



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 08:26 AM UTC

PDB ID : 1ML3 / pdb_00001ml3
Title : Evidences for a flip-flop catalytic mechanism of Trypanosoma cruzi glyceraldehyde-3-phosphate dehydrogenase, from its crystal structure in complex with reacted irreversible inhibitor 2-(2-phosphono-ethyl)-acrylic acid 4-nitro-phenyl ester
Authors : Castilho, M.S.; Pavao, F.; Oliva, G.
Deposited on : 2002-08-29
Resolution : 2.50 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:

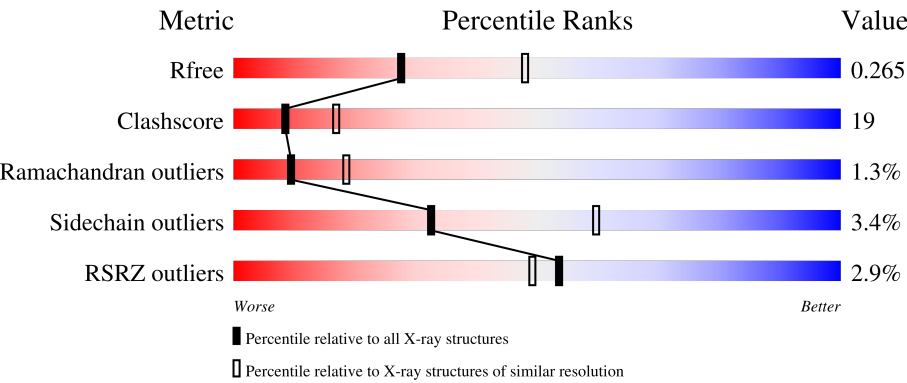
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	359	69%28%.
1	B	359	2%

62%35%.

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	CYX	D	3166	-	X	-	-

2 Entry composition [i](#)

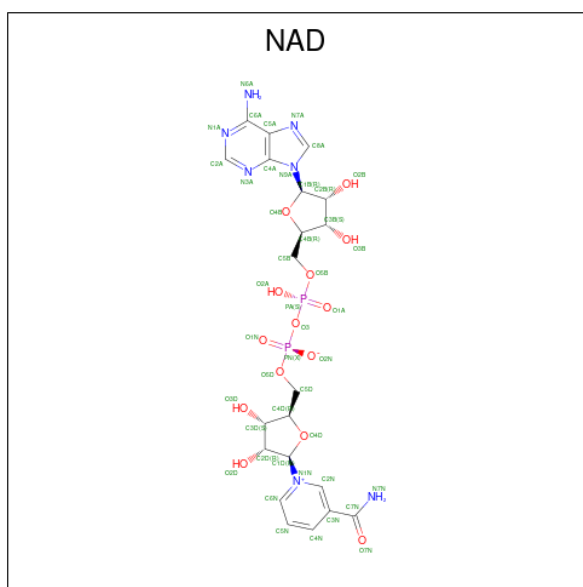
There are 4 unique types of molecules in this entry. The entry contains 11861 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glyceraldehyde 3-phosphate dehydrogenase, glycosomal.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	20	0	0
			2745	1725	486	520	14			
1	B	359	Total	C	N	O	S	52	1	0
			2747	1726	486	520	15			
1	C	359	Total	C	N	O	S	101	1	0
			2747	1726	486	520	15			
1	D	359	Total	C	N	O	S	12	0	0
			2745	1725	486	520	14			

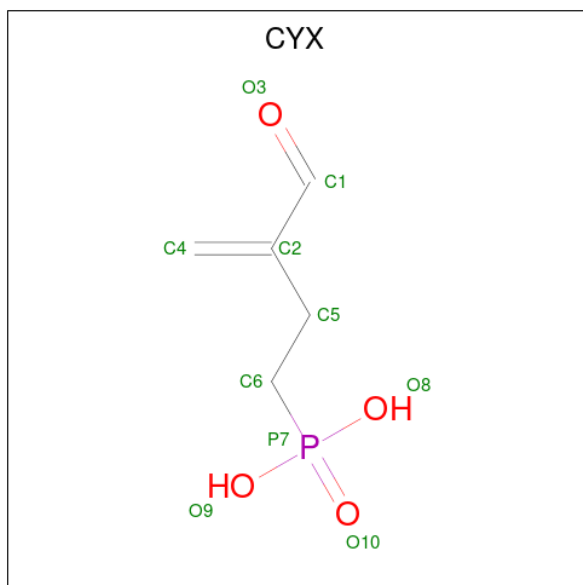
- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Continued from previous page...

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

- Molecule 3 is (3-FORMYL-BUT-3-ENYL)-PHOSPHONIC ACID (CCD ID: CYX) (formula: $C_5H_9O_4P$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	O	P	0	1
			20	10	8	2		
3	C	1	Total	C	O	P	0	1
			20	10	8	2		
3	D	1	Total	C	O	P	0	0
			10	5	4	1		

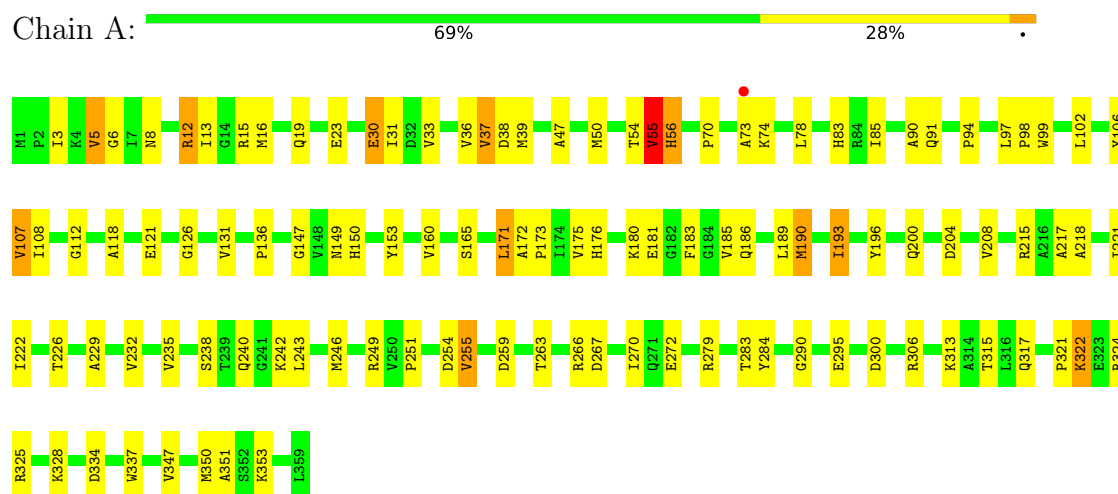
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	217	Total	O	0	0
			217	217		
4	B	161	Total	O	0	0
			161	161		
4	C	123	Total	O	0	0
			123	123		
4	D	194	Total	O	0	0
			194	194		

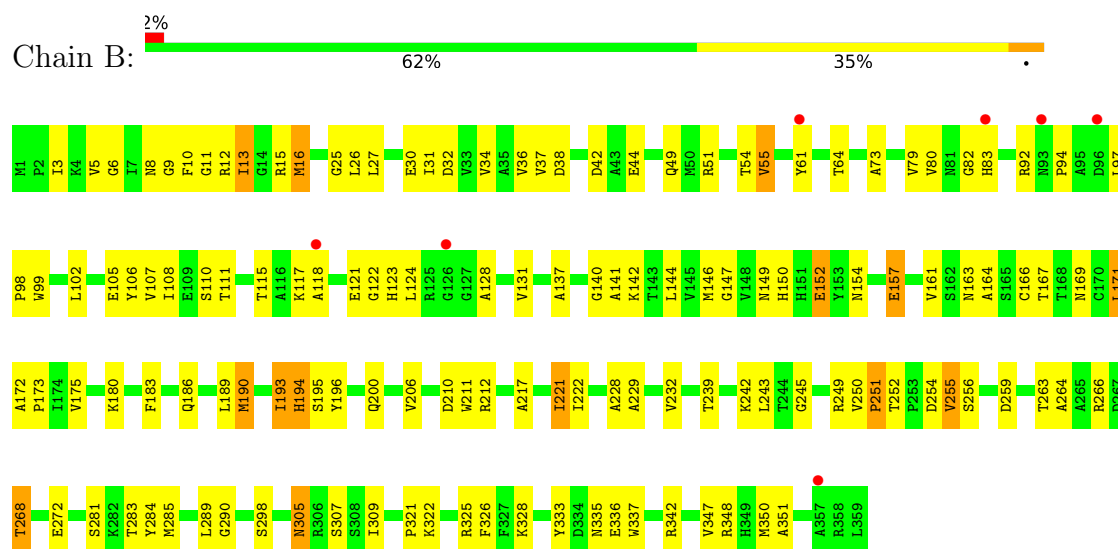
3 Residue-property plots

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: Glyceraldehyde 3-phosphate dehydrogenase, glycosomal



- Molecule 1: Glyceraldehyde 3-phosphate dehydrogenase, glycosomal

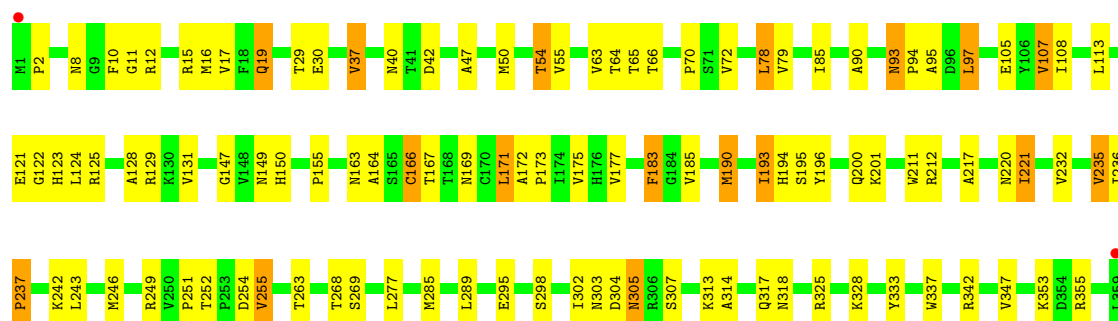


- Molecule 1: Glyceraldehyde 3-phosphate dehydrogenase, glycosomal





- Molecule 1: Glyceraldehyde 3-phosphate dehydrogenase, glycosomal



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.46Å 85.26Å 105.15Å 90.00° 95.61° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 20.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.5 (20.00-2.50) 97.3 (20.00-2.50)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.92 (at 2.50Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.199 , 0.265 0.199 , 0.265	Depositor DCC
R_{free} test set	2455 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	25.6	Xtriage
Anisotropy	0.530	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 63.0	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	0.94	EDS
Total number of atoms	11861	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.25% 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: CYX, 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	0.41	0/2798	0.94	13/3792 (0.3%)
1	B	0.39	0/2804	0.93	9/3800 (0.2%)
1	C	0.36	0/2804	0.91	7/3800 (0.2%)
1	D	0.42	0/2798	0.96	13/3792 (0.3%)
All	All	0.40	0/11204	0.94	42/15184 (0.3%)

There are no bond length outliers.

