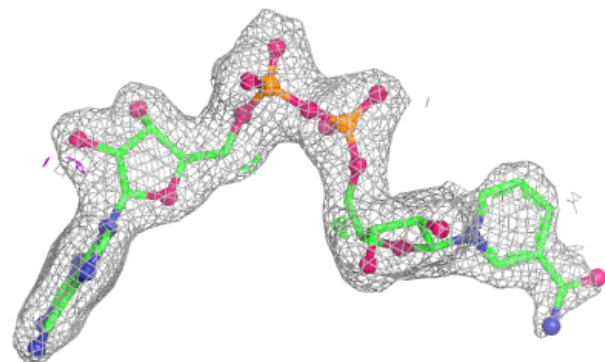


Electron density around NAD C 314:

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

**Electron density around NAD D 315:**

$2mF_o-DF_c$ (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.