



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 12:39 AM UTC

PDB ID : 1I33 / pdb_00001i33
Title : LEISHMANIA MEXICANA GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE IN COMPLEX WITH INHIBITORS
Authors : Suresh, S.; Bressi, J.C.; Kennedy, K.J.; Verlinde, C.L.M.J.; Gelb, M.H.; Hol, W.G.J.
Deposited on : 2001-02-12
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

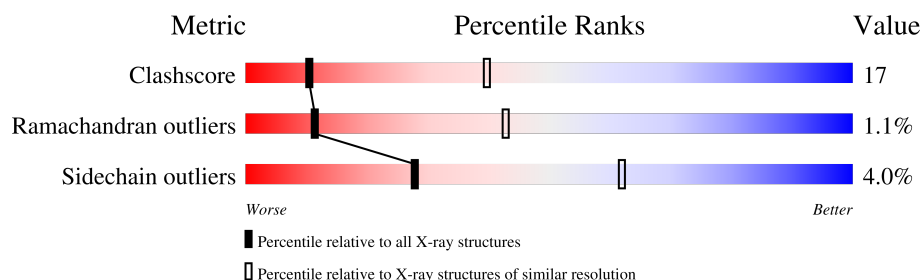
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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))
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	360	67% 29% ..
1	B	360	68% 27% ..
1	C	360	69% 27% ..
1	D	360	67% 29% ..
1	E	360	68% 27% ..
1	F	360	62% 34% ..

2 Entry composition [i](#)

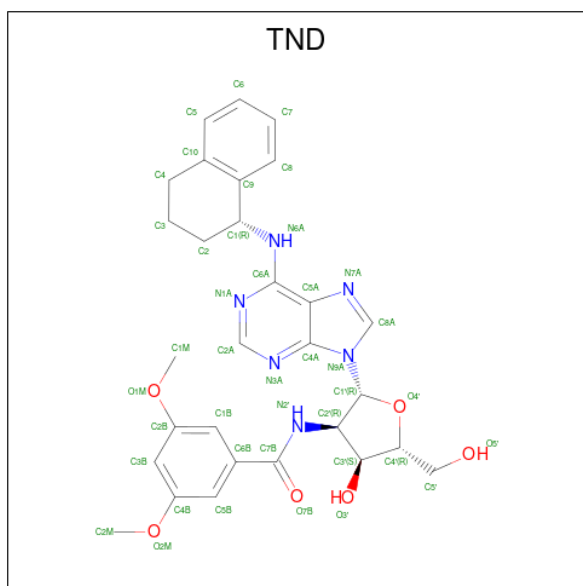
There are 2 unique types of molecules in this entry. The entry contains 16536 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	B	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	C	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	D	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	E	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			
1	F	358	Total	C	N	O	S	0	0	0
			2715	1712	474	516	13			

- Molecule 2 is N-1,2,3,4-TETRAHYDRONAPHTH-1-YL-2'-[3,5-DIMETHOXYBENZAMID O]-2'-DEOXY-ADENOSINE (CCD ID: TND) (formula: $C_{29}H_{32}N_6O_6$).