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	221	ILE	N-CA-C	-8.55	94.77	107.51
1	B	221	ILE	N-CA-C	-8.42	95.70	107.99
1	C	217	ALA	N-CA-C	8.11	119.90	111.14
1	A	222	ILE	N-CA-C	7.71	115.78	108.15
1	C	221	ILE	N-CA-C	-7.62	96.75	107.80
1	D	217	ALA	N-CA-C	7.51	119.11	111.07
1	B	217	ALA	N-CA-C	7.51	119.25	111.14
1	C	337	TRP	N-CA-C	7.26	118.98	111.14
1	A	221	ILE	N-CA-C	-6.98	97.80	107.99
1	A	208	VAL	N-CA-C	6.68	119.40	111.05
1	A	217	ALA	N-CA-C	6.52	118.18	111.14
1	B	283	THR	N-CA-C	6.41	118.30	108.30
1	D	183	PHE	N-CA-C	-6.39	103.60	111.40
1	A	193	ILE	N-CA-C	-6.34	98.37	107.37
1	A	337	TRP	N-CA-C	6.32	117.86	110.97
1	D	93	ASN	CA-C-N	6.24	126.43	119.32
1	D	93	ASN	C-N-CA	6.24	126.43	119.32
1	A	55	VAL	N-CA-C	6.18	117.12	111.81
1	A	283	THR	N-CA-C	6.17	117.92	108.30
1	D	193	ILE	N-CA-C	-6.04	97.90	107.15

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	31	ILE	N-CA-C	6.00	116.51	108.11
1	C	193	ILE	N-CA-C	-5.94	98.06	107.15
1	D	236	ILE	CA-C-N	5.74	127.01	119.84
1	D	236	ILE	C-N-CA	5.74	127.01	119.84
1	C	318	ASN	N-CA-C	5.66	119.77	112.41
1	B	193	ILE	N-CA-C	-5.66	99.44	107.98
1	A	5	VAL	N-CA-C	5.66	116.62	108.48
1	B	194	HIS	N-CA-C	5.65	118.17	109.07
1	A	334	ASP	N-CA-C	-5.61	98.58	108.23
1	B	55	VAL	N-CA-C	5.59	116.43	111.90
1	D	235	VAL	N-CA-C	-5.51	107.45	112.96
1	C	222	ILE	N-CA-C	5.39	116.23	107.71
1	B	250	VAL	N-CA-C	5.33	113.76	107.84
1	D	337	TRP	N-CA-C	5.24	116.79	111.14
1	D	304	ASP	N-CA-C	-5.21	100.81	109.46
1	B	337	TRP	N-CA-C	5.15	116.70	111.14
1	D	17	VAL	N-CA-C	-5.13	105.39	110.62
1	A	112	GLY	N-CA-C	-5.08	108.61	115.36
1	D	298	SER	N-CA-C	5.08	117.47	111.33
1	A	56	HIS	N-CA-C	5.04	119.07	113.02
1	B	152	GLU	N-CA-C	-5.03	106.98	113.02
1	C	312	SER	N-CA-C	5.01	116.43	111.07

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	2745	0	2749	98	0
1	B	2747	0	2748	133	0
1	C	2747	0	2748	115	0
1	D	2745	0	2748	92	0
2	B	44	0	26	3	0
2	C	44	0	26	0	0
2	D	44	0	26	2	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	20	0	12	2	0
3	C	20	0	12	1	0
3	D	10	0	6	0	0
4	A	217	0	0	14	0
4	B	161	0	0	13	0
4	C	123	0	0	14	0
4	D	194	0	0	5	0
All	All	11861	0	11101	413	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 19.

