



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 05:50 PM UTC

PDB ID : 1XCB / pdb_00001xcb
Title : X-ray Structure of a Rex-Family Repressor/NADH Complex from *Thermus Aquaticus*
Authors : Sickmier, E.A.; Brekasis, D.; Paranawithana, S.; Bonanno, J.B.; Burley, S.K.; Paget, M.S.; Kielkopf, C.L.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2004-09-01
Resolution : 2.90 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](#) ①) 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

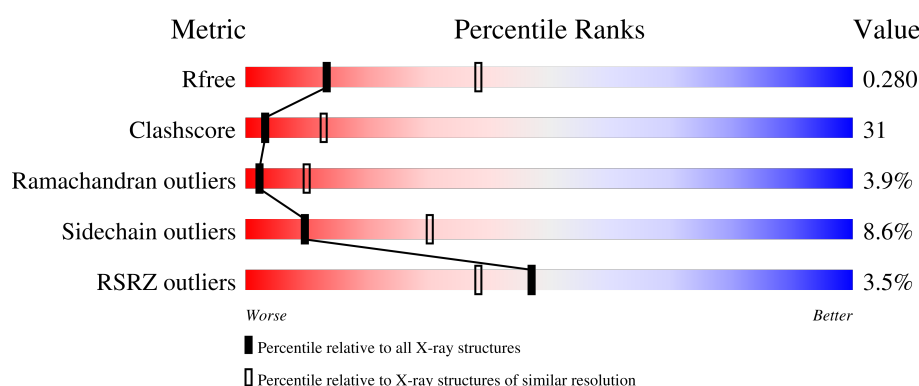
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	211	3% 45% 40% 10% • •
1	B	211	51% 35% 7% • 7%
1	C	211	3% 50% 41% 6% •
1	D	211	2% 45% 40% 8% 7%
1	E	211	% 51% 39% 5% • •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	211	2% 44% 41% 9% • 5%
1	G	211	12% 47% 35% 7% • 9%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11159 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 Redox-sensing transcriptional repressor rex.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	Se	0	0	0
			1591	1025	283	281	1	1			
1	B	197	Total	C	N	O	S	Se	0	0	0
			1530	986	271	271	1	1			
1	C	203	Total	C	N	O	S	Se	0	0	0
			1566	1008	277	279	1	1			
1	D	197	Total	C	N	O	S	Se	0	0	0
			1531	989	268	272	1	1			
1	E	203	Total	C	N	O	S	Se	0	0	0
			1565	1007	276	279	1	2			
1	F	200	Total	C	N	O	S	Se	0	0	0
			1558	1005	274	277	1	1			
1	G	192	Total	C	N	O	S	Se	0	2	0
			1505	973	263	267	1	1			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	modified residue	UNP Q9X2V5
A	88	MSE	MET	modified residue	UNP Q9X2V5
A	209	MSE	MET	modified residue	UNP Q9X2V5
A	210	MSE	MET	modified residue	UNP Q9X2V5
B	1	MSE	MET	modified residue	UNP Q9X2V5
B	88	MSE	MET	modified residue	UNP Q9X2V5
B	209	MSE	MET	modified residue	UNP Q9X2V5
B	210	MSE	MET	modified residue	UNP Q9X2V5
C	1	MSE	MET	modified residue	UNP Q9X2V5
C	88	MSE	MET	modified residue	UNP Q9X2V5
C	209	MSE	MET	modified residue	UNP Q9X2V5
C	210	MSE	MET	modified residue	UNP Q9X2V5
D	1	MSE	MET	modified residue	UNP Q9X2V5
D	88	MSE	MET	modified residue	UNP Q9X2V5
D	209	MSE	MET	modified residue	UNP Q9X2V5

Continued on next page...

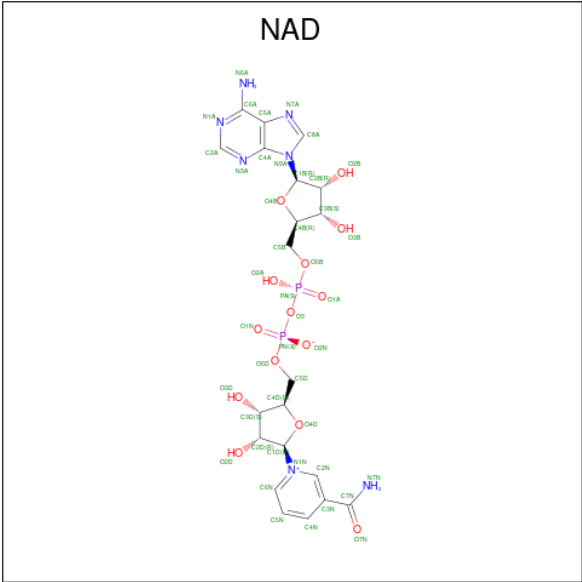
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
D	210	MSE	MET	modified residue	UNP Q9X2V5
E	1	MSE	MET	modified residue	UNP Q9X2V5
E	88	MSE	MET	modified residue	UNP Q9X2V5
E	209	MSE	MET	modified residue	UNP Q9X2V5
E	210	MSE	MET	modified residue	UNP Q9X2V5
F	1	MSE	MET	modified residue	UNP Q9X2V5
F	88	MSE	MET	modified residue	UNP Q9X2V5
F	209	MSE	MET	modified residue	UNP Q9X2V5
F	210	MSE	MET	modified residue	UNP Q9X2V5
G	1	MSE	MET	modified residue	UNP Q9X2V5
G	88	MSE	MET	modified residue	UNP Q9X2V5
G	209	MSE	MET	modified residue	UNP Q9X2V5
G	210	MSE	MET	modified residue	UNP Q9X2V5

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0
2	B	1	Total Ca 1 1	0	0
2	C	1	Total Ca 1 1	0	0
2	D	2	Total Ca 2 2	0	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).

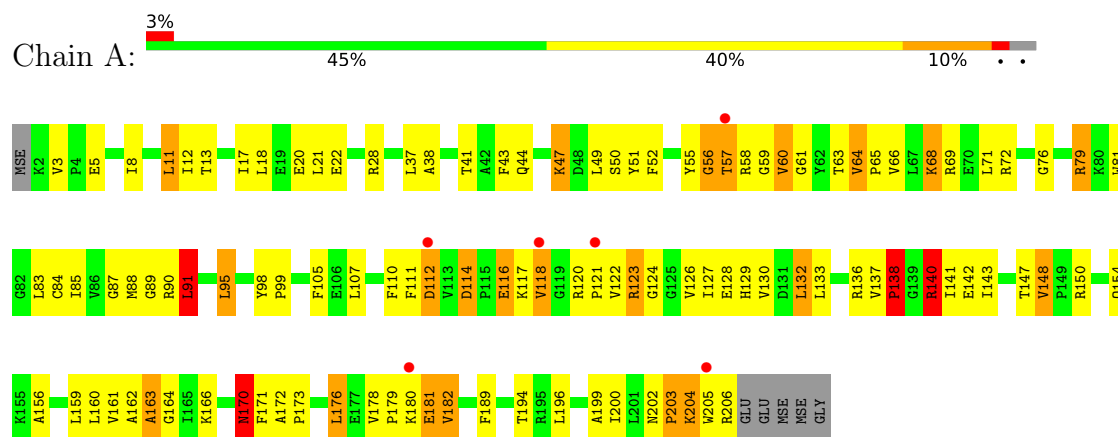


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	G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

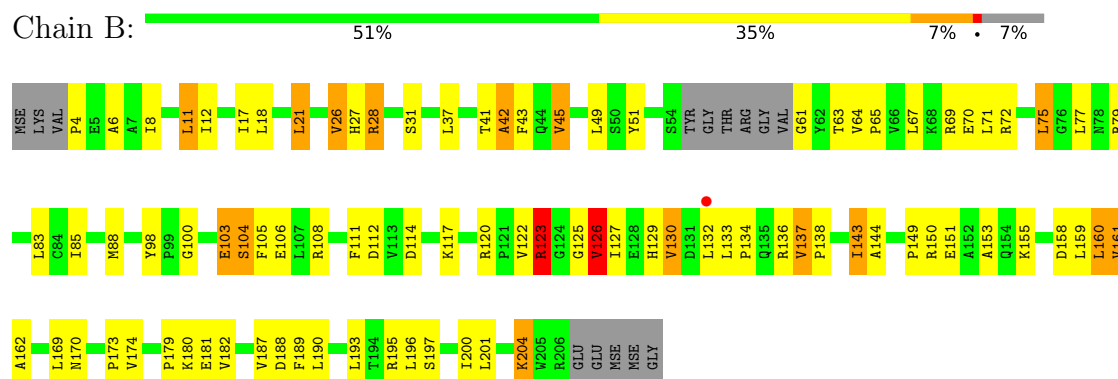
3 Residue-property plots

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

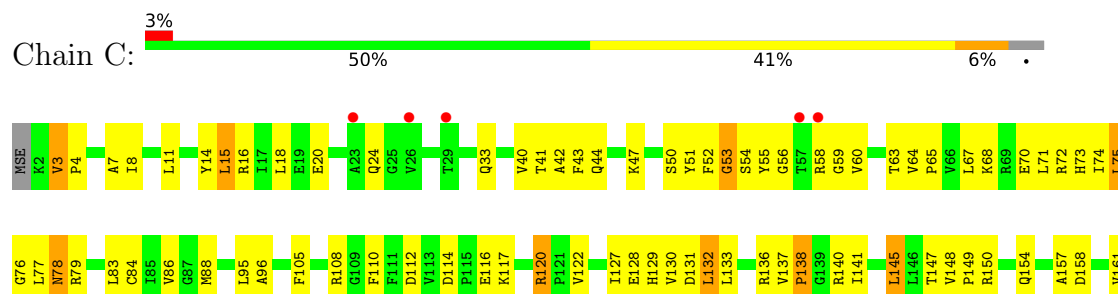
- Molecule 1: Redox-sensing transcriptional repressor rex



- Molecule 1: Redox-sensing transcriptional repressor rex

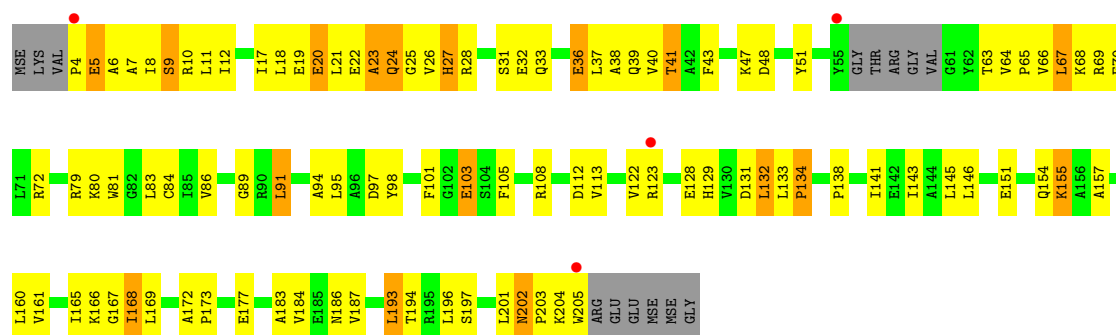
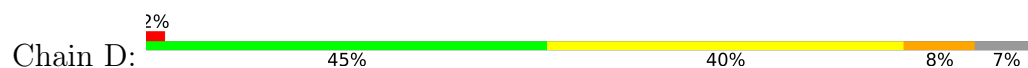


- Molecule 1: Redox-sensing transcriptional repressor rex

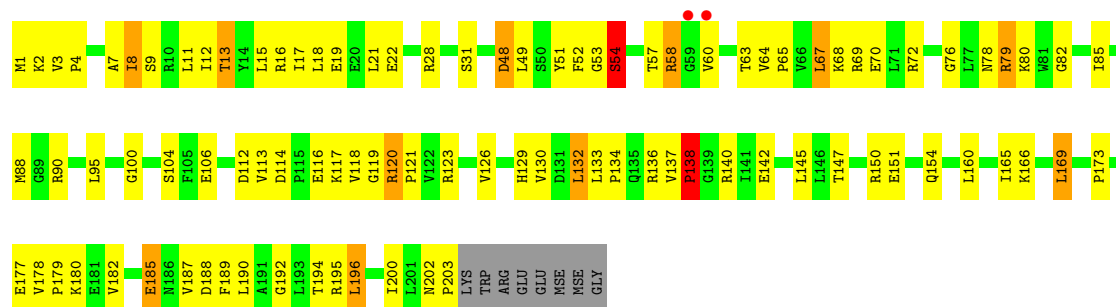




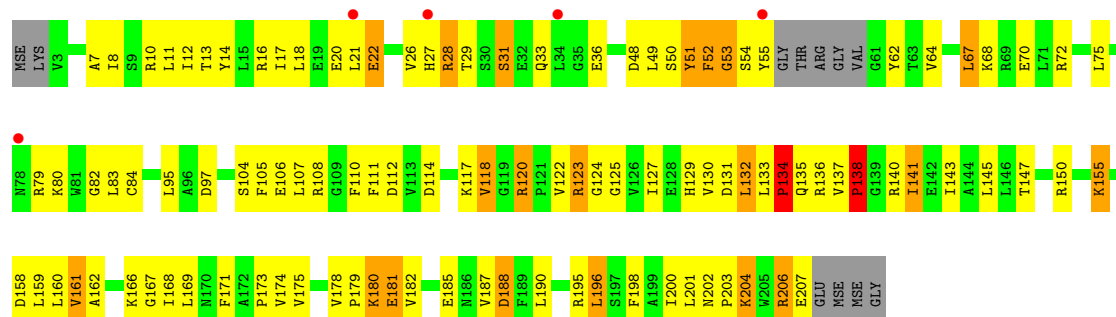
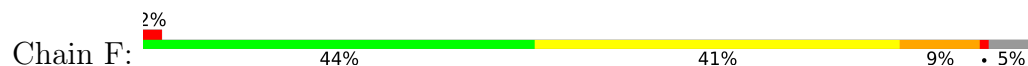
- Molecule 1: Redox-sensing transcriptional repressor rex



- Molecule 1: Redox-sensing transcriptional repressor rex

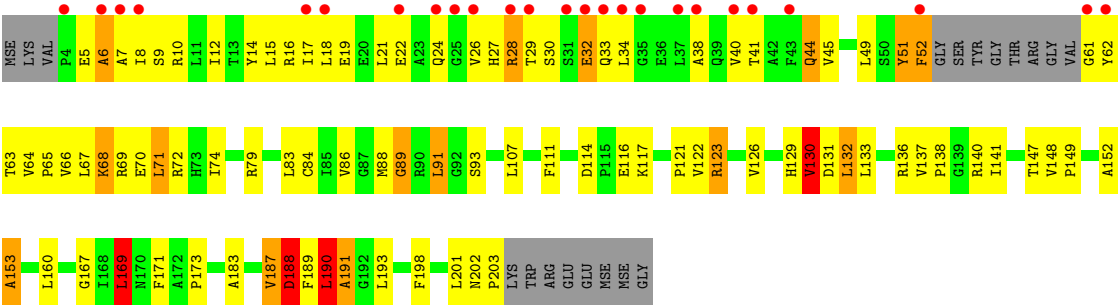


- Molecule 1: Redox-sensing transcriptional repressor rex



- Molecule 1: Redox-sensing transcriptional repressor rex





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	189.24Å 88.97Å 112.91Å 90.00° 106.09° 90.00°	Depositor
Resolution (Å)	20.00 – 2.90 20.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.90) 96.0 (20.00-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.87 (at 2.88Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.228 , 0.276 0.232 , 0.280	Depositor DCC
R_{free} test set	5215 reflections (6.68%)	wwPDB-VP
Wilson B-factor (Å ²)	35.8	Xtriage
Anisotropy	0.355	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 36.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	11159	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.03% 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: CA, NAD

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	0.45	0/1621	1.04	12/2194 (0.5%)
1	B	0.50	0/1558	0.97	7/2107 (0.3%)
1	C	0.45	0/1594	0.96	3/2157 (0.1%)
1	D	0.46	0/1560	1.03	8/2111 (0.4%)
1	E	0.52	0/1593	1.06	2/2156 (0.1%)
1	F	0.43	0/1587	0.98	8/2148 (0.4%)
1	G	0.72	9/1532 (0.6%)	1.04	11/2073 (0.5%)
All	All	0.51	9/11045 (0.1%)	1.01	51/14946 (0.3%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	G	0	2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	191	ALA	N-CA	-11.90	1.31	1.46
1	G	191	ALA	CA-C	-7.32	1.42	1.52
1	G	188	ASP	CA-CB	-7.01	1.41	1.53
1	G	188	ASP	C-O	-6.94	1.15	1.23
1	G	188	ASP	N-CA	6.40	1.54	1.46
1	G	190[A]	LEU	C-O	-5.55	1.16	1.24
1	G	190[B]	LEU	C-O	-5.55	1.16	1.24
1	G	188	ASP	C-N	5.42	1.41	1.34
1	G	191	ALA	CA-CB	-5.23	1.44	1.53