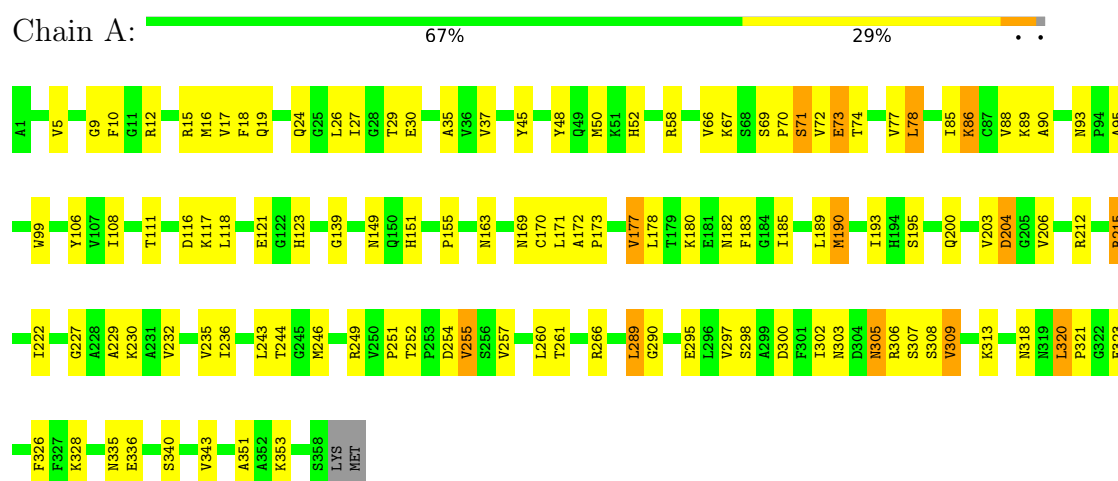
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 41	C 29	N 6	O 6	0	0
2	B	1	Total 41	C 29	N 6	O 6	0	0
2	C	1	Total 41	C 29	N 6	O 6	0	0
2	D	1	Total 41	C 29	N 6	O 6	0	0
2	E	1	Total 41	C 29	N 6	O 6	0	0
2	F	1	Total 41	C 29	N 6	O 6	0	0

3 Residue-property plots

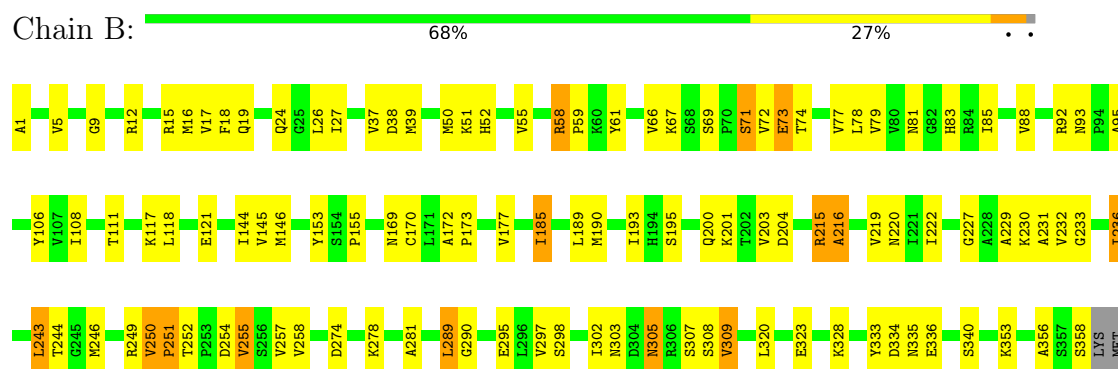
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

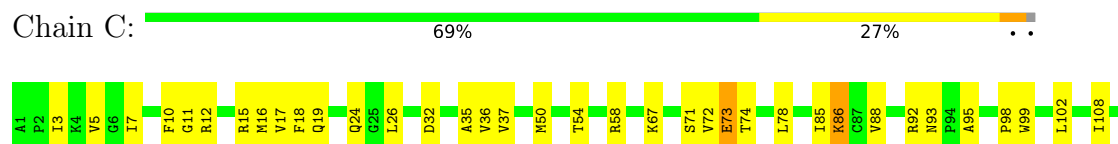
• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