All (413) 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:92:ARG:HE	1:B:92:ARG:HA	1.35	0.89
1:D:183:PHE:HD1	1:D:268:THR:HG21	1.38	0.89
1:B:94:PRO:HA	1:B:97:LEU:HD23	1.56	0.87
1:B:305:ASN:HB3	4:B:1512:HOH:O	1.75	0.85
1:C:183:PHE:HD1	1:C:268:THR:HG21	1.42	0.85
1:D:107:VAL:HG13	1:D:131:VAL:HG22	1.59	0.84
1:A:8:ASN:HA	1:A:37:VAL:HG13	1.60	0.84
1:B:92:ARG:HA	1:B:92:ARG:NE	1.93	0.83
1:D:171:LEU:HD13	1:D:232:VAL:HG21	1.63	0.81
1:D:8:ASN:HA	1:D:37:VAL:HG13	1.63	0.80
1:D:30:GLU:HG3	4:D:3305:HOH:O	1.80	0.80
1:D:50:MET:HE1	1:D:78:LEU:HG	1.65	0.79
1:A:251:PRO:HB2	1:B:251:PRO:HB2	1.63	0.79
1:C:251:PRO:HB2	1:D:251:PRO:HB2	1.65	0.78
1:C:293:ASP:O	1:C:313:LYS:HE2	1.83	0.77
1:C:37:VAL:HB	1:C:88:VAL:HG23	1.68	0.76
1:C:21:LEU:HD11	1:C:31:ILE:HG21	1.66	0.75
1:A:215:ARG:HH21	1:D:54:THR:HG22	1.51	0.75
1:B:239:THR:HB	1:B:243:LEU:HD13	1.69	0.74
1:B:11:GLY:HA3	2:B:1362:NAD:H4B	1.69	0.74
1:B:200:GLN:NE2	1:B:249:ARG:HH11	1.84	0.74
1:D:147:GLY:H	1:D:150:HIS:CD2	2.06	0.73
1:A:147:GLY:H	1:A:150:HIS:CD2	2.06	0.73
1:D:313:LYS:O	1:D:317:GLN:HG3	1.89	0.73
1:B:8:ASN:HA	1:B:37:VAL:HG13	1.69	0.73
1:D:183:PHE:CD1	1:D:268:THR:HG21	2.22	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:94:PRO:HA	1:A:97:LEU:HD23	1.71	0.73
1:B:117:LYS:O	1:B:121:GLU:HG3	1.89	0.73
1:A:8:ASN:HD22	1:A:37:VAL:HG13	1.54	0.72
1:C:3:ILE:HG22	1:C:4:LYS:H	1.53	0.72
1:B:3:ILE:HB	1:B:31:ILE:HG12	1.71	0.72
1:C:124:LEU:HA	1:C:128:ALA:O	1.89	0.72
1:C:266:ARG:C	1:C:325:ARG:HE	1.98	0.72
1:D:64:THR:CG2	1:D:79:VAL:HB	2.20	0.71
1:C:117:LYS:O	1:C:121:GLU:HB2	1.90	0.71
1:C:108:ILE:HD11	1:C:347:VAL:HG21	1.72	0.71
1:D:47:ALA:HA	1:D:50:MET:HE3	1.72	0.71
1:C:196:TYR:HA	1:C:200:GLN:NE2	2.06	0.70
1:D:147:GLY:H	1:D:150:HIS:HD2	1.37	0.70
1:B:172:ALA:HB3	1:B:173:PRO:HD3	1.75	0.69
1:B:183:PHE:CD1	1:B:268:THR:HG21	2.28	0.69
1:A:50:MET:HE1	1:A:78:LEU:HD22	1.74	0.69
1:C:183:PHE:CD1	1:C:268:THR:HG21	2.27	0.68
1:C:61:TYR:HD2	1:C:81:ASN:HB2	1.59	0.68
1:D:200:GLN:NE2	1:D:249:ARG:HH11	1.92	0.67
1:A:3:ILE:HG22	1:A:5:VAL:HG23	1.75	0.67
1:D:196:TYR:HA	1:D:200:GLN:NE2	2.09	0.67
1:D:263:THR:HG21	4:D:3332:HOH:O	1.94	0.67
1:B:26:LEU:HD13	1:B:348:ARG:HD3	1.76	0.67
1:B:110:SER:HA	4:B:1466:HOH:O	1.94	0.67
1:A:321:PRO:HG2	4:A:449:HOH:O	1.94	0.66
1:C:64:THR:HG23	1:C:79:VAL:HB	1.77	0.66
1:D:37:VAL:HG22	2:D:1361:NAD:H2A	1.76	0.66
1:B:195:SER:HB2	1:B:252:THR:O	1.96	0.66
1:D:64:THR:HG22	1:D:79:VAL:HB	1.78	0.66
1:B:268:THR:HG22	1:B:272:GLU:OE2	1.96	0.66
1:B:107:VAL:CG1	1:B:131:VAL:HG22	2.26	0.66
1:C:105:GLU:HG3	1:C:106:TYR:H	1.60	0.65
1:D:107:VAL:CG1	1:D:131:VAL:HG22	2.26	0.65
1:B:171:LEU:HD22	1:B:175:VAL:HG23	1.79	0.65
1:B:194:HIS:NE2	3:B:1166[B]:CYX:H51	2.11	0.65
1:C:200:GLN:HE21	1:C:249:ARG:NH1	1.96	0.64
1:C:263:THR:HA	1:C:325:ARG:O	1.98	0.64
1:A:16:MET:HG3	4:A:540:HOH:O	1.96	0.64
1:B:200:GLN:HE21	1:B:249:ARG:HH11	1.45	0.64
1:C:196:TYR:HA	1:C:200:GLN:HE22	1.62	0.64
1:A:108:ILE:HD11	1:A:347:VAL:HG21	1.80	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:30:GLU:HG2	4:A:573:HOH:O	1.98	0.64
1:D:200:GLN:HE21	1:D:249:ARG:HH11	1.47	0.63
1:C:279:ARG:HG2	4:C:2238:HOH:O	1.99	0.63
1:A:107:VAL:HG13	1:A:131:VAL:HG22	1.81	0.63
1:B:83:HIS:HB2	4:B:1510:HOH:O	1.99	0.63
1:C:141:ALA:HA	4:C:2275:HOH:O	1.99	0.62
1:A:215:ARG:NH2	1:D:54:THR:HG22	2.14	0.62
1:B:268:THR:HG22	1:B:272:GLU:CD	2.23	0.62
1:A:15:ARG:O	1:A:19:GLN:HG3	2.00	0.62
1:A:94:PRO:O	1:A:97:LEU:HD23	2.00	0.62
1:B:36:VAL:HG23	1:B:36:VAL:O	2.00	0.62
1:C:8:ASN:HA	1:C:37:VAL:HG13	1.80	0.62
1:B:171:LEU:HD13	1:B:232:VAL:HG21	1.83	0.61
1:A:171:LEU:HD13	1:A:232:VAL:HG21	1.83	0.61
1:A:300:ASP:OD1	1:C:52:TYR:HB3	2.00	0.61
1:A:36:VAL:HG23	1:A:36:VAL:O	2.00	0.61
1:C:115:THR:HG23	1:C:137:ALA:HA	1.83	0.61
1:A:313:LYS:O	1:A:317:GLN:HG3	2.01	0.60
1:C:37:VAL:HB	1:C:88:VAL:CG2	2.30	0.60
1:B:106:TYR:OH	1:B:351:ALA:HA	2.01	0.60
1:B:12:ARG:O	1:B:16:MET:HG2	2.01	0.60
1:B:108:ILE:HD11	1:B:347:VAL:HG21	1.84	0.60
1:B:183:PHE:CE1	1:B:268:THR:HG21	2.36	0.60
1:C:96:ASP:HA	4:C:2210:HOH:O	2.01	0.60
1:C:19:GLN:HG3	1:C:59:PHE:HE1	1.67	0.60
1:C:148:VAL:HG13	1:C:176:HIS:CD2	2.36	0.60
1:A:107:VAL:CG1	1:A:131:VAL:HG22	2.31	0.60
1:D:47:ALA:HA	1:D:50:MET:CE	2.33	0.59
1:A:147:GLY:H	1:A:150:HIS:HD2	1.51	0.59
1:C:19:GLN:HG3	1:C:59:PHE:CE1	2.37	0.59
1:A:94:PRO:HA	1:A:97:LEU:CD2	2.32	0.59
1:A:186:GLN:O	1:A:242:LYS:HD2	2.01	0.59
1:D:263:THR:HA	1:D:325:ARG:O	2.02	0.59
1:A:254:ASP:O	1:A:255:VAL:HB	2.02	0.59
1:B:194:HIS:HB3	1:B:249:ARG:HD3	1.85	0.59
1:C:309:ILE:N	1:C:309:ILE:HD12	2.18	0.58
1:C:85:ILE:N	1:C:85:ILE:HD12	2.18	0.58
1:C:149:ASN:CG	1:C:235:VAL:HG13	2.28	0.58
1:D:171:LEU:HD22	1:D:175:VAL:HG23	1.84	0.58
1:A:121:GLU:HG3	1:A:160:VAL:HG21	1.85	0.58
1:B:54:THR:HG21	1:C:220:ASN:HD21	1.68	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:194:HIS:NE2	3:C:2166[A]:CYX:H51	2.18	0.58
1:C:339:TYR:O	1:C:343:VAL:HG23	2.04	0.58
1:A:6:GLY:O	1:A:107:VAL:HA	2.04	0.57
1:B:8:ASN:HA	1:B:37:VAL:CG1	2.34	0.57
1:B:124:LEU:HA	1:B:128:ALA:O	2.04	0.57
1:A:99:TRP:HB2	1:A:126:GLY:O	2.04	0.57
1:A:176:HIS:HE1	4:A:545:HOH:O	1.88	0.57
1:C:5:VAL:HA	1:C:106:TYR:O	2.04	0.57
1:B:142:LYS:HB3	1:B:161:VAL:HG12	1.87	0.57
1:A:171:LEU:HD22	1:A:175:VAL:HG23	1.87	0.57
1:C:50:MET:HE1	1:C:78:LEU:HG	1.85	0.57
1:C:130:LYS:HE3	4:C:2289:HOH:O	2.04	0.57
1:B:206:VAL:HG21	4:C:2230:HOH:O	2.04	0.56
1:B:254:ASP:O	1:B:255:VAL:HB	2.05	0.56
1:B:147:GLY:H	1:B:150:HIS:CD2	2.23	0.56
1:D:121:GLU:HA	1:D:124:LEU:HD13	1.87	0.56
1:A:8:ASN:HA	1:A:37:VAL:CG1	2.34	0.56
1:B:64:THR:HG22	1:B:79:VAL:HB	1.87	0.56
1:B:144:LEU:HD22	1:B:150:HIS:HA	1.86	0.56
1:B:149:ASN:O	1:B:152:GLU:HB2	2.06	0.56
1:C:132:VAL:HG21	4:C:2231:HOH:O	2.05	0.56
1:B:124:LEU:HD23	1:B:128:ALA:O	2.05	0.56
1:C:35:ALA:HA	1:C:85:ILE:HG23	1.86	0.56
1:D:167:THR:HG21	1:D:190:MET:HE1	1.86	0.56
1:B:196:TYR:HA	1:B:200:GLN:NE2	2.21	0.56
1:D:85:ILE:HD12	1:D:85:ILE:N	2.21	0.55
1:B:200:GLN:HE21	1:B:249:ARG:NH1	2.03	0.55
1:D:8:ASN:HD22	1:D:37:VAL:CG1	2.20	0.55
1:C:200:GLN:C	1:C:201:LYS:HD2	2.32	0.55
1:D:108:ILE:HD11	1:D:347:VAL:HG21	1.89	0.55