All (51) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	51	TYR	N-CA-C	-9.10	101.36	111.28
1	D	6	ALA	N-CA-C	-8.26	104.07	114.56
1	A	140	ARG	N-CA-C	7.87	123.06	113.38
1	C	129	HIS	N-CA-C	-7.22	101.21	110.53
1	F	202	ASN	CA-C-N	6.95	126.20	118.97
1	F	202	ASN	C-N-CA	6.95	126.20	118.97
1	A	170	ASN	N-CA-C	6.46	119.26	108.73
1	G	51	TYR	N-CA-C	-6.37	106.72	114.75
1	A	163	ALA	N-CA-C	-6.35	105.91	113.21
1	G	6	ALA	N-CA-C	-6.32	105.55	113.20
1	E	31	SER	N-CA-C	-6.22	104.95	112.54
1	G	169	LEU	N-CA-C	-6.20	97.07	107.99
1	B	42	ALA	N-CA-C	-6.18	104.55	111.28
1	A	136	ARG	N-CA-C	-6.09	106.83	114.56
1	A	91	LEU	N-CA-C	-6.00	104.65	111.07
1	D	24	GLN	N-CA-C	-5.98	105.91	112.72
1	F	171	PHE	N-CA-C	-5.92	106.39	113.97
1	D	23	ALA	N-CA-C	-5.91	104.91	111.71
1	F	31	SER	N-CA-C	-5.90	104.85	111.28
1	G	188	ASP	N-CA-C	5.83	117.75	107.60
1	D	20	GLU	N-CA-C	-5.79	105.89	113.12
1	G	111	PHE	N-CA-C	5.78	118.83	109.40
1	A	114	ASP	CA-C-N	5.71	125.39	119.56
1	A	114	ASP	C-N-CA	5.71	125.39	119.56
1	G	44	GLN	N-CA-C	-5.70	104.75	110.97
1	A	172	ALA	CA-C-N	5.68	126.94	119.84
1	A	172	ALA	C-N-CA	5.68	126.94	119.84
1	B	189	PHE	N-CA-C	-5.63	106.25	113.23
1	B	195	ARG	N-CA-C	-5.50	105.39	111.71
1	A	38	ALA	N-CA-C	-5.48	106.64	113.38
1	B	137	VAL	N-CA-C	5.48	120.72	108.88
1	B	170	ASN	N-CA-C	5.46	117.60	109.25
1	D	9	SER	N-CA-C	-5.43	105.47	111.71
1	F	195	ARG	N-CA-C	-5.40	105.48	111.36
1	A	20	GLU	N-CA-C	-5.38	105.49	111.36
1	F	120	ARG	N-CA-C	5.37	117.21	109.48
1	G	191	ALA	CB-CA-C	5.36	120.95	110.67
1	G	188	ASP	CA-C-N	-5.35	111.32	121.54
1	G	188	ASP	C-N-CA	-5.35	111.32	121.54
1	F	22	GLU	N-CA-C	-5.35	105.53	111.36
1	D	202	ASN	CA-C-N	5.32	126.49	119.84
1	D	202	ASN	C-N-CA	5.32	126.49	119.84
1	G	198	PHE	N-CA-C	-5.29	105.42	111.14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	156	ALA	N-CA-C	-5.21	106.42	112.89
1	C	131	ASP	N-CA-C	5.21	118.74	112.38
1	B	28	ARG	N-CA-C	5.21	118.06	109.72
1	D	12	ILE	N-CA-C	-5.19	105.33	110.62
1	G	89	GLY	N-CA-C	-5.12	105.29	112.60
1	F	141	ILE	N-CA-C	5.11	115.71	106.61
1	B	143	ILE	N-CA-C	5.07	115.27	108.17
1	C	42	ALA	N-CA-C	-5.07	105.76	111.28

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	G	188	ASP	Mainchain
1	G	190[A]	LEU	Mainchain

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	1591	0	1649	125	0
1	B	1530	0	1583	100	0
1	C	1566	0	1626	105	0
1	D	1531	0	1579	110	0
1	E	1565	0	1625	93	0
1	F	1558	0	1606	120	0
1	G	1505	0	1558	101	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	2	0	0	0	0
3	A	44	0	26	4	0
3	B	44	0	26	3	0
3	C	44	0	26	4	0
3	D	44	0	26	1	0
3	E	44	0	26	2	0
3	F	44	0	26	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	44	0	26	5	0
All	All	11159	0	11408	697	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 31.

All (697) 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:E:132:LEU:HD13	1:E:132:LEU:H	1.15	1.06
1:E:154:GLN:NE2	1:E:177:GLU:HB3	1.71	1.06
1:G:122:VAL:HG12	1:G:123:ARG:H	1.20	1.06
1:A:60:VAL:HG23	1:A:61:GLY:H	1.26	1.01
1:C:132:LEU:HD12	1:C:132:LEU:H	1.19	1.01
1:A:176:LEU:H	1:A:176:LEU:HD22	1.28	0.98
1:F:180:LYS:H	1:F:180:LYS:HD3	1.28	0.97
1:C:195:ARG:HH22	1:D:9:SER:HB3	1.28	0.97
1:A:57:THR:HG23	1:A:58:ARG:H	1.31	0.95
1:C:114:ASP:HB3	1:C:117:LYS:HG3	1.47	0.94
1:D:21:LEU:HD23	1:D:26:VAL:HB	1.48	0.92
1:B:122:VAL:HG12	1:B:123:ARG:HG2	1.52	0.91
1:F:80:LYS:HZ3	1:F:106:GLU:HB3	1.32	0.91
1:F:137:VAL:HB	1:F:138:PRO:HD3	1.53	0.91
1:D:86:VAL:HG21	1:D:160:LEU:HD21	1.54	0.90
1:C:63:THR:HG22	1:C:65:PRO:HD2	1.54	0.89
1:F:80:LYS:NZ	1:F:108:ARG:HH21	1.69	0.89
1:E:132:LEU:HD13	1:E:132:LEU:N	1.87	0.89
1:G:27:HIS:HB2	1:G:65:PRO:HD3	1.54	0.89
1:B:88:MSE:HA	1:B:88:MSE:HE2	1.55	0.89
1:A:90:ARG:HB2	3:A:213:NAD:O2N	1.73	0.88
1:C:132:LEU:HD12	1:C:132:LEU:N	1.87	0.88
1:A:132:LEU:N	1:A:132:LEU:HD12	1.91	0.86
1:E:4:PRO:HG2	1:E:7:ALA:HB2	1.57	0.85
1:E:196:LEU:HD13	1:F:185:GLU:HB2	1.57	0.85
1:A:170:ASN:ND2	1:A:176:LEU:HD21	1.92	0.84
1:A:84:CYS:HB3	1:A:141:ILE:HD13	1.58	0.83
1:E:200:ILE:HD13	1:F:166:LYS:HB3	1.60	0.83
1:F:161:VAL:HG11	1:F:178:VAL:HB	1.61	0.83
1:E:189:PHE:C	1:E:190:LEU:HD12	2.04	0.82
1:E:154:GLN:HE22	1:E:177:GLU:HB3	1.45	0.81
1:A:85:ILE:HB	1:A:88:MSE:HE3	1.63	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:30:SER:HA	1:G:61:GLY:HA2	1.61	0.81
1:F:16:ARG:HB3	1:F:16:ARG:NH1	1.94	0.81
1:F:204:LYS:HB2	1:F:204:LYS:NZ	1.95	0.80
1:C:150:ARG:HG3	1:C:173:PRO:HG2	1.64	0.80
1:C:137:VAL:HB	1:C:138:PRO:HD3	1.66	0.78
1:D:132:LEU:N	1:D:132:LEU:HD23	2.00	0.77
1:F:84:CYS:HB3	1:F:141:ILE:HD13	1.66	0.77
1:D:83:LEU:HD22	1:D:143:ILE:HB	1.66	0.77
1:C:132:LEU:H	1:C:132:LEU:CD1	1.98	0.77
1:A:128:GLU:OE2	1:A:132:LEU:HD22	1.85	0.77
1:F:18:LEU:HA	1:F:21:LEU:HG	1.66	0.76
1:F:120:ARG:HB3	1:F:127:ILE:HD12	1.65	0.76
1:G:63:THR:HG22	1:G:65:PRO:HD2	1.67	0.76
1:A:176:LEU:H	1:A:176:LEU:CD2	1.99	0.76
1:F:10:ARG:HD2	1:F:48:ASP:OD1	1.86	0.76
1:E:200:ILE:HD13	1:F:166:LYS:CB	2.15	0.75
1:F:16:ARG:HB3	1:F:16:ARG:HH11	1.50	0.75
1:F:188:ASP:OD2	1:F:190:LEU:HB2	1.86	0.75
1:D:7:ALA:O	1:D:11:LEU:HG	1.86	0.75
1:F:21:LEU:HD13	1:F:26:VAL:HG11	1.69	0.75
1:D:68:LYS:O	1:D:72:ARG:HG2	1.87	0.75
1:G:41:THR:OG1	1:G:44:GLN:HG3	1.87	0.75
1:A:22:GLU:OE1	1:A:68:LYS:HE3	1.87	0.74
1:A:176:LEU:HD22	1:A:176:LEU:N	2.02	0.74
1:G:121:PRO:HA	1:G:126:VAL:HG12	1.69	0.74
1:E:178:VAL:HB	1:E:179:PRO:HD2	1.68	0.74
1:B:129:HIS:CG	1:B:130:VAL:H	2.05	0.74
1:C:84:CYS:HB3	1:C:141:ILE:HG21	1.70	0.74
1:A:88:MSE:HE2	1:A:88:MSE:HA	1.69	0.73
1:G:17:ILE:O	1:G:21:LEU:HD23	1.89	0.73
1:A:91:LEU:HD22	1:A:95:LEU:HD22	1.69	0.73
1:B:75:LEU:HB3	1:B:77:LEU:CD2	2.19	0.73
1:G:24:GLN:HB2	1:G:26:VAL:HG22	1.71	0.73
1:C:3:VAL:HG13	1:D:205:TRP:CH2	2.24	0.73
1:A:60:VAL:HG23	1:A:61:GLY:N	2.03	0.73
1:C:190:LEU:HD21	1:D:101:PHE:CE1	2.24	0.72
1:G:122:VAL:HG12	1:G:123:ARG:N	1.98	0.72
1:A:170:ASN:CG	1:A:176:LEU:HD21	2.14	0.72
1:E:19:GLU:HG2	1:E:68:LYS:NZ	2.04	0.72
1:D:157:ALA:O	1:D:161:VAL:HG23	1.89	0.72
1:G:189[B]:PHE:C	1:G:191:ALA:N	2.44	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:155:LYS:O	1:F:159:LEU:HD23	1.89	0.71
1:G:173:PRO:HD3	3:G:212:NAD:O2D	1.90	0.71
1:D:72:ARG:HG3	1:D:72:ARG:HH11	1.55	0.71
1:A:64:VAL:HB	1:A:65:PRO:HD3	1.71	0.71
1:B:75:LEU:HB3	1:B:77:LEU:HD23	1.71	0.70
1:F:180:LYS:HD3	1:F:180:LYS:N	2.03	0.70
1:B:21:LEU:HG	1:B:26:VAL:HG21	1.72	0.70
1:A:120:ARG:HE	1:A:127:ILE:HD12	1.55	0.70
1:B:28:ARG:NH2	1:B:61:GLY:N	2.39	0.70
1:A:112:ASP:OD1	3:A:213:NAD:H1B	1.91	0.70
1:A:57:THR:HG23	1:A:58:ARG:HG3	1.73	0.70
1:D:89:GLY:HA3	3:D:214:NAD:O5B	1.92	0.70
1:F:133:LEU:HB2	1:F:134:PRO:HD3	1.72	0.69
1:C:114:ASP:CB	1:C:117:LYS:HG3	2.21	0.69
1:C:204:LYS:HD2	1:D:5:GLU:HG3	1.74	0.69
1:C:88:MSE:HE1	1:C:96:ALA:HB2	1.75	0.69
1:F:80:LYS:NZ	1:F:108:ARG:NH2	2.41	0.69
1:G:45:VAL:O	1:G:49:LEU:HD13	1.93	0.68
1:C:64:VAL:HB	1:C:65:PRO:HD3	1.75	0.68
1:A:132:LEU:HD12	1:A:132:LEU:H	1.56	0.68
1:B:120:ARG:HB3	1:B:127:ILE:HD12	1.75	0.68
1:E:169:LEU:HD22	1:E:187:VAL:HG23	1.74	0.68
1:A:122:VAL:O	1:A:124:GLY:N	2.27	0.67
1:G:189[B]:PHE:O	1:G:191:ALA:N	2.27	0.67
1:G:169:LEU:HD22	1:G:187:VAL:HG12	1.77	0.67
1:E:79:ARG:O	1:E:80:LYS:HB3	1.95	0.67
1:F:49:LEU:HB3	1:F:54:SER:OG	1.95	0.67
1:D:27:HIS:ND1	1:D:28:ARG:HG3	2.09	0.66
1:D:122:VAL:HG12	1:D:123:ARG:N	2.10	0.66
1:G:83:LEU:HB3	1:G:107:LEU:HD23	1.77	0.66
1:G:171:PHE:CE2	1:G:187:VAL:HG21	2.30	0.66
1:A:117:LYS:NZ	3:A:213:NAD:O3B	2.23	0.66
1:C:70:GLU:O	1:C:74:ILE:HG13	1.95	0.66
1:D:63:THR:HB	1:D:66:VAL:HB	1.77	0.66
1:G:15:LEU:O	1:G:19:GLU:HG3	1.95	0.66
1:A:83:LEU:HD23	1:A:143:ILE:HB	1.78	0.65
1:G:28:ARG:N	1:G:64:VAL:HG23	2.12	0.65
1:B:117:LYS:NZ	3:B:213:NAD:O3B	2.28	0.65
1:G:169:LEU:HD22	1:G:187:VAL:CG1	2.26	0.65
1:A:57:THR:HG23	1:A:58:ARG:N	2.09	0.65
1:B:83:LEU:HD11	1:B:105:PHE:HB3	1.79	0.65

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:117:LYS:NZ	3:E:212:NAD:O3B	2.29	0.65
1:A:120:ARG:HE	1:A:127:ILE:CD1	2.10	0.64
1:C:58:ARG:NH1	1:C:60:VAL:HB	2.12	0.64
1:G:137:VAL:HG13	1:G:141:ILE:O	1.97	0.64
1:B:150:ARG:HG3	1:B:174:VAL:CG1	2.27	0.64
1:A:81:TRP:CZ2	1:B:201:LEU:HD11	2.33	0.64
1:A:95:LEU:HD21	1:A:171:PHE:CZ	2.33	0.64
1:G:17:ILE:HD11	1:G:34:LEU:HG	1.80	0.64
1:E:132:LEU:H	1:E:132:LEU:CD1	1.89	0.63
1:F:160:LEU:C	1:F:162:ALA:H	2.05	0.63
1:B:27:HIS:CD2	1:B:28:ARG:HG3	2.33	0.63
1:C:3:VAL:HG13	1:D:205:TRP:HH2	1.63	0.63
1:D:202:ASN:O	1:D:205:TRP:HB2	1.98	0.63
1:A:81:TRP:CH2	1:B:201:LEU:HD11	2.34	0.63
1:F:204:LYS:HB2	1:F:204:LYS:HZ2	1.64	0.63
1:D:32:GLU:O	1:D:36:GLU:HB2	1.97	0.63
1:F:131:ASP:O	1:F:134:PRO:HD2	1.99	0.63
1:B:149:PRO:HD3	3:B:213:NAD:C5B	2.28	0.63
1:E:19:GLU:HG2	1:E:68:LYS:HZ2	1.63	0.63
1:D:41:THR:HG21	1:G:116:GLU:HA	1.79	0.62
1:E:11:LEU:HD11	1:E:52:PHE:CE1	2.33	0.62
1:F:28:ARG:HA	1:F:62:TYR:O	1.99	0.62
1:A:68:LYS:NZ	1:A:68:LYS:HB3	2.14	0.62
1:A:132:LEU:N	1:A:132:LEU:CD1	2.60	0.62
1:C:148:VAL:HG13	1:C:149:PRO:HD2	1.80	0.62
1:D:38:ALA:O	1:D:39:GLN:HB2	1.97	0.62
1:G:84:CYS:HB3	1:G:141:ILE:HG21	1.82	0.62
1:A:84:CYS:HB2	1:A:111:PHE:HE1	1.64	0.62
1:E:54:SER:HB3	1:E:70:GLU:OE2	1.99	0.62
1:E:64:VAL:HB	1:E:65:PRO:HD3	1.82	0.62
1:E:200:ILE:HG21	1:F:166:LYS:HB3	1.81	0.62
1:A:43:PHE:O	1:A:47:LYS:HB2	2.00	0.62
1:F:80:LYS:NZ	1:F:106:GLU:OE1	2.32	0.62
1:B:132:LEU:O	1:B:136:ARG:HG2	1.99	0.62
1:C:161:VAL:C	1:C:163:ALA:H	2.07	0.61
1:F:150:ARG:HB2	1:F:174:VAL:CG1	2.30	0.61
1:A:162:ALA:C	1:A:164:GLY:H	2.08	0.61
1:E:196:LEU:CD1	1:F:185:GLU:HB2	2.30	0.61
1:F:132:LEU:HB3	1:F:136:ARG:NH1	2.15	0.61
1:C:181:GLU:CD	1:C:181:GLU:H	2.09	0.60
1:G:22:GLU:HB2	1:G:64:VAL:CG1	2.30	0.60