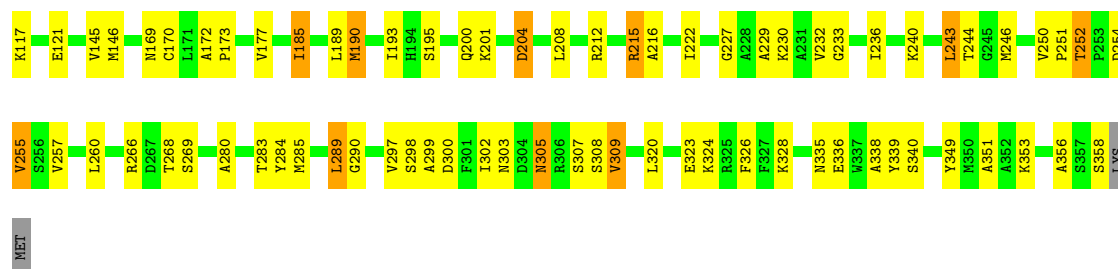


• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE



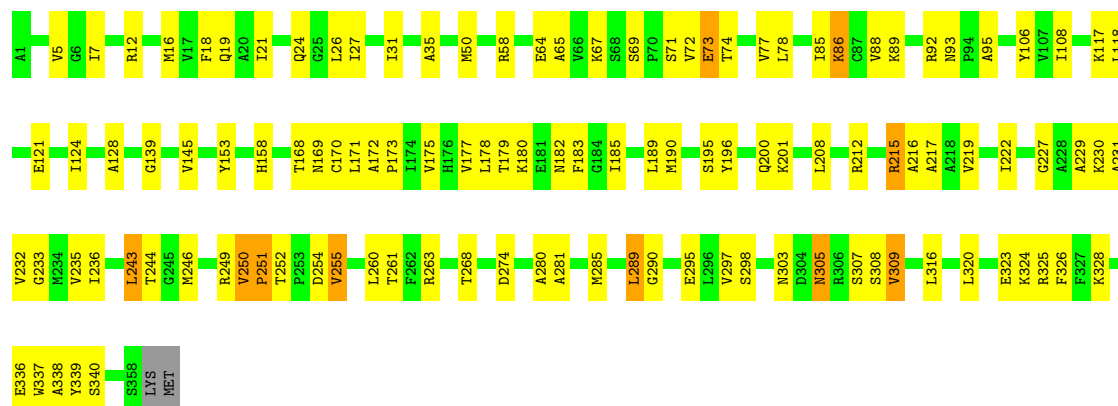
• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE





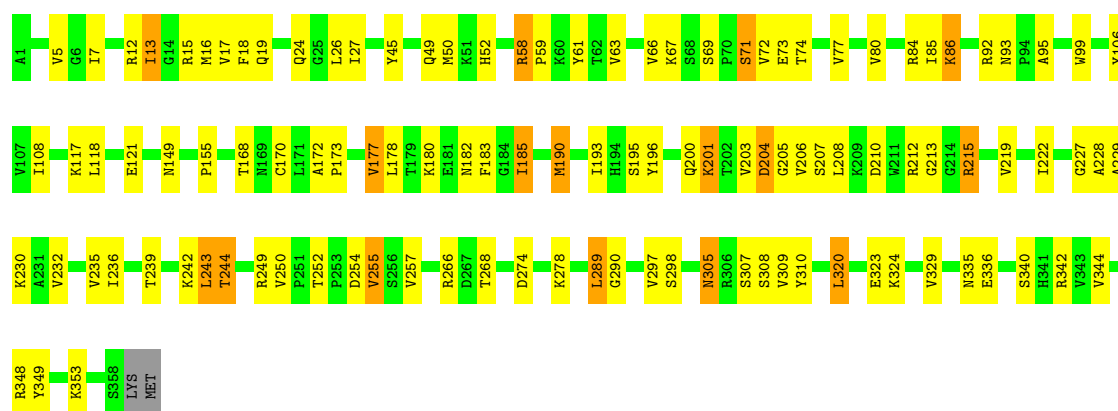
• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

Chain D: 67% 29% ..



• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

Chain E: 68% 27% ..



• Molecule 1: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE

Chain F: 62% 34% ..





4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	80.52Å 393.56Å 70.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	15.00 – 3.00	Depositor
% Data completeness (in resolution range)	(Not available) (15.00-3.00)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.211 , 0.327	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	16536	wwPDB-VP
Average B, all atoms (Å ²)	46.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: TND

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	0.48	0/2767	0.90	5/3752 (0.1%)
1	B	0.54	0/2767	0.96	8/3752 (0.2%)
1	C	0.56	0/2767	0.93	7/3752 (0.2%)
1	D	0.51	0/2767	0.90	5/3752 (0.1%)
1	E	0.47	0/2767	0.90	6/3752 (0.2%)
1	F	0.43	0/2767	0.89	7/3752 (0.2%)
All	All	0.50	0/16602	0.91	38/22512 (0.2%)

There are no bond length outliers.