1:D:185:VAL:HG11	1:D:243:LEU:HD11	1.89	0.55
1:B:167:THR:HG22	1:B:190:MET:HE1	1.88	0.55
1:B:239:THR:HA	1:B:242:LYS:HD2	1.89	0.55
1:D:94:PRO:HA	1:D:97:LEU:HD23	1.89	0.55
1:A:13:ILE:HG21	4:A:566:HOH:O	2.06	0.55
1:C:21:LEU:HD11	1:C:31:ILE:CG2	2.35	0.55
1:A:189:LEU:HD13	1:B:328:LYS:HB2	1.89	0.54
1:C:254:ASP:OD1	1:C:336:GLU:HG3	2.08	0.54
1:C:108:ILE:CD1	1:C:347:VAL:HG21	2.36	0.54
1:D:8:ASN:HD22	1:D:37:VAL:HG13	1.72	0.54
1:D:254:ASP:O	1:D:255:VAL:HB	2.07	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:THR:HA	1:A:325:ARG:O	2.07	0.54
1:B:64:THR:CG2	1:B:79:VAL:HB	2.38	0.54
1:C:136:PRO:HG3	4:C:2201:HOH:O	2.07	0.54
1:B:118:ALA:O	1:B:121:GLU:HB2	2.08	0.54
1:C:318:ASN:CG	1:D:246:MET:HB3	2.33	0.54
1:D:65:THR:HG22	1:D:78:LEU:HD12	1.89	0.54
1:A:70:PRO:HD3	4:A:453:HOH:O	2.07	0.54
1:A:193:ILE:HG22	1:B:221:ILE:HD13	1.90	0.54
1:B:190:MET:HG3	1:B:245:GLY:HA3	1.88	0.54
1:C:91:GLN:HG3	1:C:96:ASP:O	2.08	0.54
1:C:200:GLN:NE2	1:C:249:ARG:HH11	2.06	0.54
1:D:193:ILE:HD12	1:D:193:ILE:N	2.23	0.54
1:B:27:LEU:HD11	1:B:83:HIS:HD2	1.72	0.53
1:B:193:ILE:HD12	1:B:193:ILE:N	2.23	0.53
1:B:228:ALA:O	1:B:232:VAL:HG23	2.07	0.53
1:D:302:ILE:O	1:D:303:ASN:HB2	2.07	0.53
1:A:200:GLN:NE2	1:A:249:ARG:HD2	2.22	0.53
1:D:155:PRO:HG3	1:D:353:LYS:HB3	1.91	0.53
1:C:180:LYS:NZ	4:C:2190:HOH:O	2.32	0.52
1:D:94:PRO:HA	1:D:97:LEU:CD2	2.39	0.52
1:A:149:ASN:CG	1:A:235:VAL:HG13	2.35	0.52
1:C:105:GLU:HG3	1:C:106:TYR:N	2.24	0.52
1:C:189:LEU:CD2	1:C:244:THR:HG22	2.38	0.52
1:C:200:GLN:NE2	1:C:249:ARG:NH1	2.57	0.52
1:C:94:PRO:O	1:C:97:LEU:HD23	2.09	0.52
1:C:254:ASP:O	1:C:255:VAL:HB	2.09	0.52
1:B:27:LEU:HD11	1:B:83:HIS:CD2	2.45	0.52
1:D:200:GLN:C	1:D:201:LYS:HD2	2.34	0.52
1:D:305:ASN:C	1:D:305:ASN:HD22	2.16	0.52
1:B:97:LEU:HD11	4:B:1495:HOH:O	2.10	0.52
1:B:190:MET:HG2	1:B:229:ALA:HB2	1.91	0.52
1:C:64:THR:CG2	1:C:79:VAL:HB	2.38	0.52
1:C:302:ILE:O	1:C:303:ASN:HB2	2.10	0.52
1:C:6:GLY:HA3	1:C:99:TRP:HZ3	1.74	0.52
1:A:290:GLY:HA3	1:A:306:ARG:NH1	2.25	0.52
1:B:5:VAL:HG12	1:B:6:GLY:N	2.25	0.52
1:B:263:THR:HA	1:B:325:ARG:O	2.10	0.52
1:C:212:ARG:HG2	1:D:295:GLU:HB3	1.92	0.52
1:D:124:LEU:N	1:D:124:LEU:HD12	2.25	0.52
1:A:172:ALA:HB3	1:A:173:PRO:HD3	1.91	0.51
1:B:98:PRO:O	1:B:102:LEU:HD13	2.09	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:321:PRO:O	1:B:322:LYS:HB2	2.10	0.51
1:A:54:THR:HG21	1:D:220:ASN:HD21	1.74	0.51
1:D:64:THR:HG23	1:D:79:VAL:HB	1.92	0.51
1:A:196:TYR:HA	1:A:200:GLN:NE2	2.26	0.51
1:B:38:ASP:HA	2:B:1362:NAD:H2A	1.91	0.51
1:C:83:HIS:ND1	1:C:84:ARG:N	2.58	0.51
1:B:37:VAL:HG21	4:B:1495:HOH:O	2.10	0.51
1:C:21:LEU:C	1:C:21:LEU:HD23	2.36	0.51
1:C:195:SER:HB3	1:C:252:THR:O	2.10	0.51
1:B:98:PRO:HB2	1:B:102:LEU:HD13	1.92	0.51
1:B:171:LEU:HG	1:B:190:MET:HE2	1.93	0.51
1:C:3:ILE:HG22	1:C:4:LYS:N	2.23	0.51
1:A:16:MET:CG	4:A:540:HOH:O	2.56	0.50
1:B:254:ASP:OD1	1:B:336:GLU:HG3	2.12	0.50
1:B:9:GLY:HA3	1:B:111:THR:HG22	1.93	0.50
1:B:79:VAL:HG12	4:B:1487:HOH:O	2.10	0.50
1:D:194:HIS:HB3	1:D:249:ARG:HD3	1.93	0.50
1:A:218:ALA:HB1	4:A:404:HOH:O	2.11	0.50
1:B:8:ASN:HD22	1:B:37:VAL:HG13	1.75	0.50
1:B:115:THR:HG23	1:B:137:ALA:HA	1.93	0.50
1:D:307:SER:OG	1:D:342:ARG:HD2	2.11	0.50
1:C:61:TYR:HD2	1:C:81:ASN:CB	2.25	0.49
1:D:105:GLU:HG3	1:D:129:ARG:HD3	1.94	0.49
1:A:200:GLN:HE22	1:A:249:ARG:HD2	1.76	0.49
1:B:99:TRP:HA	1:B:99:TRP:CE3	2.47	0.49
1:B:239:THR:HB	1:B:243:LEU:CD1	2.40	0.49
1:B:249:ARG:HH21	3:B:1166[B]:CYX:P7	2.36	0.49
1:C:180:LYS:HA	1:C:180:LYS:HE3	1.94	0.49
1:B:32:ASP:HB2	1:B:83:HIS:CE1	2.48	0.49
1:C:295:GLU:HG3	1:D:211:TRP:HB2	1.95	0.49
1:A:8:ASN:ND2	1:A:37:VAL:HG13	2.24	0.48
1:A:33:VAL:O	1:A:83:HIS:HE1	1.95	0.48
1:A:153:TYR:CE1	1:A:350:MET:HE3	2.48	0.48
1:A:183:PHE:CZ	1:A:272:GLU:HG2	2.47	0.48
1:C:172:ALA:HB3	1:C:173:PRO:HD3	1.95	0.48
1:D:149:ASN:CG	1:D:235:VAL:HG13	2.38	0.48
1:B:200:GLN:NE2	1:B:249:ARG:NH1	2.58	0.48
1:C:94:PRO:HA	1:C:97:LEU:HD23	1.95	0.48
1:A:204:ASP:OD1	1:D:54:THR:HG23	2.13	0.48
1:A:118:ALA:O	1:A:121:GLU:HB2	2.14	0.48
1:C:119:ALA:C	1:C:121:GLU:H	2.21	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:193:ILE:N	1:C:193:ILE:HD12	2.28	0.48
1:C:296:LEU:O	1:D:212:ARG:HD3	2.13	0.48
1:A:118:ALA:HA	1:A:121:GLU:OE2	2.14	0.48
1:B:98:PRO:HB2	1:B:102:LEU:CD1	2.44	0.48
1:A:185:VAL:HG11	1:A:243:LEU:HD11	1.94	0.48
1:A:190:MET:HG2	1:A:229:ALA:HB2	1.95	0.48
1:B:285:MET:HB3	1:B:289:LEU:HB3	1.95	0.48
1:A:5:VAL:HG22	1:A:106:TYR:HB2	1.95	0.47
1:B:266:ARG:NH1	1:B:268:THR:HG23	2.29	0.47
1:C:141:ALA:HB1	1:C:160:VAL:O	2.14	0.47
1:C:8:ASN:ND2	1:C:37:VAL:HG13	2.29	0.47
1:D:12:ARG:O	1:D:16:MET:HG2	2.14	0.47
1:A:54:THR:CG2	1:D:220:ASN:HD21	2.28	0.47
1:A:324:ARG:HD2	4:A:569:HOH:O	2.14	0.47
1:B:350:MET:O	1:B:351:ALA:C	2.56	0.47
1:A:322:LYS:NZ	1:A:322:LYS:HA	2.29	0.47
1:D:169:ASN:O	1:D:307:SER:HB3	2.14	0.47
1:D:195:SER:HB3	1:D:252:THR:O	2.14	0.47
1:D:166:CYS:HB2	1:D:333:TYR:HE2	1.79	0.47
1:A:91:GLN:HG3	1:A:97:LEU:HD13	1.97	0.47
1:B:242:LYS:C	1:B:243:LEU:HD12	2.40	0.47
1:C:109:GLU:HA	1:C:109:GLU:OE2	2.14	0.47
1:A:259:ASP:OD1	1:A:328:LYS:NZ	2.48	0.47
1:B:99:TRP:HA	1:B:99:TRP:HE3	1.79	0.47
1:C:171:LEU:HD22	1:C:175:VAL:HG23	1.97	0.47
1:B:61:TYR:CD1	1:B:61:TYR:N	2.83	0.47
1:C:230:LYS:HD2	4:C:2234:HOH:O	2.15	0.47
1:D:19:GLN:HE21	1:D:19:GLN:HB3	1.60	0.47
1:C:147:GLY:H	1:C:150:HIS:CD2	2.33	0.46
1:A:295:GLU:HG3	1:B:211:TRP:HB2	1.98	0.46
1:B:194:HIS:O	1:B:249:ARG:HA	2.15	0.46
1:B:281:SER:HB2	1:B:289:LEU:O	2.15	0.46
1:B:298:SER:HB2	4:B:1412:HOH:O	2.14	0.46
1:A:226:THR:HG22	1:A:246:MET:HA	1.97	0.46
1:C:113:LEU:N	4:C:2232:HOH:O	2.48	0.46
1:C:36:VAL:HG13	1:C:85:ILE:HG21	1.98	0.46
1:C:38:ASP:CG	1:C:39:MET:H	2.24	0.46
1:D:50:MET:HE3	1:D:63:VAL:HG11	1.96	0.46
1:A:94:PRO:C	1:A:97:LEU:HD23	2.41	0.46
1:B:49:GLN:HA	4:B:1364:HOH:O	2.15	0.46
1:D:242:LYS:O	1:D:243:LEU:HD12	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:94:PRO:HB2	1:B:122:GLY:C	2.41	0.46
1:C:222:ILE:HA	1:C:223:PRO:HD3	1.82	0.46
1:A:183:PHE:CE1	1:A:272:GLU:HG2	2.51	0.46
1:C:266:ARG:HA	1:C:325:ARG:HH21	1.81	0.46
1:A:106:TYR:OH	1:A:351:ALA:HA	2.16	0.46
1:A:12:ARG:HG2	1:A:12:ARG:HH11	1.80	0.46