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:GLY:HA3	1:A:148:VAL:HG23	1.82	0.60
1:E:154:GLN:HE21	1:E:177:GLU:HB3	1.65	0.60
1:D:17:ILE:O	1:D:21:LEU:HB2	2.01	0.60
1:F:80:LYS:CE	1:F:108:ARG:HH21	2.14	0.60
1:F:80:LYS:HZ1	1:F:108:ARG:HH21	1.50	0.60
1:F:16:ARG:O	1:F:20:GLU:HG2	2.01	0.60
1:F:158:ASP:HA	1:F:161:VAL:HG22	1.83	0.60
1:A:83:LEU:HD11	1:A:105:PHE:HB3	1.82	0.60
1:C:70:GLU:HA	1:C:70:GLU:OE1	2.01	0.60
1:D:83:LEU:CD2	1:D:143:ILE:HB	2.32	0.60
1:F:67:LEU:O	1:F:70:GLU:HB2	2.02	0.60
1:B:106:GLU:OE1	1:B:108:ARG:HD2	2.02	0.60
1:A:204:LYS:HB3	1:A:204:LYS:HZ2	1.66	0.59
1:E:185:GLU:HB2	1:F:196:LEU:HG	1.82	0.59
1:F:33:GLN:O	1:F:36:GLU:HG2	2.01	0.59
1:B:181:GLU:CD	1:B:181:GLU:H	2.10	0.59
1:B:193:LEU:O	1:B:196:LEU:HB3	2.01	0.59
1:D:83:LEU:HD11	1:D:105:PHE:HB3	1.82	0.59
1:F:150:ARG:HB2	1:F:174:VAL:HG13	1.84	0.59
1:G:27:HIS:HB2	1:G:64:VAL:HB	1.84	0.59
1:A:3:VAL:HG22	1:A:51:TYR:HB3	1.84	0.59
1:G:114:ASP:OD2	1:G:117:LYS:HG3	2.02	0.59
1:F:80:LYS:HZ3	1:F:106:GLU:CB	2.09	0.59
1:B:161:VAL:HG22	1:B:182:VAL:HG21	1.84	0.59
1:F:137:VAL:HB	1:F:138:PRO:CD	2.28	0.59
1:B:28:ARG:HH21	1:B:61:GLY:N	2.01	0.58
1:F:82:GLY:HA3	1:F:140:ARG:O	2.04	0.58
1:B:129:HIS:CG	1:B:130:VAL:N	2.72	0.58
1:A:85:ILE:CB	1:A:88:MSE:HE3	2.32	0.58
1:A:121:PRO:HA	1:A:126:VAL:HG12	1.86	0.58
1:C:3:VAL:O	1:D:205:TRP:CH2	2.57	0.58
1:D:10:ARG:HD2	1:D:48:ASP:OD1	2.03	0.58
1:A:91:LEU:HD13	1:A:147:THR:HG22	1.86	0.58
1:B:180:LYS:HG3	1:B:181:GLU:OE2	2.04	0.58
1:E:160:LEU:O	1:E:165:ILE:HG13	2.04	0.58
1:G:40:VAL:HB	1:G:44:GLN:NE2	2.19	0.57
1:C:132:LEU:HD23	1:C:136:ARG:NH2	2.18	0.57
1:C:178:VAL:HB	1:C:179:PRO:HD2	1.85	0.57
1:F:80:LYS:HZ2	1:F:108:ARG:NH2	2.00	0.57
1:G:189[B]:PHE:O	1:G:190[B]:LEU:C	2.47	0.57
1:E:100:GLY:O	1:F:190:LEU:HD11	2.05	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:28:ARG:HD3	1:F:28:ARG:H	1.69	0.57
1:G:64:VAL:HB	1:G:65:PRO:HD3	1.85	0.57
1:B:72:ARG:HB3	1:B:72:ARG:HH11	1.68	0.57
1:B:129:HIS:CD2	1:B:130:VAL:H	2.22	0.57
1:E:63:THR:HG22	1:E:65:PRO:HD2	1.86	0.57
1:D:205:TRP:HA	1:D:205:TRP:CE3	2.39	0.57
1:F:21:LEU:HD12	1:F:22:GLU:N	2.19	0.57
1:A:133:LEU:HD21	1:A:160:LEU:HD23	1.87	0.56
1:B:149:PRO:HD3	3:B:213:NAD:H51A	1.85	0.56
1:E:169:LEU:HD22	1:E:187:VAL:CG2	2.35	0.56
1:E:121:PRO:HA	1:E:126:VAL:HG12	1.86	0.56
1:F:130:VAL:HG11	3:F:212:NAD:H2A	1.87	0.56
1:G:66:VAL:O	1:G:70:GLU:HG3	2.05	0.56
1:F:7:ALA:HA	1:F:10:ARG:NH1	2.21	0.56
1:E:165:ILE:O	1:E:165:ILE:HD12	2.04	0.56
1:F:51:TYR:HB2	1:F:52:PHE:CE1	2.41	0.56
1:F:188:ASP:OD2	1:F:190:LEU:HD12	2.04	0.56
1:C:195:ARG:NH2	1:D:9:SER:HB3	2.11	0.56
1:D:21:LEU:CD2	1:D:26:VAL:HB	2.30	0.56
1:D:72:ARG:HG3	1:D:72:ARG:NH1	2.19	0.56
1:G:122:VAL:CG1	1:G:123:ARG:H	2.04	0.56
1:A:111:PHE:O	1:A:112:ASP:HB2	2.05	0.55
1:A:194:THR:HG23	1:B:77:LEU:HD21	1.87	0.55
1:D:63:THR:HG22	1:D:65:PRO:HD2	1.87	0.55
1:B:204:LYS:HE2	1:B:204:LYS:HA	1.89	0.55
1:C:43:PHE:CE2	1:G:114:ASP:HA	2.41	0.55
1:D:128:GLU:OE2	1:D:132:LEU:HD12	2.07	0.55
1:G:22:GLU:HB2	1:G:64:VAL:HG12	1.86	0.55
1:C:190:LEU:HD21	1:D:101:PHE:CZ	2.40	0.55
1:E:76:GLY:C	1:E:78:ASN:H	2.13	0.55
1:G:66:VAL:HG12	1:G:70:GLU:CD	2.32	0.55
1:G:130:VAL:O	1:G:133:LEU:HB2	2.06	0.55
1:A:60:VAL:CG2	1:A:61:GLY:H	2.09	0.55
1:A:150:ARG:HG3	1:A:150:ARG:HH11	1.71	0.55
1:A:196:LEU:O	1:A:200:ILE:HG13	2.07	0.55
1:C:150:ARG:CG	1:C:173:PRO:HG2	2.36	0.55
1:G:70:GLU:O	1:G:74:ILE:HG13	2.06	0.55
1:A:57:THR:CG2	1:A:58:ARG:H	2.13	0.55
1:C:161:VAL:O	1:C:163:ALA:N	2.40	0.55
1:C:204:LYS:CD	1:D:5:GLU:HG3	2.36	0.55
1:G:148:VAL:HB	1:G:149:PRO:HD2	1.89	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:166:LYS:O	1:A:182:VAL:HG23	2.07	0.55
1:E:13:THR:O	1:E:16:ARG:HG3	2.07	0.55
1:F:49:LEU:HB3	1:F:54:SER:CB	2.37	0.55
1:A:89:GLY:HA3	3:A:213:NAD:O5B	2.05	0.55
1:A:132:LEU:H	1:A:132:LEU:CD1	2.17	0.55
1:F:118:VAL:HG12	1:F:118:VAL:O	2.07	0.55
1:E:80:LYS:HD2	1:E:106:GLU:OE1	2.07	0.54
1:A:111:PHE:HB3	1:A:130:VAL:HG12	1.90	0.54
1:B:8:ILE:O	1:B:12:ILE:HG13	2.06	0.54
1:C:110:PHE:O	1:C:127:ILE:HA	2.07	0.54
1:D:132:LEU:H	1:D:132:LEU:CD2	2.19	0.54
1:F:180:LYS:H	1:F:180:LYS:CD	2.10	0.54
1:F:18:LEU:HD23	1:F:21:LEU:HD21	1.88	0.54
1:A:63:THR:O	1:A:64:VAL:C	2.50	0.54
1:B:132:LEU:HB3	1:B:136:ARG:CG	2.37	0.54
1:C:204:LYS:CE	1:D:5:GLU:HG3	2.38	0.54
1:G:28:ARG:HG3	1:G:28:ARG:HH11	1.72	0.54
1:B:17:ILE:HD12	1:B:37:LEU:HB3	1.89	0.54
1:B:122:VAL:O	1:B:123:ARG:C	2.51	0.54
1:B:132:LEU:HB3	1:B:136:ARG:HG2	1.90	0.54
1:B:150:ARG:HG3	1:B:174:VAL:HG11	1.89	0.54
1:D:8:ILE:N	1:D:8:ILE:HD12	2.22	0.54
1:B:144:ALA:CB	1:B:160:LEU:HD21	2.37	0.54
1:A:28:ARG:HA	1:A:63:THR:HA	1.90	0.53
1:C:79:ARG:NH1	1:D:201:LEU:HD21	2.23	0.53
1:G:84:CYS:HB3	1:G:141:ILE:HD13	1.91	0.53
1:D:5:GLU:HA	1:D:8:ILE:HD11	1.89	0.53
1:E:28:ARG:HG2	1:E:28:ARG:HH11	1.73	0.53
1:C:16:ARG:HG2	1:C:16:ARG:HH11	1.73	0.53
1:C:88:MSE:HE1	1:C:96:ALA:CB	2.37	0.53
1:G:28:ARG:HA	1:G:63:THR:HA	1.90	0.53
1:C:108:ARG:HD2	1:C:140:ARG:O	2.08	0.53
1:D:122:VAL:HG12	1:D:123:ARG:H	1.71	0.53
1:A:137:VAL:HB	1:A:138:PRO:HD3	1.91	0.53
1:B:43:PHE:CE1	1:E:118:VAL:HG11	2.43	0.53
1:B:64:VAL:HB	1:B:65:PRO:HD3	1.89	0.53
1:B:201:LEU:N	1:B:201:LEU:HD12	2.24	0.53
1:C:168:ILE:HG23	1:C:184:VAL:HG12	1.91	0.53
1:E:136:ARG:HG2	1:E:136:ARG:HH11	1.74	0.53
1:B:173:PRO:O	1:B:174:VAL:HG13	2.09	0.53
1:D:154:GLN:HB3	1:D:155:LYS:NZ	2.24	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:28:ARG:H	1:G:64:VAL:HG23	1.74	0.53
1:G:41:THR:HG23	1:G:44:GLN:OE1	2.09	0.53
1:B:31:SER:OG	1:B:42:ALA:HB1	2.09	0.53
1:C:11:LEU:HD11	1:C:52:PHE:HE1	1.74	0.53
1:G:68:LYS:HB2	1:G:68:LYS:NZ	2.24	0.53
1:A:98:TYR:CD1	1:A:99:PRO:HD2	2.44	0.52
1:E:8:ILE:O	1:E:12:ILE:HG13	2.09	0.52
1:E:28:ARG:HD2	1:E:60:VAL:O	2.09	0.52
1:F:18:LEU:HA	1:F:21:LEU:CG	2.37	0.52
1:A:8:ILE:O	1:A:12:ILE:HG13	2.09	0.52
1:C:75:LEU:HB3	1:C:77:LEU:HD13	1.90	0.52
1:F:33:GLN:HA	1:F:36:GLU:HG2	1.90	0.52
1:A:137:VAL:HA	1:A:141:ILE:HB	1.90	0.52
1:D:20:GLU:O	1:D:24:GLN:HG2	2.09	0.52
1:E:68:LYS:O	1:E:72:ARG:HG3	2.08	0.52
1:C:40:VAL:HB	1:C:44:GLN:HG2	1.90	0.52
1:B:77:LEU:H	1:B:77:LEU:HD22	1.74	0.52
1:D:26:VAL:O	1:D:64:VAL:HG21	2.09	0.52
1:C:145:LEU:HA	1:C:169:LEU:O	2.09	0.52
1:E:100:GLY:O	1:F:190:LEU:HD21	2.09	0.52
1:B:4:PRO:HG2	1:B:51:TYR:OH	2.10	0.52
1:D:18:LEU:HD11	1:D:67:LEU:HD13	1.92	0.52
1:C:172:ALA:O	1:C:174:VAL:N	2.37	0.52
1:A:88:MSE:HB2	1:A:112:ASP:HB2	1.92	0.52
1:C:14:TYR:O	1:C:18:LEU:HG	2.09	0.52
1:G:65:PRO:O	1:G:69:ARG:HG3	2.10	0.52
1:C:95:LEU:HD12	1:C:147:THR:HG21	1.91	0.51
1:G:91:LEU:HD13	1:G:147:THR:HG22	1.91	0.51
1:E:130:VAL:O	1:E:133:LEU:HB2	2.10	0.51
1:E:82:GLY:HA3	1:E:140:ARG:O	2.10	0.51
1:G:67:LEU:O	1:G:71:LEU:HB2	2.10	0.51
1:B:43:PHE:CD1	1:E:118:VAL:HG11	2.46	0.51
1:C:79:ARG:NH1	1:D:201:LEU:CD2	2.73	0.51
1:D:5:GLU:HA	1:D:8:ILE:CD1	2.39	0.51
1:F:8:ILE:O	1:F:12:ILE:HG13	2.10	0.51
1:F:204:LYS:HB2	1:F:204:LYS:HZ3	1.73	0.51
1:A:204:LYS:HD2	1:A:204:LYS:N	2.26	0.51
1:C:201:LEU:HD12	1:E:138:PRO:HG2	1.93	0.51
1:D:19:GLU:O	1:D:23:ALA:HB2	2.11	0.51
1:G:117:LYS:NZ	3:G:212:NAD:O3B	2.44	0.51
1:D:91:LEU:HD22	1:D:95:LEU:HD12	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:132:LEU:HD23	1:D:132:LEU:H	1.74	0.51
1:G:34:LEU:O	1:G:38:ALA:N	2.44	0.51
1:A:91:LEU:HD13	1:A:147:THR:CG2	2.41	0.51
1:C:195:ARG:HH22	1:D:9:SER:CB	2.13	0.51
1:E:19:GLU:O	1:E:22:GLU:HB3	2.11	0.51
1:A:199:ALA:O	1:A:206:ARG:HD3	2.11	0.50
1:E:69:ARG:HH21	1:E:70:GLU:CG	2.24	0.50
1:E:85:ILE:HB	1:E:88:MSE:HE1	1.92	0.50
1:F:26:VAL:HG22	1:F:27:HIS:N	2.25	0.50
1:G:190[B]:LEU:O	1:G:193:LEU:HB2	2.11	0.50
1:B:83:LEU:HD23	1:B:143:ILE:HB	1.92	0.50
1:G:12:ILE:O	1:G:16:ARG:HG2	2.11	0.50
1:A:202:ASN:HB3	1:A:205:TRP:HB3	1.93	0.50
1:A:204:LYS:H	1:A:204:LYS:HZ3	1.60	0.50
1:D:22:GLU:HB2	1:D:64:VAL:HG11	1.93	0.50
1:A:69:ARG:HG3	1:A:72:ARG:HH22	1.77	0.50
1:B:159:LEU:O	1:B:160:LEU:C	2.54	0.50
1:F:135:GLN:HG3	1:F:136:ARG:HD2	1.94	0.50
1:G:29:THR:HG23	1:G:64:VAL:CG2	2.41	0.50
1:C:3:VAL:O	1:D:205:TRP:HH2	1.95	0.50
1:C:18:LEU:CD1	1:C:71:LEU:HD12	2.41	0.50
1:C:120:ARG:HB3	1:C:127:ILE:HD12	1.93	0.50
1:F:83:LEU:HD12	1:F:105:PHE:HB3	1.94	0.50
1:A:83:LEU:HB2	1:A:107:LEU:HD23	1.92	0.50
1:D:8:ILE:HD12	1:D:8:ILE:H	1.77	0.50
1:F:13:THR:O	1:F:17:ILE:HG12	2.11	0.50
1:G:149:PRO:HD3	3:G:212:NAD:H51A	1.94	0.50
1:F:29:THR:O	1:F:62:TYR:HB2	2.11	0.49
1:G:10:ARG:HB3	1:G:14:TYR:CZ	2.47	0.49
1:G:188:ASP:C	1:G:190[A]:LEU:N	2.67	0.49
1:D:97:ASP:O	1:D:98:TYR:C	2.54	0.49
1:D:103:GLU:CD	1:D:103:GLU:H	2.19	0.49
1:D:201:LEU:C	1:D:203:PRO:HD3	2.37	0.49
1:A:79:ARG:NH1	1:B:201:LEU:HD21	2.28	0.49
1:A:110:PHE:CD1	1:A:110:PHE:N	2.80	0.49
1:C:8:ILE:HA	1:C:11:LEU:HD12	1.94	0.49
1:D:79:ARG:O	1:D:80:LYS:HB3	2.11	0.49
1:B:122:VAL:CG2	1:B:127:ILE:HG13	2.42	0.49
1:D:122:VAL:CG1	1:D:123:ARG:N	2.76	0.49
1:E:133:LEU:HB3	1:E:134:PRO:HD3	1.93	0.49
1:G:8:ILE:O	1:G:12:ILE:HG13	2.13	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:72:ARG:HB3	1:B:72:ARG:NH1	2.28	0.49
1:F:7:ALA:HB2	1:F:10:ARG:HH12	1.77	0.49
1:A:178:VAL:HB	1:A:179:PRO:HD2	1.94	0.49
1:B:85:ILE:HG21	1:B:88:MSE:HE1	1.93	0.49
1:A:133:LEU:O	1:A:163:ALA:HB1	2.13	0.49
1:D:43:PHE:CZ	1:D:47:LYS:HD3	2.48	0.49
1:F:158:ASP:HA	1:F:161:VAL:CG2	2.42	0.49
1:A:205:TRP:O	1:A:206:ARG:C	2.55	0.49
1:B:77:LEU:HD22	1:B:77:LEU:N	2.27	0.49
1:C:136:ARG:HG2	1:C:136:ARG:HH11	1.77	0.49
1:F:18:LEU:CA	1:F:21:LEU:HG	2.40	0.49
1:F:18:LEU:HD21	1:F:29:THR:HG21	1.94	0.49
1:B:28:ARG:HH21	1:B:61:GLY:CA	2.26	0.48
1:D:166:LYS:NZ	1:E:166:LYS:NZ	2.62	0.48
1:A:87:GLY:CA	1:A:148:VAL:HG23	2.43	0.48
1:G:63:THR:CG2	1:G:65:PRO:HD2	2.39	0.48
1:A:112:ASP:OD2	1:A:117:LYS:HD2	2.13	0.48
1:B:123:ARG:NH1	1:B:123:ARG:HB2	2.28	0.48
1:G:30:SER:C	1:G:32:GLU:H	2.21	0.48
1:G:65:PRO:O	1:G:68:LYS:HG2	2.13	0.48
1:A:114:ASP:O	1:A:118:VAL:HG23	2.13	0.48
1:A:114:ASP:OD2	1:A:116:GLU:HB2	2.14	0.48
1:D:146:LEU:HB2	1:D:168:ILE:CD1	2.43	0.48
1:F:72:ARG:HH11	1:F:72:ARG:HG2	1.78	0.48
1:A:59:GLY:HA3	1:E:150:ARG:CD	2.44	0.48
1:B:123:ARG:C	1:B:125:GLY:H	2.22	0.48
1:D:20:GLU:HA	1:D:23:ALA:HB3	1.96	0.48
1:D:41:THR:CG2	1:G:116:GLU:HA	2.43	0.48
1:D:63:THR:HG22	1:D:65:PRO:HG2	1.95	0.48
1:B:21:LEU:O	1:B:26:VAL:HG13	2.14	0.48
1:E:88:MSE:CA	1:E:88:MSE:HE2	2.44	0.48
1:G:89:GLY:HA3	3:G:212:NAD:O5B	2.14	0.48
1:A:85:ILE:CG2	1:A:88:MSE:HE3	2.43	0.48
1:A:111:PHE:N	1:A:111:PHE:CD1	2.82	0.48
1:B:83:LEU:CD1	1:B:105:PHE:HB3	2.44	0.48
1:B:149:PRO:HB2	1:B:151:GLU:HG2	1.95	0.48
1:E:132:LEU:N	1:E:132:LEU:CD1	2.59	0.48
1:E:133:LEU:O	1:E:137:VAL:HG23	2.14	0.48
1:F:131:ASP:O	1:F:133:LEU:N	2.47	0.48
1:A:161:VAL:HG22	1:A:182:VAL:HG11	1.96	0.47
1:C:149:PRO:HD3	3:C:213:NAD:O4B	2.14	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:6:ALA:O	1:G:9:SER:HB2	2.14	0.47
1:B:41:THR:O	1:B:45:VAL:HG12	2.13	0.47
1:B:88:MSE:HA	1:B:88:MSE:CE	2.37	0.47
1:B:196:LEU:O	1:B:200:ILE:HG13	2.14	0.47
1:C:50:SER:C	1:C:52:PHE:H	2.22	0.47
1:C:73:HIS:HA	1:C:78:ASN:HD21	1.77	0.47
1:C:76:GLY:CA	1:D:201:LEU:HD11	2.45	0.47
1:D:168:ILE:O	1:D:168:ILE:HG13	2.12	0.47
1:F:83:LEU:HB3	1:F:107:LEU:HD23	1.96	0.47
1:C:67:LEU:HA	1:C:70:GLU:HB2	1.95	0.47
1:C:137:VAL:CB	1:C:138:PRO:HD3	2.42	0.47
1:F:107:LEU:HD13	1:F:110:PHE:HE2	1.80	0.47
1:A:17:ILE:HD13	1:A:37:LEU:CB	2.44	0.47
1:A:129:HIS:ND1	1:A:130:VAL:N	2.63	0.47
1:B:149:PRO:O	1:B:150:ARG:C	2.57	0.47
1:D:146:LEU:HB2	1:D:168:ILE:HD13	1.96	0.47
1:E:150:ARG:HD2	1:E:173:PRO:HG2	1.95	0.47
1:B:159:LEU:O	1:B:162:ALA:N	2.47	0.47
1:D:33:GLN:O	1:D:37:LEU:HG	2.14	0.47
1:D:66:VAL:O	1:D:70:GLU:HG3	2.15	0.47
1:D:91:LEU:HD22	1:D:95:LEU:CD1	2.45	0.47
1:D:151:GLU:CD	1:D:151:GLU:H	2.23	0.47
1:G:17:ILE:HD11	1:G:34:LEU:CG	2.43	0.47
1:G:188:ASP:OD1	1:G:190[B]:LEU:HD12	2.14	0.47
1:D:83:LEU:HD12	1:D:101:PHE:CE2	2.50	0.47
1:G:201:LEU:O	1:G:203:PRO:HD3	2.14	0.47
1:A:17:ILE:O	1:A:17:ILE:HG22	2.14	0.47
1:A:41:THR:O	1:A:44:GLN:N	2.44	0.47
1:A:69:ARG:HG3	1:A:72:ARG:NH2	2.30	0.47
1:A:79:ARG:CZ	1:B:201:LEU:HD21	2.45	0.47
1:A:204:LYS:HB3	1:A:204:LYS:NZ	2.29	0.47
1:C:83:LEU:HD13	1:C:105:PHE:HB3	1.97	0.47
1:E:142:GLU:HB3	1:E:166:LYS:HB2	1.96	0.47
1:E:188:ASP:CG	1:E:188:ASP:O	2.57	0.47
1:F:16:ARG:HH11	1:F:16:ARG:CB	2.22	0.47
1:F:28:ARG:HD3	1:F:28:ARG:N	2.29	0.47
1:G:34:LEU:HD23	1:G:45:VAL:HG13	1.97	0.47
1:C:58:ARG:HH12	1:C:60:VAL:HB	1.78	0.47
1:A:162:ALA:C	1:A:164:GLY:N	2.73	0.47
1:E:18:LEU:HA	1:E:21:LEU:HD12	1.96	0.47
1:E:160:LEU:HB3	1:E:165:ILE:HG12	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:LYS:O	1:A:118:VAL:C	2.58	0.47
1:B:169:LEU:HG	1:B:187:VAL:CG2	2.44	0.47
1:C:18:LEU:HD12	1:C:71:LEU:HD12	1.97	0.47
1:E:16:ARG:HG3	1:E:17:ILE:H	1.80	0.47
1:F:187:VAL:O	1:F:187:VAL:HG23	2.15	0.47
1:A:11:LEU:HD21	1:A:52:PHE:CE1	2.50	0.46
1:F:52:PHE:O	1:F:53:GLY:C	2.58	0.46
1:E:49:LEU:HD22	1:E:67:LEU:HD21	1.97	0.46
1:B:103:GLU:CG	1:B:104:SER:H	2.28	0.46
1:A:83:LEU:CD2	1:A:143:ILE:HB	2.43	0.46
1:B:88:MSE:N	1:B:112:ASP:OD2	2.48	0.46
1:F:21:LEU:HD13	1:F:26:VAL:CG1	2.43	0.46
1:F:53:GLY:HA2	1:F:55:TYR:CE1	2.49	0.46
1:F:80:LYS:NZ	1:F:106:GLU:HB3	2.15	0.46
1:A:204:LYS:HG2	1:A:205:TRP:N	2.31	0.46
1:A:59:GLY:HA3	1:E:150:ARG:NE	2.30	0.46
1:A:150:ARG:HD3	1:A:150:ARG:C	2.41	0.46
1:C:54:SER:C	1:C:55:TYR:CD1	2.94	0.46
1:G:152:ALA:O	1:G:153:ALA:C	2.58	0.46
1:A:55:TYR:O	1:A:56:GLY:C	2.58	0.46
1:E:9:SER:HA	1:E:12:ILE:HD12	1.96	0.46
1:F:97:ASP:HA	1:F:123:ARG:HE	1.80	0.46
1:G:51:TYR:HB2	1:G:52:PHE:CE1	2.51	0.46
1:C:161:VAL:C	1:C:163:ALA:N	2.72	0.46
1:D:63:THR:O	1:D:64:VAL:C	2.59	0.46
1:D:154:GLN:HB3	1:D:155:LYS:HZ2	1.81	0.46
1:E:136:ARG:HG2	1:E:136:ARG:NH1	2.31	0.46
1:E:169:LEU:CD2	1:E:187:VAL:HG23	2.44	0.46
1:F:54:SER:OG	1:F:55:TYR:N	2.44	0.46
1:F:108:ARG:HH11	1:F:140:ARG:HB3	1.80	0.46
1:G:5:GLU:C	1:G:7:ALA:H	2.23	0.46
1:G:10:ARG:HD2	1:G:14:TYR:OH	2.16	0.46
1:G:17:ILE:HD11	1:G:34:LEU:CD1	2.45	0.46
1:G:188:ASP:C	1:G:188:ASP:OD2	2.57	0.46
1:A:179:PRO:HB2	1:A:181:GLU:HG2	1.97	0.46
1:B:125:GLY:C	1:B:126:VAL:HG12	2.40	0.46
1:D:40:VAL:O	1:D:41:THR:C	2.57	0.46
1:F:50:SER:C	1:F:52:PHE:N	2.74	0.46
1:F:118:VAL:O	1:F:118:VAL:CG1	2.63	0.46
1:C:130:VAL:O	1:C:133:LEU:HD13	2.15	0.45
1:D:22:GLU:HB2	1:D:64:VAL:CG1	2.47	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:194:THR:HG21	1:F:75:LEU:HD13	1.98	0.45
1:F:122:VAL:O	1:F:123:ARG:C	2.60	0.45
1:A:17:ILE:HD13	1:A:37:LEU:HB3	1.98	0.45
1:A:127:ILE:HG22	1:A:128:GLU:N	2.31	0.45
1:B:21:LEU:HD12	1:B:21:LEU:HA	1.86	0.45
1:C:50:SER:O	1:C:52:PHE:N	2.50	0.45
1:F:161:VAL:HG12	1:F:182:VAL:HG11	1.99	0.45
1:F:196:LEU:O	1:F:200:ILE:HG13	2.17	0.45
1:G:68:LYS:O	1:G:72:ARG:HG3	2.16	0.45
1:A:18:LEU:HD12	1:A:71:LEU:HD12	1.98	0.45
1:C:50:SER:C	1:C:52:PHE:N	2.74	0.45
1:D:63:THR:HG22	1:D:65:PRO:CD	2.47	0.45
1:F:83:LEU:HD23	1:F:143:ILE:O	2.16	0.45
1:G:132:LEU:C	1:G:132:LEU:HD12	2.41	0.45
1:F:129:HIS:ND1	1:F:130:VAL:N	2.65	0.45
1:F:133:LEU:CB	1:F:134:PRO:HD3	2.43	0.45
1:C:88:MSE:HE2	1:C:122:VAL:HG11	1.99	0.45
1:A:202:ASN:O	1:A:206:ARG:HB2	2.16	0.45
1:E:52:PHE:CD1	1:E:52:PHE:N	2.85	0.45
1:E:57:THR:O	1:E:58:ARG:C	2.60	0.45
1:G:140:ARG:HB3	1:G:140:ARG:NH1	2.31	0.45
1:A:170:ASN:ND2	1:A:176:LEU:CD2	2.75	0.45
1:C:77:LEU:HD11	1:D:194:THR:HG23	1.99	0.45
1:B:41:THR:CG2	1:E:116:GLU:HG3	2.47	0.45
1:C:8:ILE:HD11	1:D:205:TRP:CZ2	2.51	0.45
1:C:86:VAL:HG12	1:C:148:VAL:HG23	1.99	0.45
1:D:84:CYS:SG	1:D:141:ILE:HG21	2.57	0.45
1:G:169:LEU:HD23	1:G:169:LEU:HA	1.73	0.45
1:A:111:PHE:CE2	1:A:133:LEU:HD12	2.52	0.44
1:B:111:PHE:HB3	1:B:129:HIS:O	2.17	0.44
1:B:169:LEU:HG	1:B:187:VAL:HG21	1.99	0.44
1:B:12:ILE:HG12	1:B:75:LEU:HD21	1.99	0.44
1:B:69:ARG:HA	1:B:69:ARG:NE	2.33	0.44
1:E:76:GLY:C	1:E:78:ASN:N	2.75	0.44
1:F:114:ASP:O	1:F:118:VAL:HG23	2.18	0.44
1:A:203:PRO:HD2	1:A:204:LYS:HE2	2.00	0.44
1:B:155:LYS:O	1:B:158:ASP:HB2	2.17	0.44
1:C:60:VAL:HG12	1:C:60:VAL:O	2.18	0.44
1:C:128:GLU:OE2	1:C:132:LEU:HD22	2.18	0.44
1:F:79:ARG:HG2	1:F:79:ARG:HH11	1.82	0.44
1:F:169:LEU:HD23	1:F:169:LEU:HA	1.69	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:4:PRO:HB3	1:D:39:GLN:OE1	2.18	0.44
1:E:90:ARG:HE	1:E:90:ARG:HB2	1.57	0.44
1:E:129:HIS:CE1	1:E:130:VAL:HG22	2.53	0.44
1:F:201:LEU:C	1:F:203:PRO:HD3	2.41	0.44
1:E:133:LEU:HD21	1:E:160:LEU:HD23	1.98	0.44
1:A:159:LEU:O	1:A:162:ALA:HB3	2.17	0.44
1:A:194:THR:CG2	1:B:75:LEU:HG	2.48	0.44
1:C:41:THR:O	1:C:44:GLN:HB3	2.17	0.44
1:D:21:LEU:HD22	1:D:64:VAL:HG21	2.00	0.44
1:D:79:ARG:HD2	1:D:81:TRP:CZ2	2.52	0.44
1:D:168:ILE:HD12	1:D:169:LEU:N	2.32	0.44
1:E:166:LYS:HB3	1:F:200:ILE:HD13	1.98	0.44
1:E:188:ASP:C	1:E:190:LEU:H	2.26	0.44
1:F:167:GLY:O	1:F:168:ILE:HD13	2.17	0.44
1:G:32:GLU:O	1:G:33:GLN:C	2.61	0.44
1:G:167:GLY:HA2	1:G:183:ALA:O	2.17	0.44
1:B:122:VAL:O	1:B:125:GLY:N	2.51	0.44
1:C:3:VAL:HG23	1:C:7:ALA:HB3	1.98	0.44
1:C:132:LEU:O	1:C:136:ARG:HG2	2.18	0.44
1:C:132:LEU:CD2	1:C:136:ARG:NH2	2.80	0.44
1:E:190:LEU:HD12	1:E:190:LEU:N	2.33	0.44
1:D:168:ILE:HG23	1:D:184:VAL:HG22	2.00	0.44
1:B:43:PHE:CE2	1:E:118:VAL:HG21	2.53	0.43
1:F:173:PRO:HD3	3:F:212:NAD:O2D	2.18	0.43
1:G:17:ILE:HD12	1:G:34:LEU:HA	1.99	0.43
1:D:21:LEU:HD22	1:D:64:VAL:CG2	2.48	0.43
1:F:133:LEU:O	1:F:135:GLN:N	2.51	0.43
1:G:188:ASP:C	1:G:190[A]:LEU:H	2.26	0.43
1:B:111:PHE:N	1:B:111:PHE:CD1	2.85	0.43
1:D:41:THR:HG21	1:G:116:GLU:CA	2.45	0.43
1:D:172:ALA:HA	1:D:173:PRO:HD3	1.85	0.43
1:B:133:LEU:N	1:B:134:PRO:HD2	2.33	0.43
1:G:88:MSE:CE	1:G:93:SER:HA	2.49	0.43
1:A:68:LYS:HB3	1:A:68:LYS:HZ2	1.80	0.43
1:B:11:LEU:HD12	1:B:11:LEU:HA	1.87	0.43
1:B:181:GLU:CD	1:B:181:GLU:N	2.75	0.43
1:D:122:VAL:CG1	1:D:123:ARG:H	2.30	0.43
1:E:48:ASP:O	1:E:49:LEU:C	2.62	0.43
1:F:67:LEU:HA	1:F:70:GLU:HG3	2.01	0.43
1:A:150:ARG:HG3	1:A:150:ARG:NH1	2.33	0.43
1:C:15:LEU:HD12	1:C:75:LEU:HD23	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:52:PHE:O	1:C:53:GLY:C	2.59	0.43
1:C:73:HIS:HA	1:C:78:ASN:ND2	2.34	0.43
1:C:86:VAL:O	1:C:148:VAL:HG23	2.18	0.43
1:F:132:LEU:HD13	1:F:136:ARG:CZ	2.48	0.43
1:A:107:LEU:HD13	1:A:110:PHE:HE2	1.83	0.43
1:F:84:CYS:HB2	1:F:111:PHE:HE1	1.82	0.43
1:A:59:GLY:O	1:A:60:VAL:C	2.61	0.43
1:B:49:LEU:HD22	1:B:67:LEU:HD11	2.00	0.43
1:E:119:GLY:O	1:E:120:ARG:C	2.61	0.43
1:A:13:THR:O	1:A:17:ILE:HG13	2.18	0.43
1:C:20:GLU:O	1:C:24:GLN:HG3	2.19	0.43
1:C:154:GLN:O	1:C:158:ASP:OD1	2.37	0.43
1:D:167:GLY:HA2	1:D:183:ALA:O	2.18	0.43
1:D:27:HIS:ND1	1:D:28:ARG:CG	2.80	0.43
1:D:112:ASP:O	1:D:129:HIS:HA	2.18	0.43
1:F:50:SER:O	1:F:52:PHE:N	2.52	0.43
1:B:197:SER:O	1:B:201:LEU:HD13	2.19	0.42
1:C:148:VAL:HG13	1:C:149:PRO:CD	2.48	0.42
1:E:49:LEU:CD1	1:E:67:LEU:HD11	2.49	0.42
1:F:131:ASP:C	1:F:133:LEU:N	2.77	0.42
1:C:58:ARG:O	1:C:60:VAL:HG23	2.19	0.42
1:A:59:GLY:H	1:E:150:ARG:HD3	1.84	0.42
1:A:63:THR:OG1	1:A:66:VAL:HG23	2.20	0.42
1:C:15:LEU:HD11	1:C:72:ARG:HG3	2.01	0.42
1:C:171:PHE:O	3:C:213:NAD:H2N	2.20	0.42
1:C:201:LEU:CD1	1:D:81:TRP:HH2	2.33	0.42
1:G:123:ARG:HA	1:G:123:ARG:HD3	1.75	0.42
1:C:47:LYS:O	1:C:50:SER:HB2	2.20	0.42
1:B:150:ARG:HG3	1:B:174:VAL:HG13	2.00	0.42
1:D:186:ASN:O	1:D:187:VAL:HG23	2.19	0.42
1:G:16:ARG:HD3	1:G:16:ARG:HA	1.79	0.42
1:B:4:PRO:C	1:B:6:ALA:N	2.78	0.42
1:B:28:ARG:HG2	1:B:63:THR:HG22	2.01	0.42
1:B:42:ALA:HA	1:B:45:VAL:CG1	2.50	0.42
1:B:114:ASP:HB3	1:B:117:LYS:HE3	2.01	0.42
1:E:95:LEU:HD12	1:E:147:THR:HG21	2.02	0.42
1:F:150:ARG:HB2	1:F:174:VAL:HG11	1.99	0.42
1:D:165:ILE:HD12	1:D:165:ILE:HA	1.89	0.42
1:C:114:ASP:OD1	1:C:116:GLU:HB2	2.18	0.42
1:F:137:VAL:CB	1:F:138:PRO:CD	2.93	0.42
1:F:206:ARG:O	1:F:207:GLU:C	2.63	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:18:LEU:HD13	1:C:68:LYS:HA	2.02	0.42
1:C:56:GLY:O	1:C:59:GLY:N	2.52	0.42
1:C:114:ASP:OD1	1:C:116:GLU:N	2.53	0.42
1:D:113:VAL:HG22	1:D:113:VAL:O	2.19	0.42
1:F:114:ASP:HB3	1:F:117:LYS:HD2	2.01	0.42
1:C:204:LYS:HZ2	1:D:5:GLU:HG3	1.85	0.42
1:D:201:LEU:O	1:D:203:PRO:HD3	2.20	0.42
1:E:63:THR:CG2	1:E:65:PRO:HD2	2.49	0.42
1:E:69:ARG:HH21	1:E:70:GLU:HG3	1.85	0.42
1:G:132:LEU:H	1:G:132:LEU:HG	1.50	0.42
1:A:47:LYS:HA	1:A:50:SER:OG	2.20	0.41
1:A:58:ARG:O	1:A:60:VAL:HG22	2.20	0.41
1:A:122:VAL:O	1:A:123:ARG:C	2.62	0.41
1:A:160:LEU:O	1:A:161:VAL:C	2.62	0.41
1:F:112:ASP:OD1	3:F:212:NAD:O2B	2.38	0.41
1:G:18:LEU:HD21	1:G:67:LEU:HD23	2.02	0.41
1:G:28:ARG:H	1:G:64:VAL:H	1.67	0.41
1:A:114:ASP:OD1	1:A:116:GLU:HB2	2.20	0.41
1:B:138:PRO:O	1:G:79:ARG:NH1	2.51	0.41
1:B:190:LEU:O	1:B:193:LEU:HB2	2.20	0.41
1:E:179:PRO:HG2	1:E:182:VAL:HG23	2.02	0.41
1:A:76:GLY:O	1:A:79:ARG:HD3	2.20	0.41
1:A:140:ARG:HG3	1:A:140:ARG:HH11	1.84	0.41
1:C:112:ASP:OD1	3:C:213:NAD:O2B	2.25	0.41
3:C:213:NAD:O1N	1:D:94:ALA:HB1	2.21	0.41
1:D:80:LYS:O	1:D:80:LYS:HG3	2.20	0.41
1:F:122:VAL:O	1:F:124:GLY:N	2.53	0.41
1:G:137:VAL:O	1:G:138:PRO:C	2.63	0.41
1:A:85:ILE:CG2	1:A:88:MSE:CE	2.98	0.41
1:A:203:PRO:HD2	1:A:204:LYS:CE	2.50	0.41
1:E:8:ILE:HD11	1:F:198:PHE:CZ	2.56	0.41
1:G:34:LEU:HD23	1:G:45:VAL:CG1	2.50	0.41
1:C:171:PHE:CD1	1:C:171:PHE:N	2.88	0.41
1:D:4:PRO:HD2	1:D:51:TYR:OH	2.20	0.41
1:G:17:ILE:HG13	1:G:18:LEU:N	2.36	0.41
1:B:85:ILE:CG2	1:B:88:MSE:CE	2.99	0.41
1:G:88:MSE:HE3	1:G:93:SER:HA	2.03	0.41
1:B:21:LEU:HG	1:B:26:VAL:CG2	2.47	0.41
1:B:79:ARG:O	1:B:104:SER:HB3	2.21	0.41
1:C:72:ARG:HG2	1:C:72:ARG:HH11	1.84	0.41
1:D:166:LYS:NZ	1:E:166:LYS:HZ3	2.19	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:175:VAL:O	1:F:175:VAL:HG13	2.21	0.41
1:A:142:GLU:HB3	1:A:166:LYS:HB2	2.01	0.41
1:B:123:ARG:CZ	1:B:123:ARG:CB	2.99	0.41
1:B:133:LEU:O	1:B:137:VAL:HG23	2.20	0.41
1:C:73:HIS:CG	1:C:78:ASN:ND2	2.89	0.41
1:C:105:PHE:CE2	1:D:193:LEU:HD22	2.55	0.41
1:E:80:LYS:HA	1:E:104:SER:O	2.20	0.41
1:E:147:THR:O	3:E:212:NAD:H51N	2.21	0.41
1:F:13:THR:HA	1:F:16:ARG:NH1	2.36	0.41
1:A:95:LEU:HD22	1:A:147:THR:HG21	2.02	0.41
1:B:72:ARG:HH11	1:B:72:ARG:CB	2.33	0.41
1:B:122:VAL:HG23	1:B:127:ILE:HG13	2.02	0.41
1:C:76:GLY:HA2	1:D:201:LEU:HD11	2.03	0.41
1:C:76:GLY:HA3	1:D:201:LEU:HD11	2.03	0.41
1:C:136:ARG:HG2	1:C:136:ARG:NH1	2.36	0.41
1:F:21:LEU:O	1:F:26:VAL:HG12	2.21	0.41
1:F:95:LEU:HD12	1:F:147:THR:HG21	2.01	0.41
1:G:27:HIS:HA	1:G:64:VAL:HG21	2.03	0.41
1:G:121:PRO:CA	1:G:126:VAL:HG12	2.46	0.41
1:G:132:LEU:HD22	1:G:136:ARG:NH2	2.36	0.41
1:A:37:LEU:HD23	1:A:37:LEU:HA	1.89	0.41
1:B:18:LEU:HD11	1:B:67:LEU:HG	2.02	0.41
1:E:1:MSE:HG2	1:E:3:VAL:HG12	2.03	0.41
1:E:112:ASP:OD1	1:E:113:VAL:N	2.54	0.41
1:F:145:LEU:HD22	1:F:169:LEU:HD12	2.03	0.41
1:F:179:PRO:HB3	1:F:181:GLU:OE2	2.21	0.41
1:B:28:ARG:CG	1:B:63:THR:HG22	2.51	0.40
1:D:63:THR:HG22	1:D:65:PRO:CG	2.51	0.40
1:E:114:ASP:HB3	1:E:117:LYS:HD2	2.03	0.40
1:F:11:LEU:O	1:F:14:TYR:HB2	2.20	0.40
1:G:18:LEU:HG	1:G:34:LEU:HD11	2.03	0.40
1:G:149:PRO:HA	3:G:212:NAD:H3D	2.03	0.40
1:D:133:LEU:HB2	1:D:134:PRO:HD3	2.03	0.40
1:D:145:LEU:HD12	1:D:145:LEU:N	2.35	0.40
1:A:154:GLN:O	1:A:154:GLN:HG3	2.19	0.40
1:B:169:LEU:HA	1:B:169:LEU:HD12	1.85	0.40
1:C:63:THR:O	1:C:64:VAL:C	2.64	0.40
1:E:180:LYS:NZ	1:F:207:GLU:HA	2.37	0.40
1:E:202:ASN:N	1:E:203:PRO:HD3	2.36	0.40
1:G:86:VAL:HG21	1:G:160:LEU:HD21	2.03	0.40
1:C:157:ALA:O	1:C:158:ASP:C	2.64	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:138:PRO:HG2	1:F:201:LEU:CD2	2.52	0.40
1:D:197:SER:O	1:D:201:LEU:HG	2.21	0.40
1:G:12:ILE:HG22	1:G:16:ARG:HE	1.87	0.40
1:G:129:HIS:O	1:G:131:ASP:N	2.54	0.40
1:A:84:CYS:CB	1:A:141:ILE:HD13	2.41	0.40
1:B:98:TYR:CE2	1:B:100:GLY:HA3	2.56	0.40
1:E:192:GLY:HA2	1:E:195:ARG:HE	1.87	0.40
1:G:52:PHE:CG	1:G:74:ILE:HD13	2.56	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	203/211 (96%)	170 (84%)	22 (11%)	11 (5%)	1	5
1	B	193/211 (92%)	165 (86%)	23 (12%)	5 (3%)	4	17
1	C	201/211 (95%)	161 (80%)	33 (16%)	7 (4%)	3	12
1	D	193/211 (92%)	169 (88%)	19 (10%)	5 (3%)	4	17
1	E	201/211 (95%)	177 (88%)	16 (8%)	8 (4%)	2	9
1	F	196/211 (93%)	156 (80%)	27 (14%)	13 (7%)	1	3
1	G	190/211 (90%)	153 (80%)	31 (16%)	6 (3%)	3	13
All	All	1377/1477 (93%)	1151 (84%)	171 (12%)	55 (4%)	2	9