1:A:266:ARG:HD2	1:A:267:ASP:O	2.16	0.46
1:D:342:ARG:HA	1:D:342:ARG:NE	2.30	0.46
1:D:122:GLY:HA2	1:D:125:ARG:NH1	2.31	0.45
1:B:189:LEU:HD23	1:B:189:LEU:HA	1.82	0.45
1:B:305:ASN:H	1:B:305:ASN:ND2	2.13	0.45
1:A:238:SER:O	1:A:242:LYS:HE2	2.17	0.45
1:C:163:ASN:O	1:C:164:ALA:HB3	2.16	0.45
1:C:268:THR:O	1:C:324:ARG:HG2	2.17	0.45
1:B:328:LYS:NZ	4:B:1386:HOH:O	2.49	0.45
1:B:118:ALA:HA	1:B:121:GLU:CD	2.42	0.45
1:C:151:HIS:C	1:C:153:TYR:H	2.25	0.45
1:B:239:THR:O	1:B:242:LYS:HB2	2.16	0.45
1:D:200:GLN:HE21	1:D:249:ARG:NH1	2.13	0.45
1:A:38:ASP:OD1	1:A:39:MET:N	2.49	0.45
1:A:263:THR:HG23	1:B:326:PHE:CE1	2.52	0.45
1:B:117:LYS:HB2	1:B:141:ALA:HB2	1.99	0.45
1:C:307:SER:OG	1:C:342:ARG:HD2	2.16	0.45
1:A:47:ALA:HA	1:A:50:MET:HE3	1.98	0.44
1:A:99:TRP:HA	1:A:99:TRP:CE3	2.52	0.44
1:B:115:THR:CG2	1:B:137:ALA:HA	2.47	0.44
1:C:105:GLU:CG	1:C:106:TYR:H	2.29	0.44
1:D:124:LEU:HA	1:D:128:ALA:O	2.16	0.44
1:A:204:ASP:CG	1:D:54:THR:HG23	2.43	0.44
1:B:51:ARG:HG3	4:B:1409:HOH:O	2.16	0.44
1:D:200:GLN:HB3	4:D:3171:HOH:O	2.17	0.44
1:C:50:MET:O	1:C:59:PHE:HB2	2.17	0.44
1:B:309:ILE:HD12	1:B:309:ILE:N	2.33	0.44
1:D:40:ASN:OD1	1:D:42:ASP:HB3	2.17	0.44
1:A:85:ILE:HD12	1:A:85:ILE:N	2.32	0.44
1:B:13:ILE:HG12	2:B:1362:NAD:O2N	2.17	0.44
1:B:34:VAL:HG11	1:B:102:LEU:HB3	1.99	0.44
1:D:37:VAL:CG2	1:D:90:ALA:HA	2.48	0.44
1:B:12:ARG:HH11	1:B:12:ARG:HG3	1.82	0.44
1:B:25:GLY:HA2	4:B:1464:HOH:O	2.17	0.44
1:B:196:TYR:HA	1:B:200:GLN:HE22	1.80	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:8:ASN:HD22	1:C:37:VAL:HG13	1.82	0.44
1:C:10:PHE:CE2	1:C:15:ARG:HG2	2.52	0.44
1:C:134:SER:O	1:C:135:ALA:HB2	2.18	0.44
1:B:117:LYS:HD2	1:B:140:GLY:C	2.43	0.44
1:C:227:GLY:O	1:C:228:ALA:C	2.61	0.44
1:A:246:MET:HG2	1:B:328:LYS:HE2	1.99	0.44
1:B:54:THR:CG2	1:C:220:ASN:HD21	2.30	0.44
1:B:80:VAL:C	1:B:82:GLY:N	2.76	0.44
1:A:180:LYS:HE3	1:A:284:TYR:CE2	2.53	0.43
1:A:353:LYS:HE2	4:A:544:HOH:O	2.18	0.43
1:B:200:GLN:HB3	4:B:1375:HOH:O	2.18	0.43
1:D:2:PRO:HG3	1:D:29:THR:O	2.17	0.43
1:D:254:ASP:O	1:D:255:VAL:CB	2.67	0.43
1:C:135:ALA:O	1:C:136:PRO:C	2.60	0.43
1:D:95:ALA:HA	1:D:122:GLY:O	2.19	0.43
1:D:107:VAL:HG11	1:D:123:HIS:HB3	2.01	0.43
1:C:43:ALA:HB2	1:C:76:ASP:HA	2.01	0.43
1:A:36:VAL:O	1:A:36:VAL:CG2	2.66	0.43
1:B:10:PHE:CE2	1:B:15:ARG:HG2	2.53	0.43
1:B:259:ASP:OD1	1:B:328:LYS:HE3	2.18	0.43
1:B:290:GLY:O	1:B:309:ILE:HA	2.18	0.43
1:B:44:GLU:H	1:B:44:GLU:CD	2.25	0.43
1:B:212:ARG:HB3	1:B:222:ILE:HG23	2.00	0.43
1:B:342:ARG:HA	1:B:342:ARG:NE	2.34	0.43
1:C:81:ASN:CG	1:C:81:ASN:O	2.61	0.43
1:A:270:ILE:HD11	1:A:315:THR:CG2	2.49	0.43
1:B:108:ILE:CD1	1:B:347:VAL:HG21	2.48	0.43
1:A:254:ASP:O	1:A:255:VAL:CB	2.67	0.42
1:B:30:GLU:O	1:B:31:ILE:HG13	2.18	0.42
1:C:19:GLN:NE2	4:C:2240:HOH:O	2.51	0.42
1:D:268:THR:HB	1:D:269:SER:H	1.65	0.42
1:A:180:LYS:HE2	4:A:545:HOH:O	2.18	0.42
1:A:99:TRP:HA	1:A:99:TRP:HE3	1.84	0.42
1:B:180:LYS:HD3	1:B:284:TYR:CE2	2.54	0.42
1:C:77:THR:HG23	1:C:85:ILE:O	2.19	0.42
1:C:170:CYS:HA	1:C:308:SER:HB2	2.02	0.42
1:A:136:PRO:CG	1:A:165:SER:HB3	2.49	0.42
1:B:183:PHE:HD1	1:B:268:THR:HG21	1.76	0.42
1:D:193:ILE:HD12	1:D:193:ILE:H	1.82	0.42
1:C:61:TYR:CD2	1:C:81:ASN:HB2	2.45	0.42
1:C:171:LEU:HD13	1:C:232:VAL:HG21	2.01	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:149:ASN:HA	4:D:3197:HOH:O	2.19	0.42
1:A:181:GLU:OE2	1:A:279:ARG:NH2	2.52	0.42
1:B:256:SER:HB2	1:B:333:TYR:CZ	2.54	0.42
1:C:349:HIS:C	1:C:351:ALA:H	2.28	0.42
1:B:54:THR:HG23	1:C:204:ASP:OD2	2.20	0.42
1:A:55:VAL:HG13	1:A:56:HIS:CD2	2.55	0.42
1:A:180:LYS:NZ	4:A:462:HOH:O	2.52	0.42
1:B:98:PRO:O	1:B:99:TRP:C	2.62	0.42
1:B:186:GLN:HG3	1:B:264:ALA:O	2.19	0.42
1:B:305:ASN:N	1:B:305:ASN:HD22	2.18	0.42
1:C:45:TYR:O	1:C:49:GLN:HG3	2.19	0.42
1:C:298:SER:HB3	1:D:221:ILE:HB	2.02	0.42
1:D:93:ASN:HA	1:D:94:PRO:HD3	1.93	0.42
1:D:314:ALA:O	1:D:318:ASN:ND2	2.52	0.42
1:B:9:GLY:CA	1:B:111:THR:HG22	2.48	0.42
1:D:172:ALA:HB3	1:D:173:PRO:HD3	2.01	0.42
1:D:328:LYS:NZ	4:D:3225:HOH:O	2.53	0.42
1:B:94:PRO:HB3	1:B:123:HIS:CG	2.55	0.41
1:B:169:ASN:O	1:B:307:SER:HB3	2.20	0.41
1:C:50:MET:HB3	4:C:2276:HOH:O	2.19	0.41
1:C:208:VAL:HG13	4:C:2283:HOH:O	2.18	0.41
1:D:285:MET:HB3	1:D:289:LEU:HB3	2.02	0.41
1:C:194:HIS:O	1:C:249:ARG:HA	2.20	0.41
1:D:70:PRO:C	1:D:72:VAL:H	2.28	0.41
1:A:97:LEU:C	1:A:99:TRP:H	2.27	0.41
1:A:196:TYR:HA	1:A:200:GLN:HE22	1.85	0.41
1:B:171:LEU:HD22	1:B:175:VAL:CG2	2.49	0.41
1:B:348:ARG:HD2	4:B:1461:HOH:O	2.19	0.41
1:C:113:LEU:O	1:C:113:LEU:HG	2.20	0.41
1:C:343:VAL:O	1:C:347:VAL:HG23	2.20	0.41
1:A:200:GLN:HB3	4:A:366:HOH:O	2.20	0.41
1:A:204:ASP:OD1	1:D:54:THR:CG2	2.69	0.41
1:D:177:VAL:HG11	1:D:277:LEU:HD23	2.03	0.41
1:A:74:LYS:HE2	4:A:489:HOH:O	2.20	0.41
1:B:154:ASN:HB3	1:B:157:GLU:HB3	2.02	0.41
1:A:94:PRO:CA	1:A:97:LEU:HD23	2.45	0.41
1:A:136:PRO:HG3	1:A:165:SER:HB3	2.03	0.41
1:C:295:GLU:HB3	1:D:212:ARG:HG2	2.02	0.41
1:B:146:MET:HB2	1:B:342:ARG:HD3	2.02	0.41
1:C:112:GLY:N	4:C:2232:HOH:O	2.54	0.41
1:C:256:SER:HB2	1:C:333:TYR:CZ	2.55	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:97:LEU:HD22	1:A:97:LEU:N	2.36	0.41
1:C:169:ASN:O	1:C:307:SER:HB3	2.21	0.41
1:D:163:ASN:O	1:D:164:ALA:HB3	2.21	0.41
1:C:186:GLN:HB2	1:C:263:THR:OG1	2.21	0.40
1:A:204:ASP:OD2	1:D:54:THR:HG23	2.21	0.40
1:B:163:ASN:O	1:B:164:ALA:HB3	2.20	0.40
1:B:190:MET:HG3	1:B:190:MET:O	2.21	0.40
1:D:124:LEU:HD12	1:D:124:LEU:H	1.84	0.40
1:D:235:VAL:C	1:D:237:PRO:HD3	2.47	0.40
1:A:37:VAL:CG2	1:A:90:ALA:HA	2.51	0.40
1:C:142:LYS:HG2	1:C:158:HIS:CE1	2.56	0.40
1:D:10:PHE:CZ	1:D:15:ARG:HG3	2.56	0.40
1:A:121:GLU:CG	1:A:160:VAL:HG21	2.48	0.40
1:B:305:ASN:ND2	1:B:305:ASN:N	2.68	0.40
1:D:11:GLY:HA3	2:D:1361:NAD:O5B	2.22	0.40
1:A:181:GLU:CD	1:A:279:ARG:HH21	2.28	0.40
1:B:94:PRO:CA	1:B:97:LEU:HD23	2.39	0.40
1:C:94:PRO:C	1:C:97:LEU:HD23	2.47	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	357/359 (99%)	331 (93%)	23 (6%)	3 (1%)	16	31
1	B	358/359 (100%)	323 (90%)	28 (8%)	7 (2%)	6	10
1	C	358/359 (100%)	306 (86%)	45 (13%)	7 (2%)	6	10
1	D	357/359 (99%)	331 (93%)	24 (7%)	2 (1%)	21	38
All	All	1430/1436 (100%)	1291 (90%)	120 (8%)	19 (1%)	9	18

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	73	ALA
1	C	73	ALA
1	A	73	ALA
1	A	255	VAL
1	B	42	ASP
1	B	157	GLU
1	B	255	VAL
1	C	3	ILE
1	C	39	MET
1	C	157	GLU
1	D	255	VAL
1	B	335	ASN
1	C	255	VAL
1	B	210	ASP
1	C	164	ALA
1	C	76	ASP
1	D	237	PRO
1	A	98	PRO
1	B	251	PRO

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	296/296 (100%)	285 (96%)	11 (4%)	30	57
1	B	297/296 (100%)	287 (97%)	10 (3%)	32	60
1	C	297/296 (100%)	290 (98%)	7 (2%)	43	70
1	D	296/296 (100%)	282 (95%)	14 (5%)	23	47
All	All	1186/1184 (100%)	1144 (96%)	42 (4%)	32	58

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	ARG
1	A	23	GLU
1	A	30	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	37	VAL
1	A	55	VAL
1	A	102	LEU
1	A	107	VAL
1	A	171	LEU
1	A	190	MET
1	A	240	GLN
1	A	322	LYS
1	B	13	ILE
1	B	16	MET
1	B	55	VAL
1	B	105	GLU
1	B	166[A]	CYS
1	B	166[B]	CYS
1	B	171	LEU
1	B	190	MET
1	B	268	THR
1	B	305	ASN
1	C	166[A]	CYS
1	C	166[B]	CYS
1	C	171	LEU
1	C	180	LYS
1	C	190	MET
1	C	238	SER
1	C	305	ASN
1	D	19	GLN
1	D	37	VAL
1	D	54	THR
1	D	55	VAL
1	D	66	THR
1	D	78	LEU
1	D	97	LEU
1	D	107	VAL
1	D	113	LEU
1	D	166	CYS
1	D	171	LEU
1	D	190	MET
1	D	305	ASN
1	D	355	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (33) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	8	ASN
1	A	19	GLN
1	A	150	HIS
1	A	151	HIS
1	A	159	HIS
1	A	176	HIS
1	A	200	GLN
1	B	8	ASN
1	B	19	GLN
1	B	49	GLN
1	B	83	HIS
1	B	150	HIS
1	B	176	HIS
1	B	200	GLN
1	B	305	ASN
1	C	8	ASN
1	C	19	GLN
1	C	49	GLN
1	C	150	HIS
1	C	151	HIS
1	C	159	HIS
1	C	176	HIS
1	C	200	GLN
1	C	305	ASN
1	C	349	HIS
1	D	8	ASN
1	D	19	GLN
1	D	81	ASN
1	D	150	HIS
1	D	176	HIS
1	D	200	GLN
1	D	305	ASN
1	D	341	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

8 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$
3	CYX	C	2166[A]	1	9,9,9	2.84	5 (55%)	9,12,12	0.89	0
2	NAD	C	1360	-	46,48,48	1.61	7 (15%)	64,73,73	1.61	8 (12%)
3	CYX	B	1166[B]	1	9,9,9	2.87	5 (55%)	9,12,12	0.88	0
2	NAD	B	1362	-	46,48,48	1.77	10 (21%)	64,73,73	1.64	8 (12%)
3	CYX	B	1166[A]	1	9,9,9	2.92	5 (55%)	9,12,12	0.92	0
2	NAD	D	1361	-	46,48,48	1.72	6 (13%)	64,73,73	1.59	8 (12%)
3	CYX	D	3166	1	9,9,9	2.93	5 (55%)	9,12,12	0.76	0
3	CYX	C	2166[B]	1	9,9,9	2.80	5 (55%)	9,12,12	0.91	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	CYX	C	2166[A]	1	-	2/8/8/8	-
2	NAD	C	1360	-	-	13/30/62/62	0/5/5/5
3	CYX	B	1166[B]	1	-	3/8/8/8	-
2	NAD	B	1362	-	-	17/30/62/62	0/5/5/5
3	CYX	B	1166[A]	1	-	6/8/8/8	-
2	NAD	D	1361	-	-	7/30/62/62	0/5/5/5
3	CYX	D	3166	1	-	7/8/8/8	-
3	CYX	C	2166[B]	1	-	2/8/8/8	-

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	3166	CYX	P7-O10	5.69	1.61	1.50
3	C	2166[A]	CYX	P7-O10	5.52	1.61	1.50
3	B	1166[A]	CYX	P7-O10	5.47	1.61	1.50
2	D	1361	NAD	C3N-C7N	5.40	1.58	1.50
3	C	2166[B]	CYX	P7-O10	5.32	1.61	1.50
3	B	1166[B]	CYX	P7-O10	5.22	1.60	1.50
2	B	1362	NAD	C3N-C7N	4.91	1.57	1.50
2	D	1361	NAD	C2N-N1N	4.87	1.40	1.35
2	C	1360	NAD	C3N-C7N	4.83	1.57	1.50
2	C	1360	NAD	C2N-N1N	4.69	1.40	1.35
2	B	1362	NAD	C6N-N1N	4.33	1.45	1.35
2	B	1362	NAD	C2N-N1N	4.28	1.39	1.35
2	D	1361	NAD	PA-O3	3.95	1.63	1.59
2	C	1360	NAD	C6N-N1N	3.94	1.44	1.35
2	D	1361	NAD	C6N-N1N	3.90	1.44	1.35
2	D	1361	NAD	C4N-C3N	3.72	1.45	1.39
3	B	1166[B]	CYX	P7-C6	-3.71	1.75	1.78
3	B	1166[A]	CYX	C1-C2	3.62	1.55	1.46
3	C	2166[B]	CYX	P7-C6	-3.55	1.75	1.78
3	B	1166[A]	CYX	P7-C6	-3.51	1.75	1.78
2	B	1362	NAD	PA-O3	3.39	1.63	1.59
3	D	3166	CYX	C1-C2	3.31	1.54	1.46
2	C	1360	NAD	C4N-C3N	3.25	1.44	1.39
3	C	2166[A]	CYX	P7-C6	-3.24	1.75	1.78
3	B	1166[B]	CYX	C1-C2	3.24	1.54	1.46
2	B	1362	NAD	C4N-C3N	3.11	1.44	1.39
3	C	2166[A]	CYX	C1-C2	3.11	1.54	1.46
3	C	2166[B]	CYX	C1-C2	3.02	1.54	1.46
3	D	3166	CYX	P7-O8	2.99	1.61	1.55
3	B	1166[B]	CYX	P7-O9	2.97	1.61	1.55
3	D	3166	CYX	P7-C6	-2.97	1.75	1.78
3	C	2166[A]	CYX	P7-O9	2.94	1.61	1.55
3	B	1166[B]	CYX	P7-O8	2.90	1.61	1.55
3	C	2166[B]	CYX	P7-O9	2.86	1.61	1.55
3	C	2166[A]	CYX	P7-O8	2.86	1.61	1.55
3	D	3166	CYX	P7-O9	2.84	1.61	1.55
3	B	1166[A]	CYX	P7-O9	2.74	1.61	1.55
2	B	1362	NAD	PN-O3	-2.74	1.56	1.59
3	B	1166[A]	CYX	P7-O8	2.66	1.60	1.55
3	C	2166[B]	CYX	P7-O8	2.59	1.60	1.55
2	B	1362	NAD	C2A-N1A	2.58	1.38	1.33
2	C	1360	NAD	C2A-N1A	2.43	1.38	1.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1361	NAD	C2A-N1A	2.42	1.38	1.33
2	C	1360	NAD	PA-O3	2.28	1.62	1.59
2	B	1362	NAD	PN-O2N	-2.10	1.45	1.55
2	B	1362	NAD	PA-O2A	-2.09	1.45	1.55
2	B	1362	NAD	O4B-C1B	2.03	1.46	1.42
2	C	1360	NAD	PA-O2A	-2.02	1.46	1.55

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1362	NAD	C5N-C4N-C3N	-6.14	114.33	120.36
2	C	1360	NAD	C5N-C4N-C3N	-5.99	114.47	120.36
2	D	1361	NAD	C5N-C4N-C3N	-5.99	114.48	120.36
2	B	1362	NAD	C6N-C5N-C4N	5.40	127.23	119.45
2	C	1360	NAD	C6N-C5N-C4N	5.36	127.18	119.45
2	D	1361	NAD	C6N-C5N-C4N	5.32	127.11	119.45
2	C	1360	NAD	C5N-C6N-N1N	-4.87	113.74	120.38
2	B	1362	NAD	C5N-C6N-N1N	-4.82	113.80	120.38
2	D	1361	NAD	C5N-C6N-N1N	-4.60	114.10	120.38
2	B	1362	NAD	C4N-C3N-C7N	-3.76	110.83	121.06
2	D	1361	NAD	C4N-C3N-C7N	-3.70	110.99	121.06
2	C	1360	NAD	C4N-C3N-C7N	-3.67	111.05	121.06
2	B	1362	NAD	C2N-C3N-C4N	3.44	122.26	118.26
2	C	1360	NAD	C2N-C3N-C4N	3.24	122.02	118.26
2	D	1361	NAD	C2N-C3N-C4N	3.22	122.00	118.26
2	B	1362	NAD	O2N-PN-O3	3.06	115.55	107.27
2	C	1360	NAD	O4B-C1B-C2B	-2.98	100.24	106.62
2	D	1361	NAD	O4B-C1B-C2B	-2.87	100.47	106.62
2	D	1361	NAD	C2N-C3N-C7N	2.61	127.00	119.46
2	B	1362	NAD	C2N-C3N-C7N	2.58	126.91	119.46
2	C	1360	NAD	C2N-C3N-C7N	2.57	126.89	119.46
2	D	1361	NAD	O4B-C1B-N9A	-2.13	104.00	108.09
2	C	1360	NAD	O4B-C1B-N9A	-2.13	104.00	108.09
2	B	1362	NAD	O3-PA-O1A	-2.10	104.40	110.70

There are no chirality outliers.

All (57) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	1362	NAD	C5B-O5B-PA-O1A
2	B	1362	NAD	O4D-C4D-C5D-O5D
2	B	1362	NAD	O4D-C1D-N1N-C2N