All (55) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	60	VAL
1	A	118	VAL
1	A	123	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	103	GLU
1	B	153	ALA
1	C	162	ALA
1	D	27	HIS
1	E	58	ARG
1	E	138	PRO
1	G	153	ALA
1	C	53	GLY
1	C	180	LYS
1	D	25	GLY
1	E	54	SER
1	E	123	ARG
1	F	53	GLY
1	F	123	ARG
1	F	132	LEU
1	G	123	ARG
1	A	57	THR
1	A	138	PRO
1	C	138	PRO
1	C	189	PHE
1	D	31	SER
1	F	68	LYS
1	F	138	PRO
1	F	161	VAL
1	G	130	VAL
1	A	112	ASP
1	B	123	ARG
1	C	51	TYR
1	E	48	ASP
1	F	51	TYR
1	F	206	ARG
1	G	28	ARG
1	G	190[A]	LEU
1	G	190[B]	LEU
1	A	189	PHE
1	E	120	ARG
1	F	134	PRO
1	F	155	LYS
1	C	33	GLN
1	D	5	GLU
1	D	41	THR
1	E	79	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	118	VAL
1	F	125	GLY
1	A	203	PRO
1	B	126	VAL
1	E	53	GLY
1	F	64	VAL
1	A	64	VAL
1	A	56	GLY
1	A	173	PRO
1	B	179	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	166/167 (99%)	146 (88%)	20 (12%)	5	16
1	B	160/167 (96%)	145 (91%)	15 (9%)	8	26
1	C	164/167 (98%)	153 (93%)	11 (7%)	15	43
1	D	160/167 (96%)	145 (91%)	15 (9%)	8	26
1	E	164/167 (98%)	151 (92%)	13 (8%)	11	34
1	F	163/167 (98%)	151 (93%)	12 (7%)	13	38
1	G	158/167 (95%)	147 (93%)	11 (7%)	14	40
All	All	1135/1169 (97%)	1038 (92%)	97 (8%)	10	31