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	B	1362	NAD	O4D-C1D-N1N-C6N
2	C	1360	NAD	O4D-C1D-N1N-C2N
2	C	1360	NAD	O4D-C1D-N1N-C6N
2	C	1360	NAD	C2D-C1D-N1N-C2N
2	C	1360	NAD	C2D-C1D-N1N-C6N
2	D	1361	NAD	O4D-C1D-N1N-C2N
2	D	1361	NAD	O4D-C1D-N1N-C6N
2	D	1361	NAD	C2D-C1D-N1N-C2N
2	D	1361	NAD	C2D-C1D-N1N-C6N
3	B	1166[A]	CYX	O3-C1-C2-C4
3	B	1166[A]	CYX	O3-C1-C2-C5
3	B	1166[A]	CYX	C5-C6-P7-O9
3	B	1166[A]	CYX	C5-C6-P7-O10
3	B	1166[B]	CYX	O3-C1-C2-C4
3	B	1166[B]	CYX	O3-C1-C2-C5
3	B	1166[B]	CYX	C1-C2-C5-C6
3	C	2166[A]	CYX	O3-C1-C2-C4
3	C	2166[A]	CYX	O3-C1-C2-C5
3	C	2166[B]	CYX	O3-C1-C2-C4
3	C	2166[B]	CYX	O3-C1-C2-C5
3	D	3166	CYX	O3-C1-C2-C4
3	D	3166	CYX	O3-C1-C2-C5
3	D	3166	CYX	C5-C6-P7-O8
3	D	3166	CYX	C5-C6-P7-O9
3	D	3166	CYX	C5-C6-P7-O10
2	B	1362	NAD	C3D-C4D-C5D-O5D
2	C	1360	NAD	C2N-C3N-C7N-O7N
2	B	1362	NAD	O4B-C4B-C5B-O5B
2	C	1360	NAD	C4N-C3N-C7N-N7N
2	C	1360	NAD	C4N-C3N-C7N-O7N
2	C	1360	NAD	C2N-C3N-C7N-N7N
2	B	1362	NAD	C3B-C4B-C5B-O5B
3	B	1166[A]	CYX	C5-C6-P7-O8
3	D	3166	CYX	C2-C5-C6-P7
2	C	1360	NAD	C2B-C1B-N9A-C8A
2	B	1362	NAD	C4N-C3N-C7N-O7N
2	D	1361	NAD	C2B-C1B-N9A-C8A
2	B	1362	NAD	PA-O3-PN-O2N
3	D	3166	CYX	C1-C2-C5-C6
2	B	1362	NAD	C4N-C3N-C7N-N7N
2	B	1362	NAD	C5B-O5B-PA-O2A
2	B	1362	NAD	C5B-O5B-PA-O3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	B	1362	NAD	C5D-O5D-PN-O1N
2	C	1360	NAD	C2B-C1B-N9A-C4A
2	B	1362	NAD	C2D-C1D-N1N-C6N
2	D	1361	NAD	C2B-C1B-N9A-C4A
2	B	1362	NAD	C2N-C3N-C7N-O7N
2	B	1362	NAD	C2N-C3N-C7N-N7N
2	C	1360	NAD	O4B-C1B-N9A-C8A
2	B	1362	NAD	PA-O3-PN-O1N
2	D	1361	NAD	O4B-C4B-C5B-O5B
3	B	1166[A]	CYX	C1-C2-C5-C6
2	C	1360	NAD	O4B-C4B-C5B-O5B
2	C	1360	NAD	C4B-C5B-O5B-PA

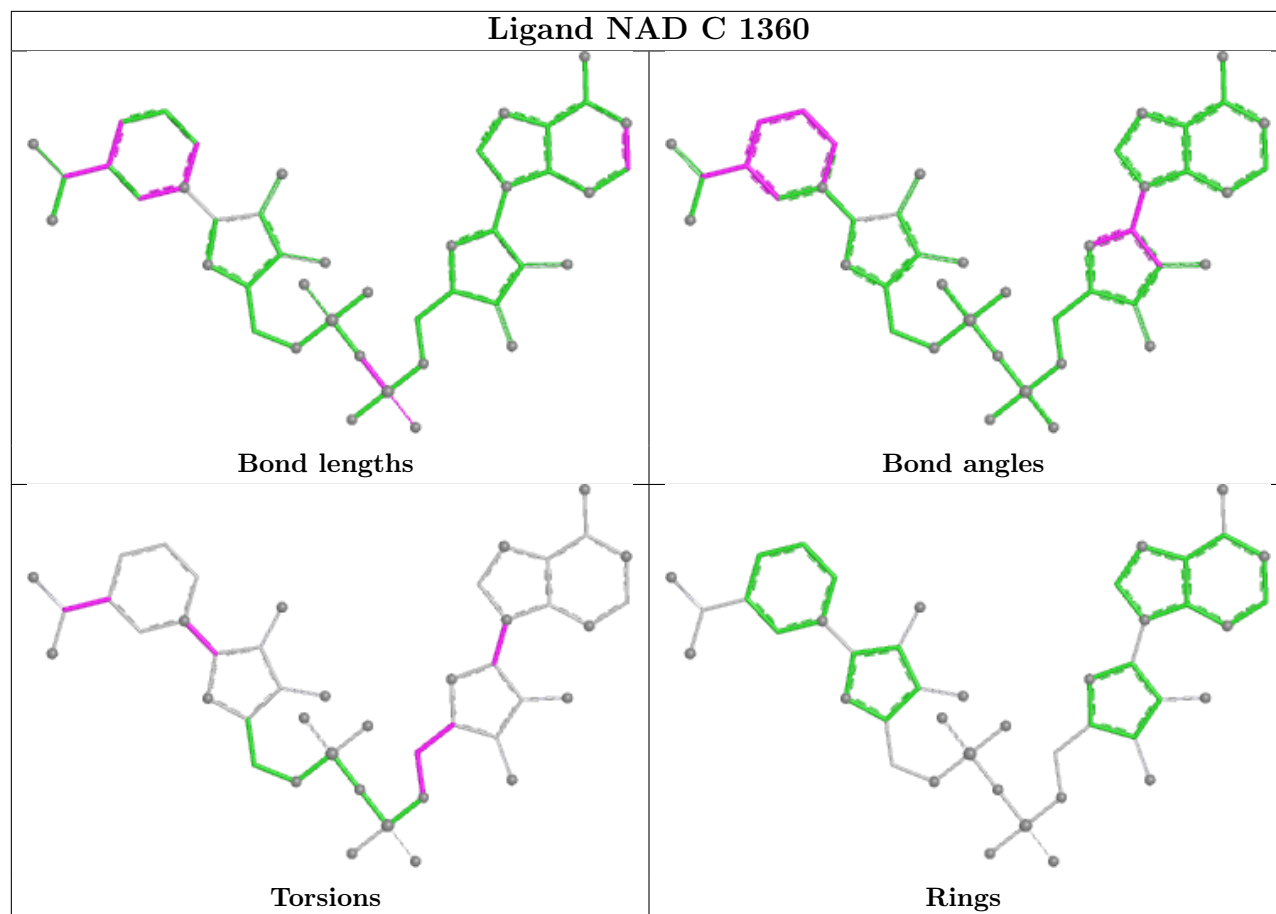
There are no ring outliers.

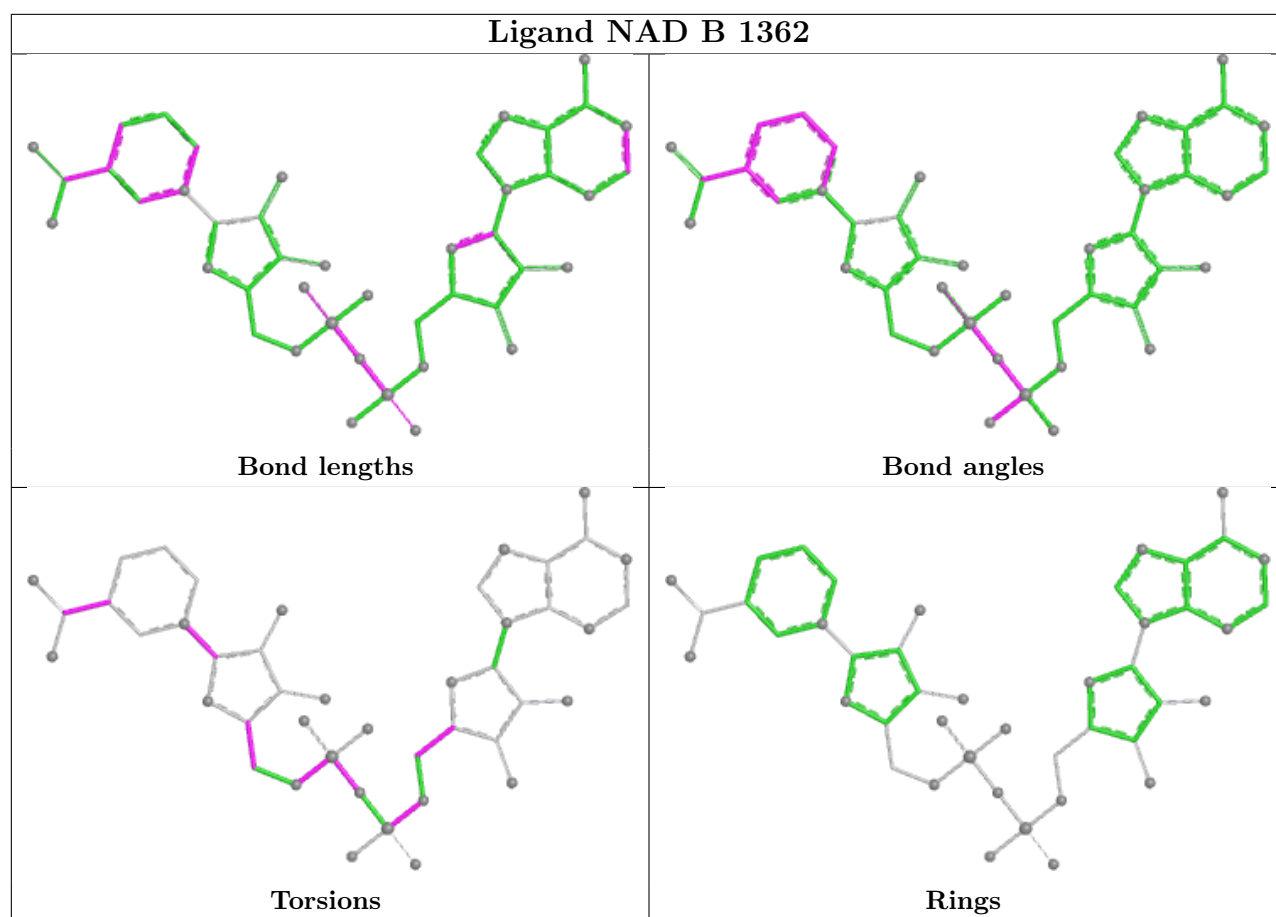
4 monomers are involved in 8 short contacts:

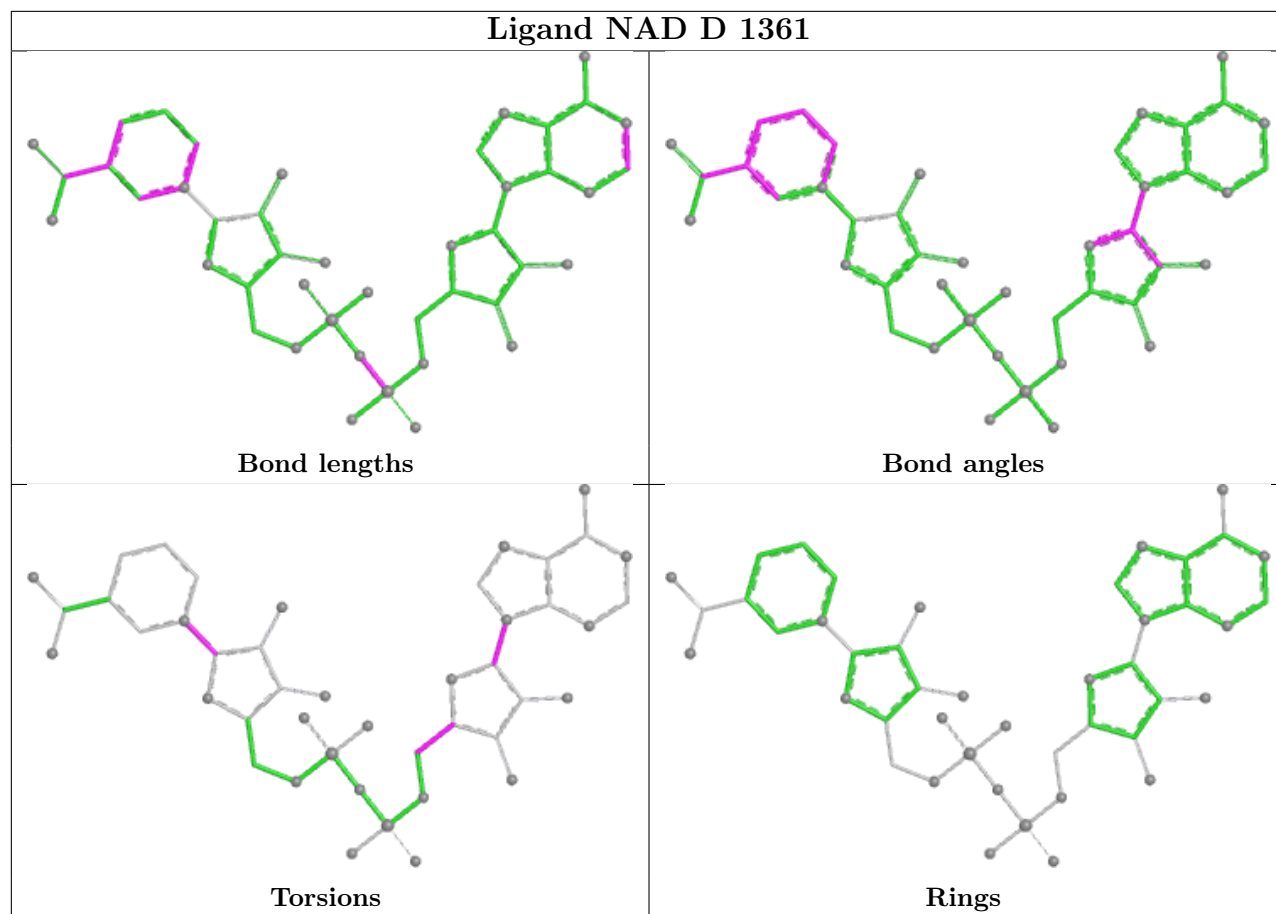
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2166[A]	CYX	1	0
3	B	1166[B]	CYX	2	0
2	B	1362	NAD	3	0
2	D	1361	NAD	2	0

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

Ligand NAD C 1360







5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	359/359 (100%)	-0.35	1 (0%) 90 87	6, 23, 43, 67	6 (1%)
1	B	359/359 (100%)	-0.10	7 (1%) 66 62	5, 25, 63, 84	18 (5%)
1	C	359/359 (100%)	0.39	31 (8%) 16 14	11, 34, 81, 101	32 (8%)
1	D	359/359 (100%)	-0.42	2 (0%) 85 83	9, 22, 40, 58	5 (1%)
All	All	1436/1436 (100%)	-0.12	41 (2%) 53 49	5, 25, 63, 101	61 (4%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	120	ALA	5.6
1	C	99	TRP	3.8
1	C	3	ILE	3.6
1	C	38	ASP	3.1
1	C	104	VAL	3.1
1	C	126	GLY	3.1
1	C	97	LEU	3.0
1	C	125	ARG	3.0
1	C	93	ASN	2.9
1	C	5	VAL	2.9
1	C	124	LEU	2.8
1	C	114	PHE	2.8
1	C	95	ALA	2.7
1	B	61	TYR	2.7
1	C	90	ALA	2.6
1	C	4	LYS	2.6
1	C	72	VAL	2.6
1	C	71	SER	2.6
1	B	118	ALA	2.6
1	C	121	GLU	2.5
1	C	2	PRO	2.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	107	VAL	2.4
1	B	96	ASP	2.4
1	A	73	ALA	2.3
1	D	359	LEU	2.3
1	B	357	ALA	2.2
1	C	7	ILE	2.2
1	C	118	ALA	2.2
1	C	9	GLY	2.2
1	C	116	ALA	2.2
1	B	126	GLY	2.2
1	D	1	MET	2.1
1	C	41	THR	2.1
1	C	70	PRO	2.1
1	B	83	HIS	2.1
1	C	357	ALA	2.1
1	B	93	ASN	2.1
1	C	122	GLY	2.1
1	C	102	LEU	2.0
1	C	353	LYS	2.0
1	C	115	THR	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 [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
3	CYX	C	2166[A]	10/10	0.63	0.23	42,45,48,48	10
3	CYX	C	2166[B]	10/10	0.63	0.23	35,38,40,41	10
2	NAD	B	1362	44/44	0.74	0.21	30,49,56,56	43

Continued on next page...

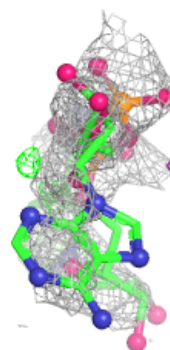
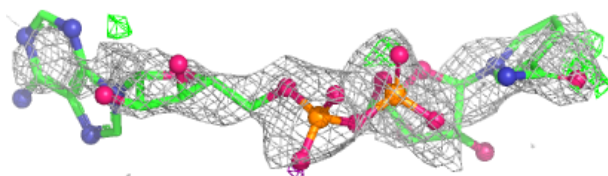
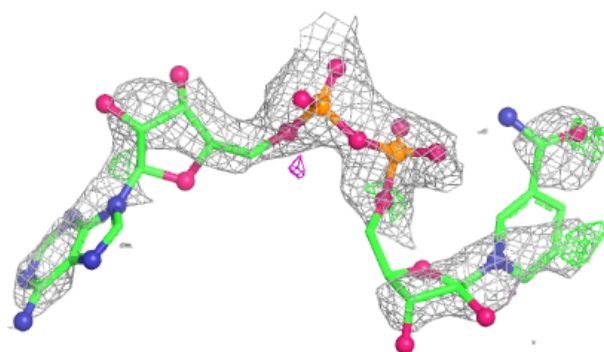
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	CYX	B	1166[A]	10/10	0.79	0.20	30,32,36,38	10
3	CYX	B	1166[B]	10/10	0.79	0.20	43,48,54,54	10
3	CYX	D	3166	10/10	0.80	0.21	39,44,50,51	0
2	NAD	C	1360	44/44	0.84	0.15	22,28,31,33	44
2	NAD	D	1361	44/44	0.97	0.06	22,26,29,30	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.

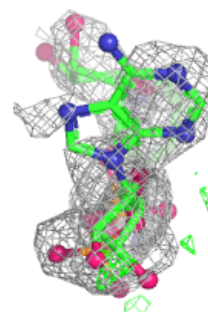
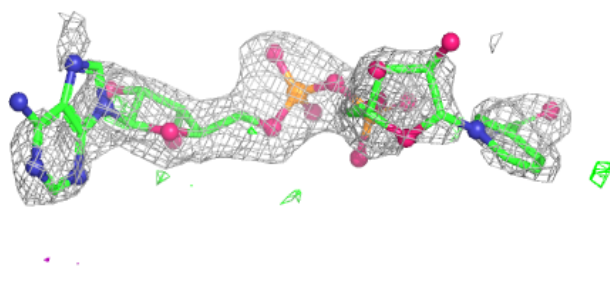
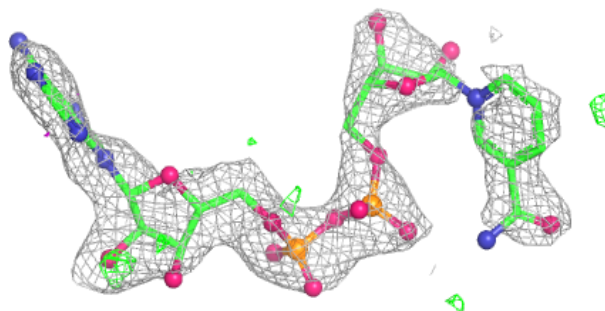
Electron density around NAD B 1362:

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

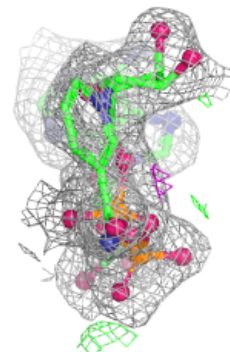
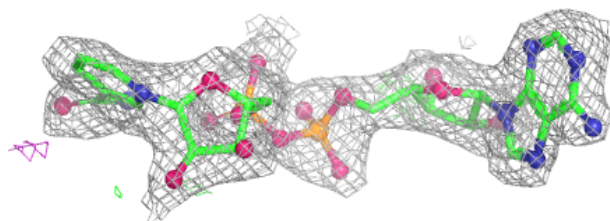
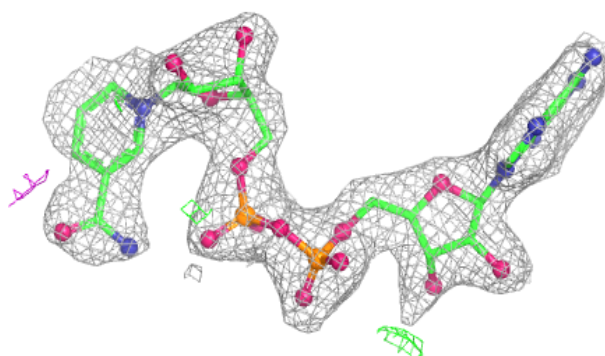


Electron density around NAD C 1360:

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

**Electron density around NAD D 1361:**

$2mF_o-DF_c$ (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.