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	GLU
1	A	11	LEU
1	A	21	LEU
1	A	47	LYS
1	A	49	LEU
1	A	68	LYS
1	A	79	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	91	LEU
1	A	95	LEU
1	A	116	GLU
1	A	132	LEU
1	A	138	PRO
1	A	140	ARG
1	A	148	VAL
1	A	170	ASN
1	A	176	LEU
1	A	180	LYS
1	A	181	GLU
1	A	182	VAL
1	A	204	LYS
1	B	11	LEU
1	B	21	LEU
1	B	26	VAL
1	B	45	VAL
1	B	70	GLU
1	B	71	LEU
1	B	75	LEU
1	B	104	SER
1	B	123	ARG
1	B	126	VAL
1	B	130	VAL
1	B	160	LEU
1	B	161	VAL
1	B	188	ASP
1	B	204	LYS
1	C	3	VAL
1	C	15	LEU
1	C	75	LEU
1	C	78	ASN
1	C	120	ARG
1	C	132	LEU
1	C	145	LEU
1	C	168	ILE
1	C	170	ASN
1	C	181	GLU
1	C	184	VAL
1	D	36	GLU
1	D	67	LEU
1	D	69	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	91	LEU
1	D	103	GLU
1	D	108	ARG
1	D	131	ASP
1	D	132	LEU
1	D	134	PRO
1	D	155	LYS
1	D	168	ILE
1	D	177	GLU
1	D	193	LEU
1	D	196	LEU
1	D	204	LYS
1	E	2	LYS
1	E	8	ILE
1	E	13	THR
1	E	15	LEU
1	E	54	SER
1	E	67	LEU
1	E	132	LEU
1	E	138	PRO
1	E	145	LEU
1	E	151	GLU
1	E	169	LEU
1	E	185	GLU
1	E	196	LEU
1	F	28	ARG
1	F	31	SER
1	F	52	PHE
1	F	67	LEU
1	F	104	SER
1	F	134	PRO
1	F	138	PRO
1	F	180	LYS
1	F	181	GLU
1	F	188	ASP
1	F	196	LEU
1	F	204	LYS
1	G	32	GLU
1	G	52	PHE
1	G	62	TYR
1	G	68	LYS
1	G	71	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	91	LEU
1	G	130	VAL
1	G	132	LEU
1	G	169	LEU
1	G	187	VAL
1	G	202	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	202	ASN
1	B	129	HIS
1	B	186	ASN
1	B	202	ASN
1	C	33	GLN
1	C	78	ASN
1	C	202	ASN
1	D	44	GLN
1	E	44	GLN
1	E	135	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 5 are monoatomic - leaving 7 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	NAD	D	214	-	46,48,48	2.83	13 (28%)	64,73,73	2.54	16 (25%)
3	NAD	G	212	-	46,48,48	2.85	15 (32%)	64,73,73	2.44	15 (23%)
3	NAD	E	212	-	46,48,48	2.87	13 (28%)	64,73,73	2.57	17 (26%)
3	NAD	B	213	-	46,48,48	2.70	12 (26%)	64,73,73	2.48	13 (20%)
3	NAD	F	212	-	46,48,48	2.86	14 (30%)	64,73,73	2.47	16 (25%)
3	NAD	A	213	-	46,48,48	3.05	13 (28%)	64,73,73	2.53	15 (23%)
3	NAD	C	213	-	46,48,48	2.93	13 (28%)	64,73,73	2.45	16 (25%)

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	D	214	-	-	4/30/62/62	0/5/5/5
3	NAD	G	212	-	-	6/30/62/62	0/5/5/5
3	NAD	E	212	-	-	4/30/62/62	0/5/5/5
3	NAD	B	213	-	-	4/30/62/62	0/5/5/5
3	NAD	F	212	-	-	8/30/62/62	0/5/5/5
3	NAD	A	213	-	-	5/30/62/62	0/5/5/5
3	NAD	C	213	-	-	6/30/62/62	0/5/5/5

All (93) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	213	NAD	C2N-N1N	10.87	1.46	1.35
3	D	214	NAD	C2N-N1N	10.00	1.46	1.35
3	E	212	NAD	C2N-N1N	9.93	1.45	1.35
3	C	213	NAD	C2N-N1N	9.64	1.45	1.35
3	F	212	NAD	C2N-N1N	9.54	1.45	1.35
3	C	213	NAD	C4N-C3N	9.33	1.53	1.39
3	A	213	NAD	C4N-C3N	9.26	1.53	1.39
3	B	213	NAD	C2N-N1N	9.09	1.45	1.35

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	212	NAD	C2N-N1N	9.07	1.44	1.35
3	G	212	NAD	C4N-C3N	8.91	1.52	1.39
3	E	212	NAD	C4N-C3N	8.88	1.52	1.39
3	D	214	NAD	C4N-C3N	8.62	1.52	1.39
3	F	212	NAD	C4N-C3N	8.61	1.52	1.39
3	B	213	NAD	C4N-C3N	8.24	1.51	1.39
3	A	213	NAD	C5N-C4N	8.15	1.52	1.38
3	F	212	NAD	C5N-C4N	7.62	1.51	1.38
3	C	213	NAD	C5N-C4N	7.54	1.51	1.38
3	E	212	NAD	C5N-C4N	7.51	1.51	1.38
3	G	212	NAD	C5N-C4N	7.41	1.51	1.38
3	D	214	NAD	C5N-C4N	7.21	1.51	1.38
3	B	213	NAD	C5N-C4N	6.95	1.50	1.38
3	G	212	NAD	PN-O3	6.20	1.66	1.59
3	A	213	NAD	C6N-N1N	5.45	1.47	1.35
3	C	213	NAD	PN-O3	5.38	1.65	1.59
3	A	213	NAD	PN-O3	5.18	1.65	1.59
3	F	212	NAD	C6N-N1N	5.16	1.47	1.35
3	C	213	NAD	C6N-N1N	5.14	1.47	1.35
3	D	214	NAD	C6N-N1N	5.04	1.46	1.35
3	E	212	NAD	C6N-N1N	5.00	1.46	1.35
3	G	212	NAD	C6N-N1N	4.92	1.46	1.35
3	E	212	NAD	PN-O3	4.80	1.64	1.59
3	F	212	NAD	PN-O3	4.75	1.64	1.59
3	D	214	NAD	PA-O3	-4.67	1.54	1.59
3	B	213	NAD	C4A-N3A	4.52	1.42	1.34
3	B	213	NAD	C6N-N1N	4.47	1.45	1.35
3	B	213	NAD	C2A-N3A	4.05	1.41	1.33
3	C	213	NAD	C2A-N3A	4.00	1.41	1.33
3	C	213	NAD	C4A-N3A	3.88	1.41	1.34
3	D	214	NAD	C2A-N3A	3.72	1.40	1.33
3	E	212	NAD	C2A-N3A	3.61	1.40	1.33
3	A	213	NAD	C3D-C4D	3.50	1.61	1.53
3	D	214	NAD	O4D-C1D	3.48	1.45	1.40
3	F	212	NAD	C4A-N3A	3.47	1.40	1.34
3	A	213	NAD	C2A-N3A	3.45	1.40	1.33
3	A	213	NAD	C4A-N3A	3.42	1.40	1.34
3	F	212	NAD	C3D-C4D	3.36	1.61	1.53
3	F	212	NAD	C2A-N3A	3.36	1.39	1.33
3	C	213	NAD	O4D-C1D	3.34	1.45	1.40
3	G	212	NAD	O4D-C1D	3.25	1.45	1.40
3	G	212	NAD	C2A-N3A	3.24	1.39	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	214	NAD	C4A-N3A	3.21	1.40	1.34
3	A	213	NAD	O4D-C1D	3.14	1.45	1.40
3	B	213	NAD	O4D-C1D	3.12	1.45	1.40
3	G	212	NAD	C2N-C3N	-3.12	1.34	1.39
3	E	212	NAD	C4A-N3A	3.00	1.40	1.34
3	B	213	NAD	PA-O3	-2.99	1.56	1.59
3	F	212	NAD	C2N-C3N	-2.97	1.34	1.39
3	G	212	NAD	C4A-N3A	2.96	1.39	1.34
3	B	213	NAD	C2N-C3N	-2.93	1.34	1.39
3	D	214	NAD	C5A-C6A	2.87	1.49	1.41
3	E	212	NAD	O4D-C4D	2.86	1.51	1.45
3	A	213	NAD	C6N-C5N	2.82	1.44	1.38
3	C	213	NAD	C3D-C4D	2.79	1.60	1.53
3	C	213	NAD	C5A-C6A	2.78	1.48	1.41
3	B	213	NAD	C5A-N7A	-2.63	1.34	1.39
3	E	212	NAD	C3D-C4D	2.63	1.59	1.53
3	F	212	NAD	C5A-C6A	2.59	1.48	1.41
3	D	214	NAD	C3D-C4D	2.58	1.59	1.53
3	E	212	NAD	C6N-C5N	2.53	1.43	1.38
3	E	212	NAD	C5A-C6A	2.52	1.48	1.41
3	G	212	NAD	PA-O3	2.52	1.62	1.59
3	F	212	NAD	C6N-C5N	2.51	1.43	1.38
3	D	214	NAD	O4D-C4D	2.50	1.50	1.45
3	C	213	NAD	C6N-C5N	2.49	1.43	1.38
3	G	212	NAD	C5A-N7A	-2.49	1.34	1.39
3	B	213	NAD	C5A-C6A	2.48	1.47	1.41
3	D	214	NAD	C2N-C3N	-2.47	1.35	1.39
3	F	212	NAD	O4D-C1D	2.38	1.44	1.40
3	A	213	NAD	C5A-N7A	-2.37	1.34	1.39
3	C	213	NAD	C2N-C3N	-2.28	1.35	1.39
3	E	212	NAD	C2N-C3N	-2.25	1.35	1.39
3	D	214	NAD	C6N-C5N	2.18	1.43	1.38
3	A	213	NAD	C2N-C3N	-2.17	1.35	1.39
3	G	212	NAD	C5A-C6A	2.16	1.47	1.41
3	B	213	NAD	O4D-C4D	2.16	1.49	1.45
3	G	212	NAD	O4D-C4D	2.12	1.49	1.45
3	F	212	NAD	C3B-C4B	2.12	1.58	1.53
3	G	212	NAD	C6N-C5N	2.12	1.43	1.38
3	A	213	NAD	C3B-C4B	2.04	1.58	1.53
3	F	212	NAD	C5A-C4A	2.03	1.42	1.39
3	C	213	NAD	O4D-C4D	2.01	1.49	1.45
3	E	212	NAD	C5A-N7A	-2.01	1.35	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	G	212	NAD	C3D-C4D	2.00	1.58	1.53

All (108) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	213	NAD	C5N-C4N-C3N	-12.78	107.80	120.36
3	E	212	NAD	C5N-C4N-C3N	-12.75	107.83	120.36
3	D	214	NAD	C5N-C4N-C3N	-12.37	108.20	120.36
3	F	212	NAD	C5N-C4N-C3N	-11.98	108.59	120.36
3	G	212	NAD	C5N-C4N-C3N	-11.84	108.72	120.36
3	A	213	NAD	C5N-C4N-C3N	-11.32	109.23	120.36
3	C	213	NAD	C5N-C4N-C3N	-11.31	109.25	120.36
3	E	212	NAD	C6N-N1N-C2N	-9.38	113.90	121.88
3	F	212	NAD	C6N-N1N-C2N	-9.36	113.92	121.88
3	D	214	NAD	C6N-N1N-C2N	-9.23	114.02	121.88
3	A	213	NAD	C6N-N1N-C2N	-9.19	114.06	121.88
3	C	213	NAD	C6N-N1N-C2N	-8.92	114.29	121.88
3	B	213	NAD	C6N-N1N-C2N	-8.77	114.42	121.88
3	G	212	NAD	C6N-N1N-C2N	-8.70	114.47	121.88
3	B	213	NAD	N3A-C2A-N1A	-4.69	121.48	128.58
3	D	214	NAD	N3A-C2A-N1A	-4.52	121.74	128.58
3	G	212	NAD	N3A-C2A-N1A	-4.46	121.83	128.58
3	A	213	NAD	N3A-C2A-N1A	-4.41	121.91	128.58
3	C	213	NAD	N3A-C2A-N1A	-4.40	121.92	128.58
3	B	213	NAD	C2A-N1A-C6A	4.35	125.87	118.73
3	A	213	NAD	C2A-N1A-C6A	4.30	125.80	118.73
3	A	213	NAD	O2N-PN-O5D	4.24	126.78	107.57
3	C	213	NAD	C2A-N1A-C6A	4.21	125.64	118.73
3	E	212	NAD	N3A-C2A-N1A	-4.17	122.27	128.58
3	F	212	NAD	C2A-N1A-C6A	4.16	125.56	118.73
3	G	212	NAD	C2A-N1A-C6A	4.15	125.55	118.73
3	E	212	NAD	C2A-N1A-C6A	4.05	125.38	118.73
3	D	214	NAD	C2A-N1A-C6A	4.03	125.35	118.73
3	F	212	NAD	N3A-C2A-N1A	-3.98	122.55	128.58
3	C	213	NAD	O2N-PN-O5D	3.50	123.41	107.57
3	D	214	NAD	C1B-N9A-C8A	3.40	134.63	127.09
3	A	213	NAD	O5D-PN-O1N	-3.34	95.70	108.94
3	E	212	NAD	O5D-C5D-C4D	-3.30	97.76	108.99
3	E	212	NAD	O2N-PN-O5D	3.29	122.49	107.57
3	F	212	NAD	O2N-PN-O5D	3.28	122.42	107.57
3	E	212	NAD	O5D-PN-O1N	-3.24	96.08	108.94
3	A	213	NAD	O3-PN-O1N	3.20	120.32	110.70

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	214	NAD	O2N-PN-O5D	3.16	121.90	107.57
3	B	213	NAD	C1B-N9A-C8A	3.14	134.07	127.09
3	F	212	NAD	C1B-N9A-C8A	3.03	133.82	127.09
3	A	213	NAD	C2N-N1N-C1D	-3.02	112.48	119.13
3	G	212	NAD	C1B-N9A-C8A	2.98	133.72	127.09
3	A	213	NAD	C1B-N9A-C8A	2.96	133.65	127.09
3	G	212	NAD	O2N-PN-O5D	2.95	120.93	107.57
3	C	213	NAD	C1B-N9A-C8A	2.91	133.54	127.09
3	G	212	NAD	C2N-N1N-C1D	-2.89	112.74	119.13
3	C	213	NAD	C2N-N1N-C1D	-2.87	112.80	119.13
3	B	213	NAD	C4A-N9A-C8A	-2.86	102.74	105.74
3	F	212	NAD	O5D-PN-O1N	-2.86	97.62	108.94
3	C	213	NAD	O5D-PN-O1N	-2.84	97.67	108.94
3	B	213	NAD	C6N-C5N-C4N	-2.83	115.37	119.45
3	E	212	NAD	C1B-N9A-C8A	2.81	133.34	127.09
3	A	213	NAD	O4B-C1B-N9A	-2.70	102.90	108.09
3	C	213	NAD	C2N-C3N-C4N	2.70	121.39	118.26
3	E	212	NAD	C2N-N1N-C1D	-2.69	113.20	119.13
3	D	214	NAD	C4D-O4D-C1D	-2.68	107.47	109.92
3	G	212	NAD	O5D-PN-O1N	-2.64	98.49	108.94
3	D	214	NAD	C6N-C5N-C4N	-2.61	115.69	119.45
3	B	213	NAD	C2N-N1N-C1D	-2.57	113.47	119.13
3	A	213	NAD	O2A-PA-O3	-2.55	100.39	107.27
3	F	212	NAD	C2N-C3N-C4N	2.54	121.21	118.26
3	B	213	NAD	C5A-N7A-C8A	2.49	107.36	103.45
3	F	212	NAD	C4A-N9A-C8A	-2.47	103.14	105.74
3	G	212	NAD	C4A-N9A-C8A	-2.46	103.16	105.74
3	C	213	NAD	O3-PN-O1N	2.42	117.97	110.70
3	C	213	NAD	O2A-PA-O3	-2.41	100.75	107.27
3	F	212	NAD	C2N-N1N-C1D	-2.39	113.85	119.13
3	C	213	NAD	C4A-N9A-C8A	-2.38	103.24	105.74
3	C	213	NAD	C6N-N1N-C1D	-2.36	115.10	119.73
3	C	213	NAD	O4B-C1B-N9A	-2.32	103.63	108.09
3	G	212	NAD	C2N-C3N-C4N	2.32	120.96	118.26
3	E	212	NAD	C2B-C3B-C4B	2.31	107.07	102.61
3	B	213	NAD	C6N-N1N-C1D	-2.30	115.21	119.73
3	C	213	NAD	C5A-N7A-C8A	2.30	107.06	103.45
3	F	212	NAD	O3-PN-O1N	2.28	117.57	110.70
3	D	214	NAD	C5A-C4A-N9A	2.25	108.27	105.81
3	A	213	NAD	C5A-N7A-C8A	2.25	106.99	103.45
3	E	212	NAD	C4A-N9A-C8A	-2.25	103.38	105.74
3	E	212	NAD	C5A-N7A-C8A	2.24	106.97	103.45

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	213	NAD	C2B-C3B-C4B	2.21	106.88	102.61
3	D	214	NAD	C5A-N7A-C8A	2.20	106.90	103.45
3	D	214	NAD	C2N-C3N-C4N	2.19	120.81	118.26
3	A	213	NAD	C2N-C3N-C4N	2.19	120.81	118.26
3	E	212	NAD	C6N-C5N-C4N	-2.19	116.29	119.45
3	E	212	NAD	C4D-O4D-C1D	-2.18	107.93	109.92
3	G	212	NAD	C6N-C5N-C4N	-2.18	116.31	119.45
3	G	212	NAD	O4B-C1B-N9A	-2.18	103.91	108.09
3	D	214	NAD	C2N-N1N-C1D	-2.18	114.33	119.13
3	D	214	NAD	O5D-PN-O1N	-2.17	100.34	108.94
3	D	214	NAD	C4A-N9A-C8A	-2.17	103.46	105.74
3	G	212	NAD	O2B-C2B-C3B	2.17	118.76	111.82
3	F	212	NAD	C5A-N7A-C8A	2.14	106.82	103.45
3	G	212	NAD	N6A-C6A-N1A	2.12	123.09	118.38
3	E	212	NAD	C2N-C3N-C4N	2.11	120.71	118.26
3	A	213	NAD	O2A-PA-O1A	2.09	122.17	112.44
3	F	212	NAD	C5A-C4A-N3A	-2.09	123.84	126.72
3	C	213	NAD	O2B-C2B-C3B	2.08	118.49	111.82
3	G	212	NAD	C5A-N7A-C8A	2.08	106.71	103.45
3	D	214	NAD	O2A-PA-O1A	2.07	122.08	112.44
3	B	213	NAD	C5A-C4A-N3A	-2.07	123.87	126.72
3	E	212	NAD	O2B-C2B-C3B	2.03	118.32	111.82
3	F	212	NAD	C6N-C5N-C4N	-2.03	116.53	119.45
3	B	213	NAD	O4B-C1B-N9A	-2.02	104.20	108.09
3	F	212	NAD	N6A-C6A-N1A	2.02	122.88	118.38
3	D	214	NAD	C4A-N9A-C1B	-2.02	121.90	126.63
3	F	212	NAD	O5D-C5D-C4D	-2.01	102.14	108.99
3	A	213	NAD	N6A-C6A-N1A	2.00	122.84	118.38
3	E	212	NAD	N6A-C6A-N1A	2.00	122.83	118.38

There are no chirality outliers.

All (37) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	213	NAD	O4D-C1D-N1N-C2N
3	B	213	NAD	C2D-C1D-N1N-C2N
3	C	213	NAD	O4D-C1D-N1N-C2N
3	C	213	NAD	C2D-C1D-N1N-C2N
3	D	214	NAD	O4D-C1D-N1N-C2N
3	D	214	NAD	C2D-C1D-N1N-C2N
3	F	212	NAD	O4D-C1D-N1N-C2N
3	F	212	NAD	C2D-C1D-N1N-C2N

Continued on next page...

Continued from previous page...

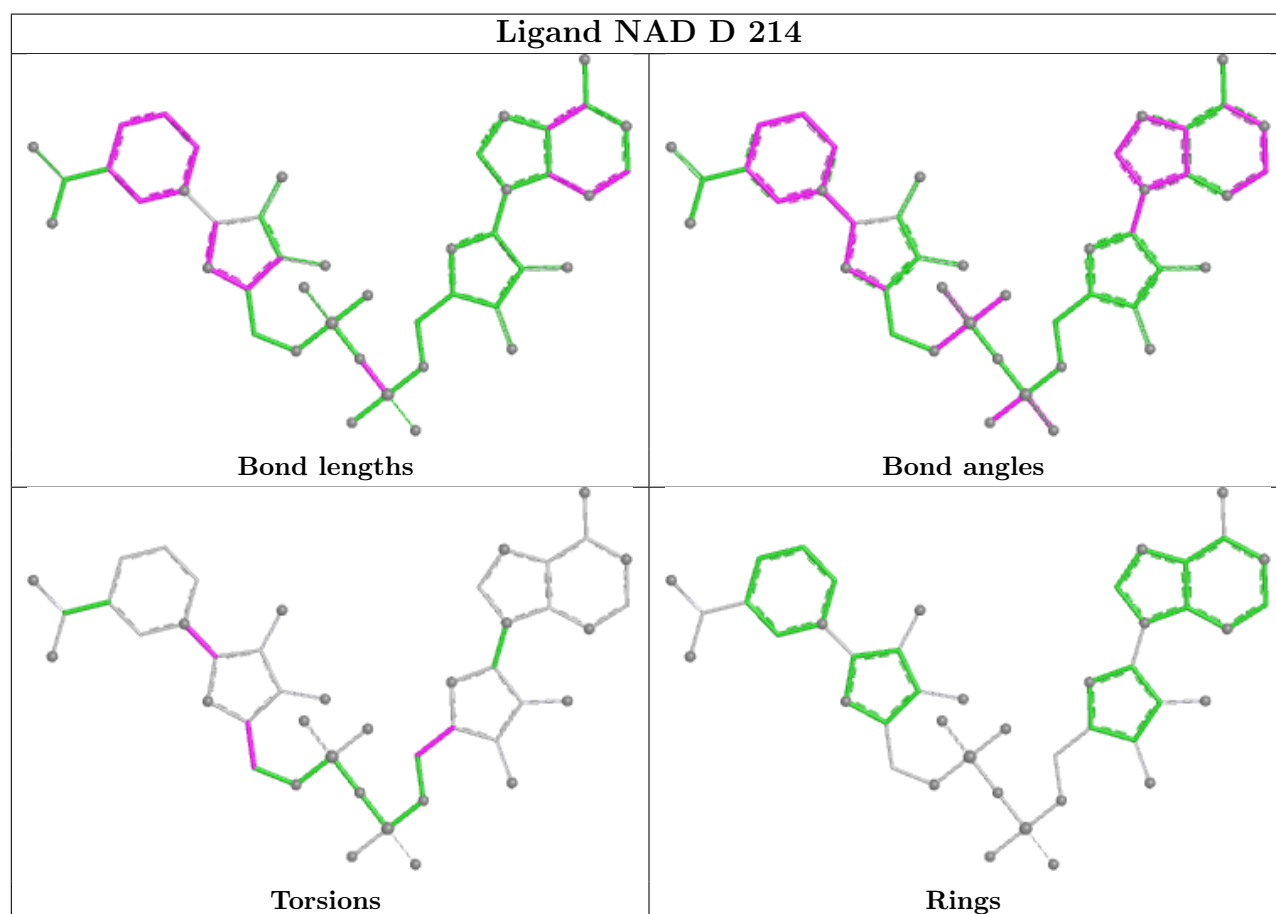
Mol	Chain	Res	Type	Atoms
3	A	213	NAD	O4D-C4D-C5D-O5D
3	F	212	NAD	C2N-C3N-C7N-O7N
3	F	212	NAD	C2N-C3N-C7N-N7N
3	F	212	NAD	C4N-C3N-C7N-O7N
3	F	212	NAD	C4N-C3N-C7N-N7N
3	G	212	NAD	O4D-C4D-C5D-O5D
3	E	212	NAD	O4D-C4D-C5D-O5D
3	A	213	NAD	C3D-C4D-C5D-O5D
3	C	213	NAD	O4D-C4D-C5D-O5D
3	G	212	NAD	PA-O3-PN-O2N
3	G	212	NAD	C3D-C4D-C5D-O5D
3	A	213	NAD	O4D-C1D-N1N-C6N
3	E	212	NAD	O4D-C1D-N1N-C2N
3	G	212	NAD	O4D-C1D-N1N-C2N
3	A	213	NAD	PA-O3-PN-O2N
3	B	213	NAD	PA-O3-PN-O1N
3	G	212	NAD	PA-O3-PN-O1N
3	C	213	NAD	C4N-C3N-C7N-N7N
3	D	214	NAD	O4D-C4D-C5D-O5D
3	C	213	NAD	C4N-C3N-C7N-O7N
3	E	212	NAD	O4B-C4B-C5B-O5B
3	B	213	NAD	PA-O3-PN-O2N
3	E	212	NAD	PA-O3-PN-O1N
3	C	213	NAD	O4B-C4B-C5B-O5B
3	D	214	NAD	O4B-C4B-C5B-O5B
3	F	212	NAD	O4B-C4B-C5B-O5B
3	A	213	NAD	O4B-C4B-C5B-O5B
3	F	212	NAD	PN-O3-PA-O2A
3	G	212	NAD	O4B-C4B-C5B-O5B

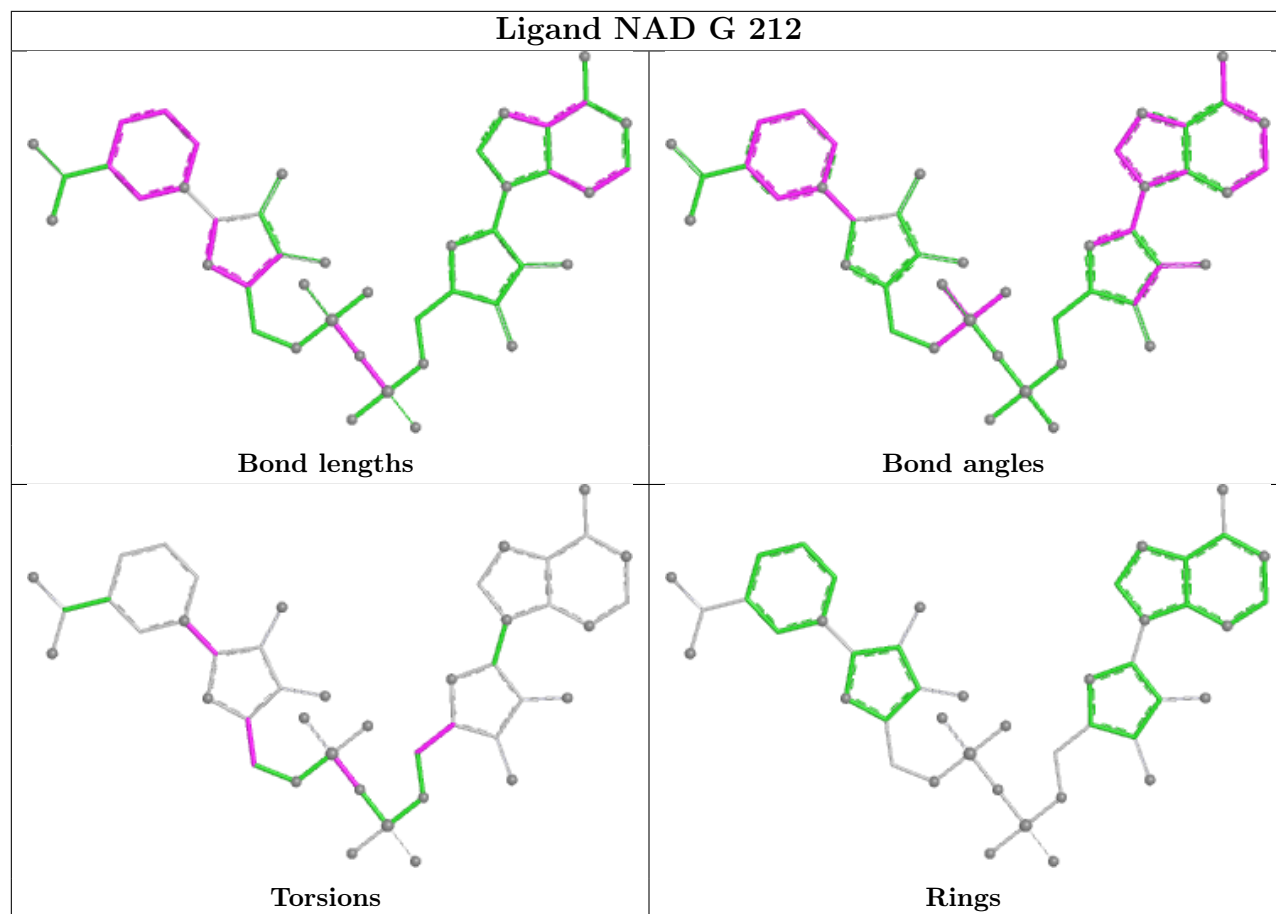
There are no ring outliers.

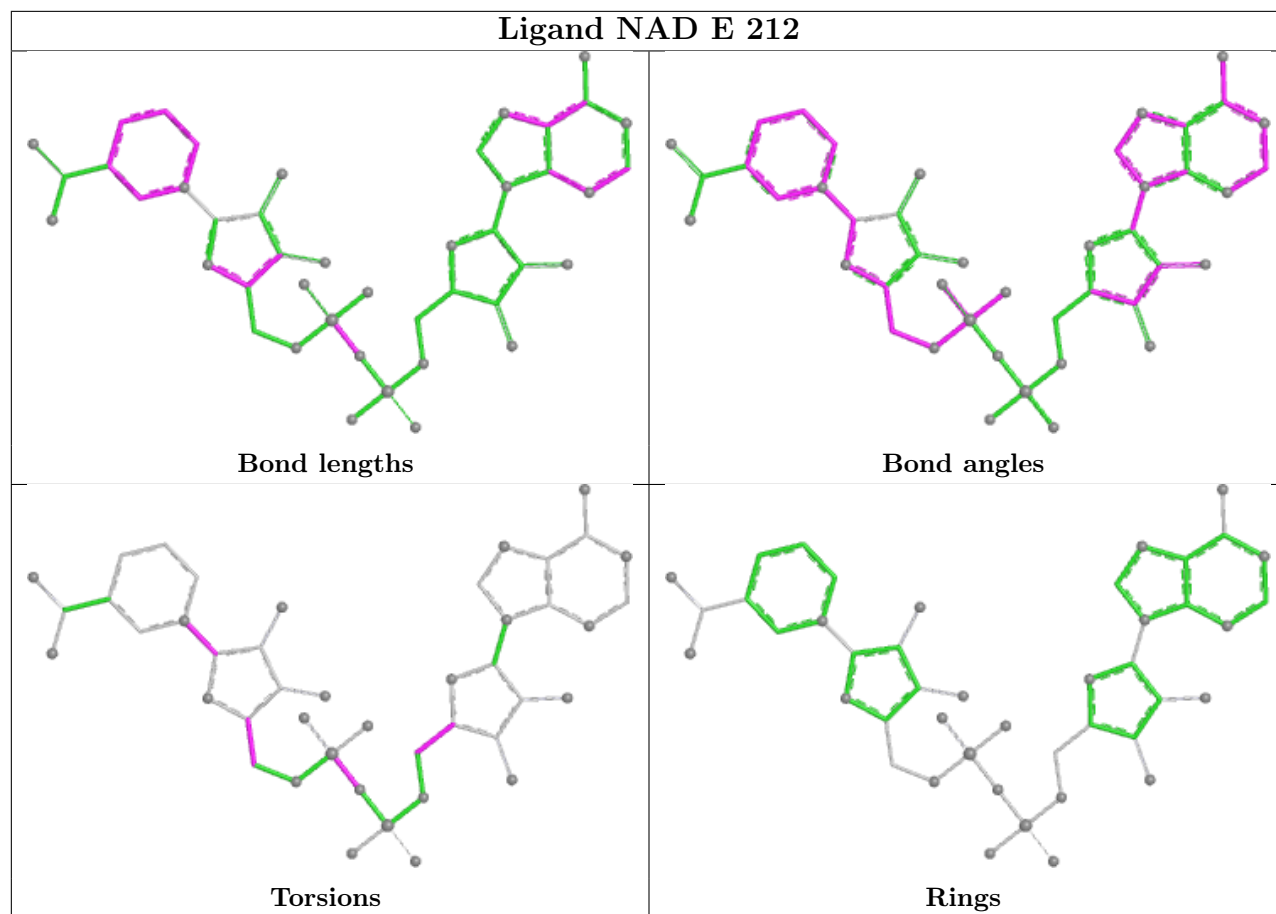
7 monomers are involved in 22 short contacts:

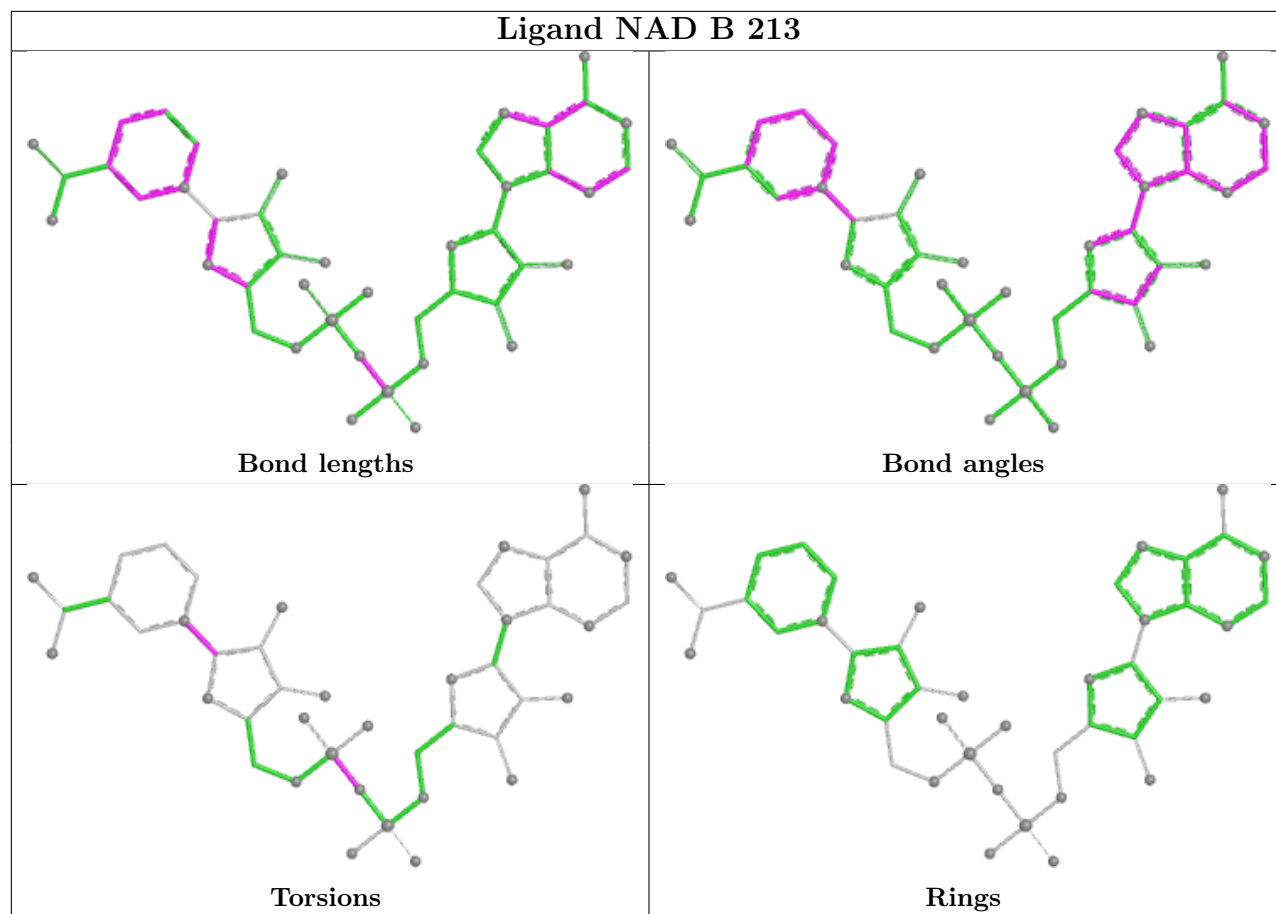
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	214	NAD	1	0
3	G	212	NAD	5	0
3	E	212	NAD	2	0
3	B	213	NAD	3	0
3	F	212	NAD	3	0
3	A	213	NAD	4	0
3	C	213	NAD	4	0

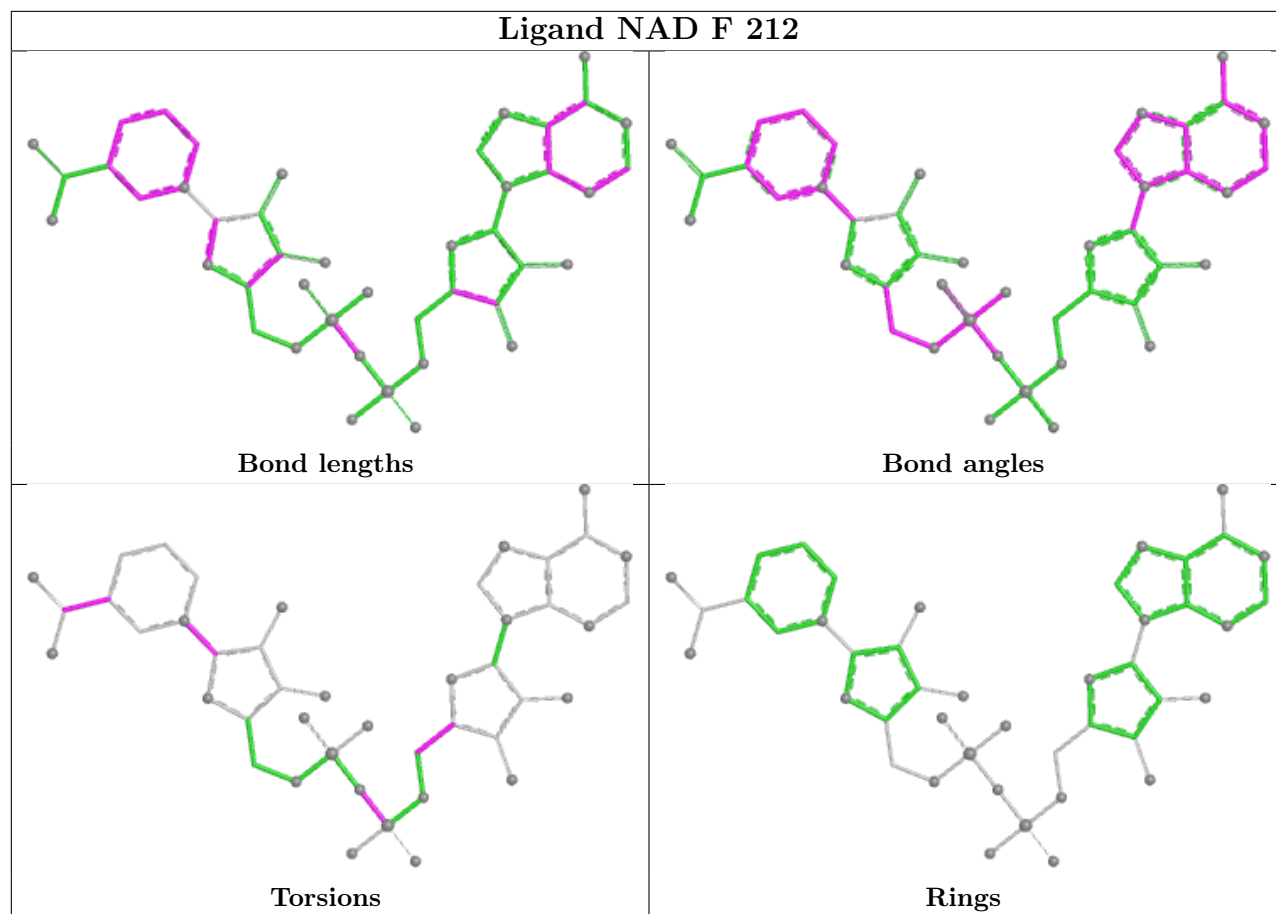
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

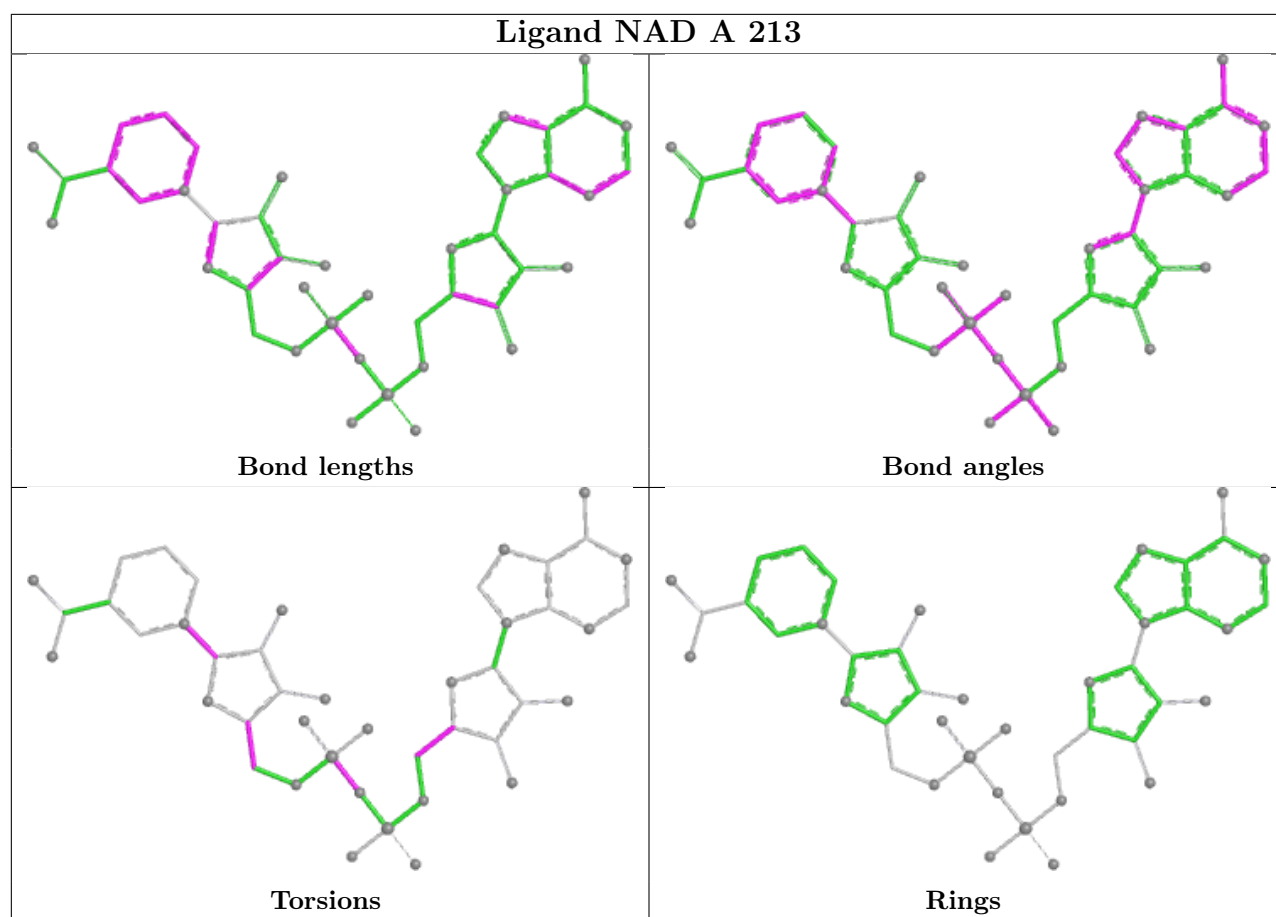


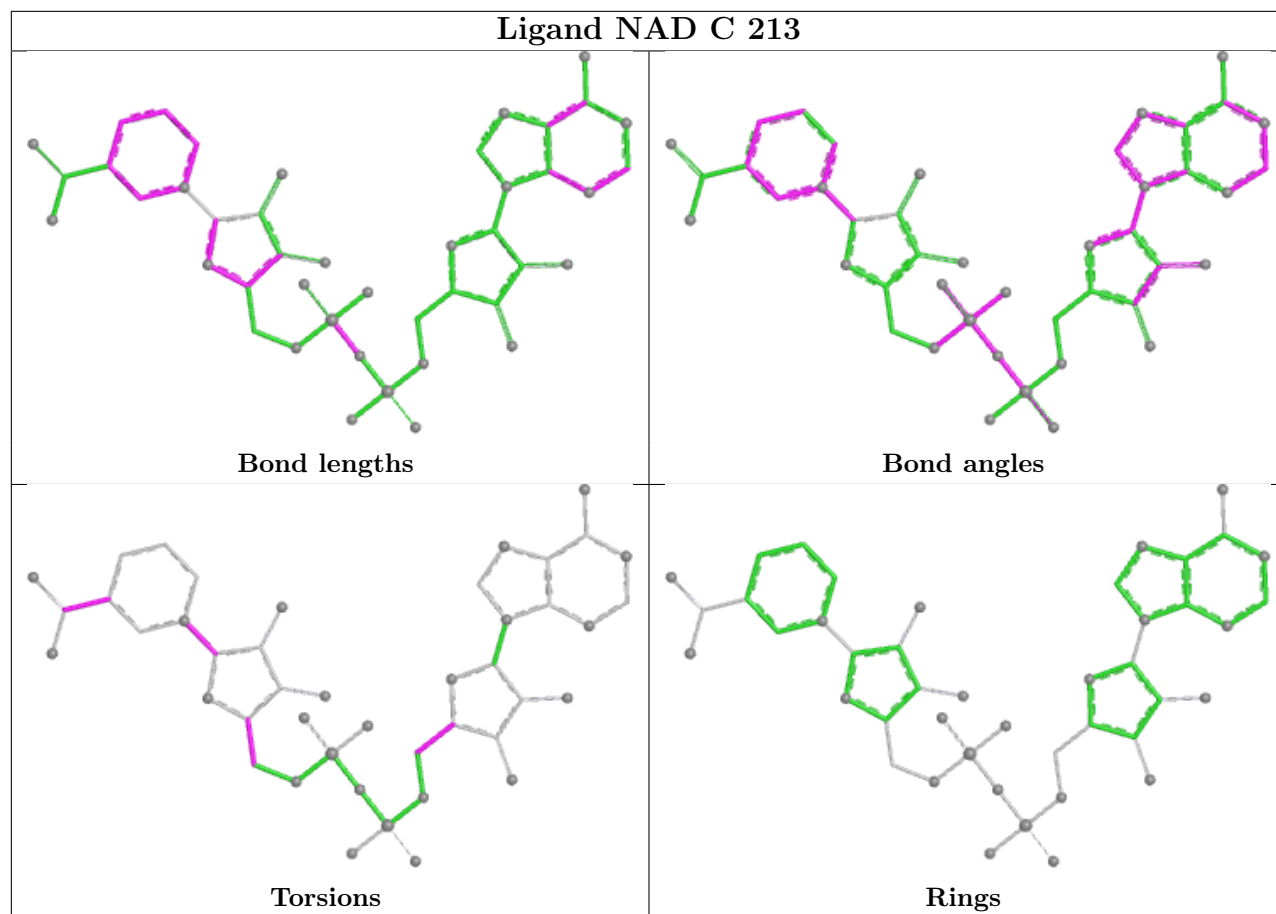












5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	G	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	G	188:ASP	C	189[A]:PHE	N	1.15
1	G	190[A]:LEU	C	191:ALA	N	1.15

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	204/211 (96%)	0.23	6 (2%) 53 45	11, 31, 54, 66	0
1	B	196/211 (92%)	-0.05	1 (0%) 87 83	11, 25, 47, 59	0
1	C	202/211 (95%)	0.23	6 (2%) 52 43	13, 32, 71, 77	0
1	D	196/211 (92%)	0.07	4 (2%) 65 56	10, 29, 64, 74	0
1	E	201/211 (95%)	-0.11	2 (0%) 79 73	10, 22, 42, 64	0
1	F	199/211 (94%)	0.48	5 (2%) 58 48	10, 42, 71, 80	0
1	G	191/211 (90%)	0.51	25 (13%) 7 6	11, 29, 91, 98	2 (1%)
All	All	1389/1477 (94%)	0.19	49 (3%) 47 38	10, 30, 69, 98	2 (0%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	4	PRO	4.6
1	G	26	VAL	4.3
1	G	31	SER	4.2
1	C	57	THR	4.1
1	G	6	ALA	3.7
1	D	4	PRO	3.6
1	G	18	LEU	3.2
1	G	62	TYR	3.2
1	A	205	TRP	3.0
1	G	38	ALA	3.0
1	G	34	LEU	3.0
1	G	41	THR	3.0
1	D	205	TRP	2.9
1	G	8	ILE	2.9
1	C	26	VAL	2.8
1	E	59	GLY	2.8
1	A	57	THR	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	G	32	GLU	2.7
1	G	28	ARG	2.7
1	F	55	TYR	2.6
1	G	61	GLY	2.6
1	B	132	LEU	2.6
1	E	60	VAL	2.6
1	C	29	THR	2.5
1	F	27	HIS	2.5
1	G	29	THR	2.4
1	G	40	VAL	2.4
1	A	112	ASP	2.3
1	D	123	ARG	2.3
1	G	25	GLY	2.3
1	G	35	GLY	2.2
1	F	21	LEU	2.2
1	G	24	GLN	2.2
1	A	118	VAL	2.2
1	F	34	LEU	2.2
1	G	17	ILE	2.2
1	G	43	PHE	2.2
1	G	33	GLN	2.1
1	G	37	LEU	2.1
1	G	52	PHE	2.1
1	D	55	TYR	2.1
1	F	78	ASN	2.1
1	C	23	ALA	2.1
1	C	204	LYS	2.1
1	A	121	PRO	2.1
1	G	22	GLU	2.1
1	G	7	ALA	2.0
1	A	180	LYS	2.0
1	C	58	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands

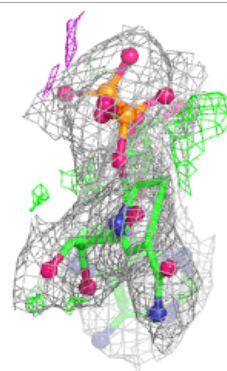
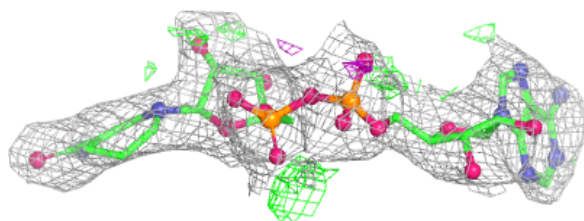
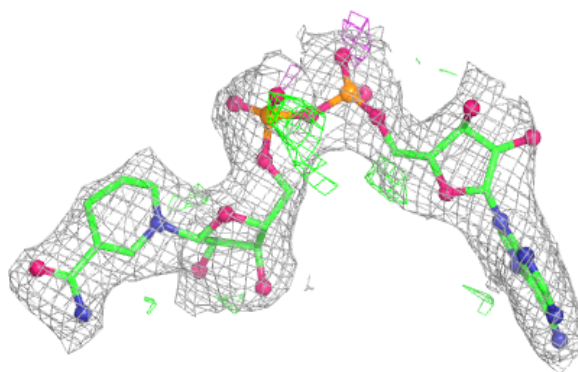
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	CA	A	212	1/1	0.90	0.33	58,58,58,58	0
3	NAD	A	213	44/44	0.90	0.11	20,27,32,37	0
2	CA	C	212	1/1	0.91	0.07	64,64,64,64	0
3	NAD	B	213	44/44	0.92	0.10	14,22,30,34	0
3	NAD	C	213	44/44	0.93	0.10	21,28,40,41	0
3	NAD	F	212	44/44	0.93	0.10	20,28,35,37	0
2	CA	B	212	1/1	0.94	0.26	45,45,45,45	0
2	CA	D	213	1/1	0.94	0.06	57,57,57,57	0
3	NAD	G	212	44/44	0.94	0.10	16,27,37,39	0
3	NAD	E	212	44/44	0.95	0.09	10,15,23,28	0
2	CA	D	212	1/1	0.95	0.19	47,47,47,47	0
3	NAD	D	214	44/44	0.95	0.09	10,20,25,31	0

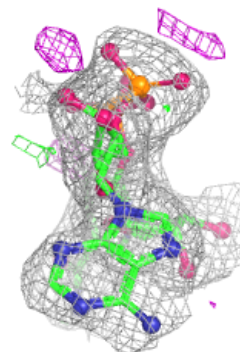
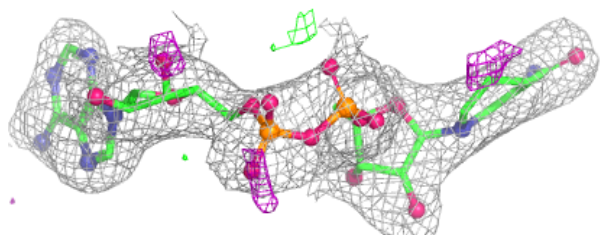
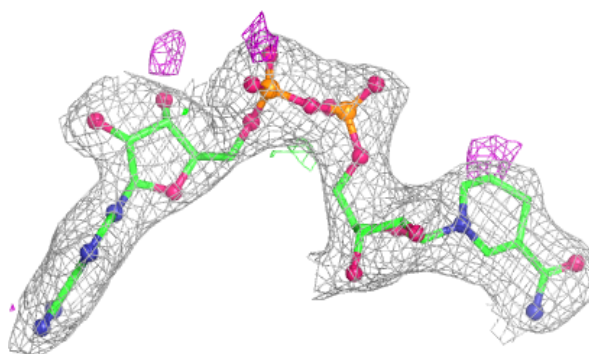
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAD A 213:

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

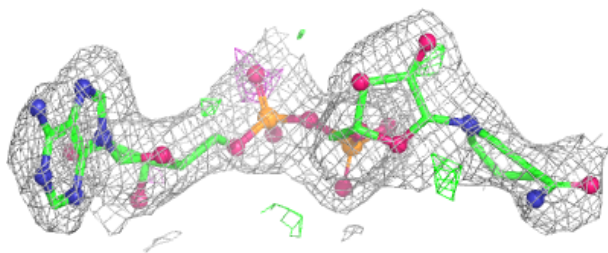
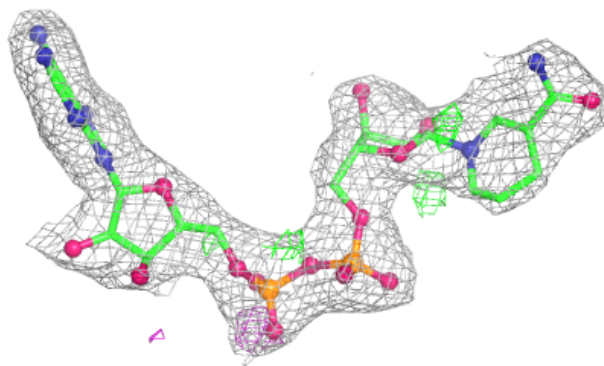
**Electron density around NAD B 213:**

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

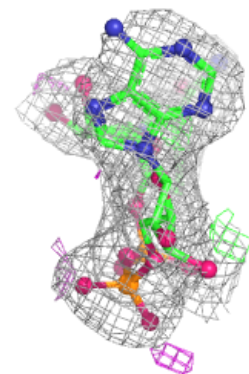
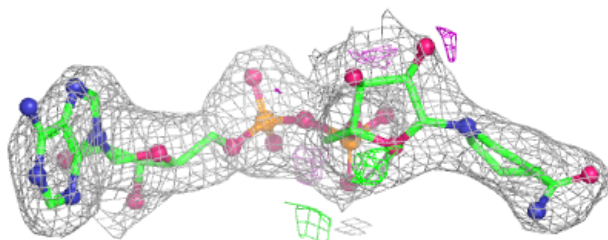
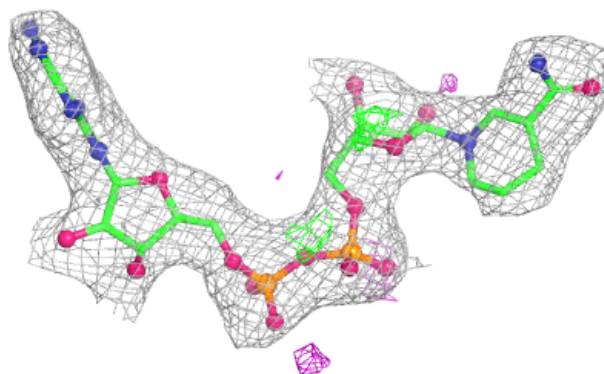


Electron density around NAD C 213:

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

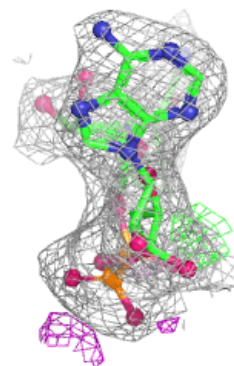
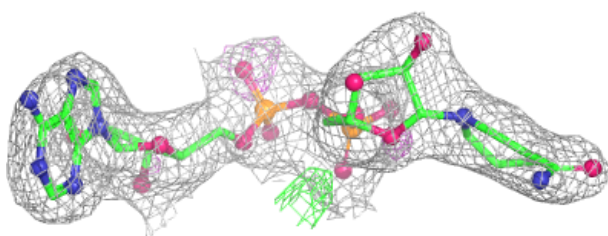
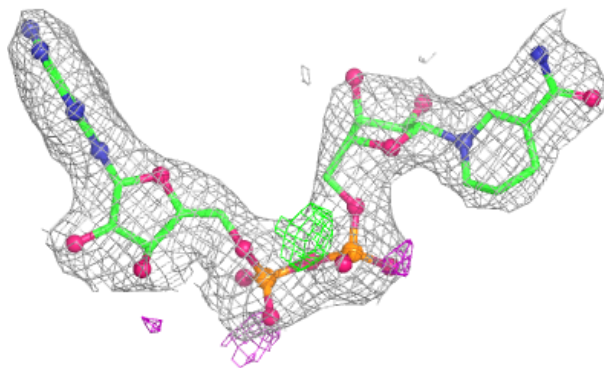
**Electron density around NAD F 212:**

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

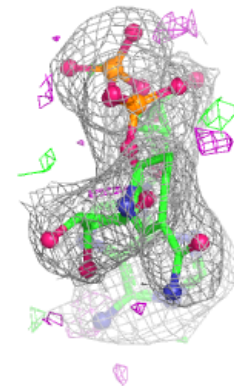
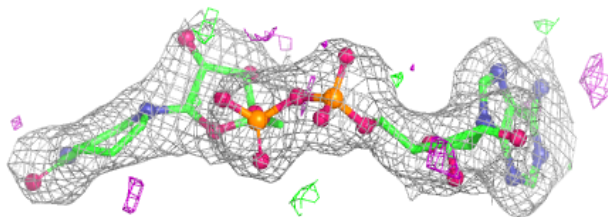
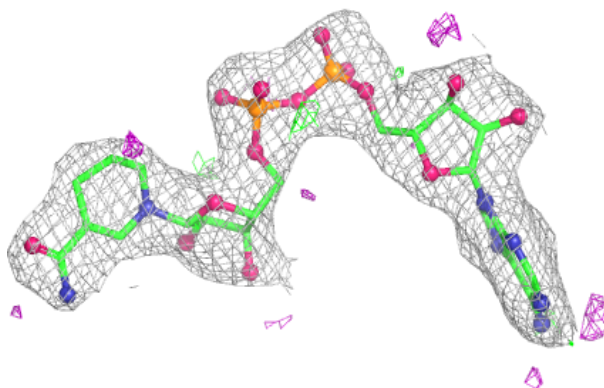


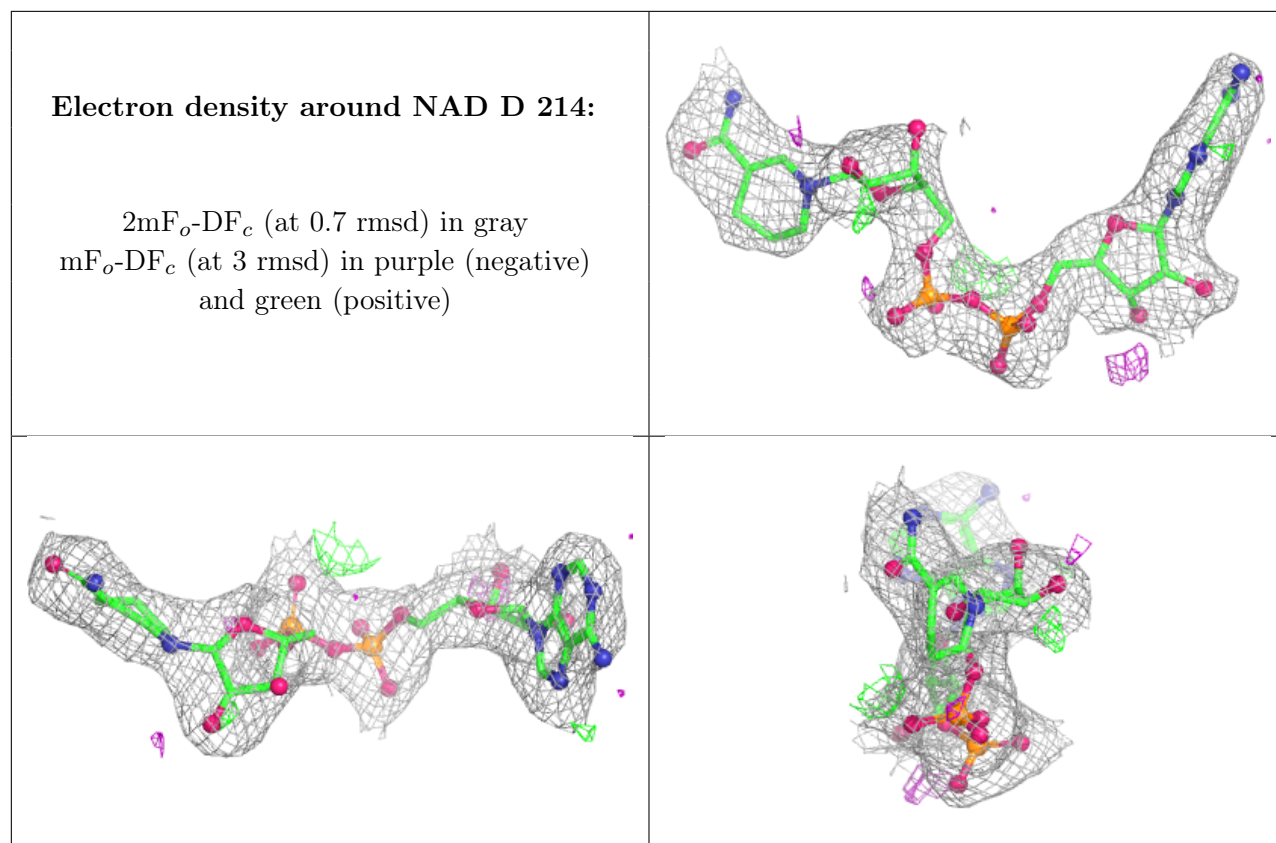
Electron density around NAD G 212:

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

**Electron density around NAD E 212:**

$2mF_o-DF_c$ (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.