All (38) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	250	VAL	CA-C-N	9.36	131.54	119.84
1	B	250	VAL	C-N-CA	9.36	131.54	119.84
1	D	250	VAL	CA-C-N	8.12	130.00	119.84
1	D	250	VAL	C-N-CA	8.12	130.00	119.84
1	A	236	ILE	CA-C-N	8.05	129.90	119.84
1	A	236	ILE	C-N-CA	8.05	129.90	119.84
1	B	236	ILE	CA-C-N	7.88	129.70	119.84
1	B	236	ILE	C-N-CA	7.88	129.70	119.84
1	F	250	VAL	CA-C-N	7.46	129.16	119.84
1	F	250	VAL	C-N-CA	7.46	129.16	119.84
1	D	222	ILE	N-CA-C	7.29	115.40	107.60
1	A	222	ILE	N-CA-C	7.17	115.27	107.60
1	B	222	ILE	N-CA-C	7.08	115.18	107.60
1	F	320	LEU	CA-C-N	6.84	128.40	119.84
1	F	320	LEU	C-N-CA	6.84	128.40	119.84
1	F	236	ILE	CA-C-N	6.79	128.32	119.84
1	F	236	ILE	C-N-CA	6.79	128.32	119.84
1	D	236	ILE	CA-C-N	6.65	128.15	119.84

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	236	ILE	C-N-CA	6.65	128.15	119.84
1	E	250	VAL	CA-C-N	6.39	127.83	119.84
1	E	250	VAL	C-N-CA	6.39	127.83	119.84
1	C	252	THR	CA-C-N	6.16	125.79	119.56
1	C	252	THR	C-N-CA	6.16	125.79	119.56
1	C	236	ILE	CA-C-N	6.10	127.47	119.84
1	C	236	ILE	C-N-CA	6.10	127.47	119.84
1	A	320	LEU	CA-C-N	6.10	127.46	119.84
1	A	320	LEU	C-N-CA	6.10	127.46	119.84
1	F	222	ILE	N-CA-C	6.06	114.08	107.60
1	C	222	ILE	N-CA-C	5.99	114.01	107.60
1	E	236	ILE	CA-C-N	5.89	127.21	119.84
1	E	236	ILE	C-N-CA	5.89	127.21	119.84
1	E	320	LEU	CA-C-N	5.55	126.77	119.84
1	E	320	LEU	C-N-CA	5.55	126.77	119.84
1	C	250	VAL	CA-C-N	5.25	126.41	119.84
1	C	250	VAL	C-N-CA	5.25	126.41	119.84
1	B	55	VAL	N-CA-C	5.15	116.24	111.81
1	B	1	ALA	CA-C-N	5.10	126.21	119.84
1	B	1	ALA	C-N-CA	5.10	126.21	119.84

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	2715	0	2736	96	0
1	B	2715	0	2736	93	0
1	C	2715	0	2736	78	0
1	D	2715	0	2736	97	0
1	E	2715	0	2736	105	0
1	F	2715	0	2736	124	0
2	A	41	0	32	0	0
2	B	41	0	32	3	0
2	C	41	0	32	4	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	41	0	32	2	0
2	E	41	0	32	4	0
2	F	41	0	32	2	0
All	All	16536	0	16608	560	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 17.

All (560) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:73:GLU:HG2	1:C:74:THR:HG23	1.44	0.98
1:E:73:GLU:HG2	1:E:74:THR:HG23	1.46	0.96
1:E:206:VAL:HG13	1:F:45:TYR:HE2	1.33	0.91
1:E:93:ASN:ND2	1:E:95:ALA:HB3	1.86	0.90
1:A:73:GLU:HG2	1:A:74:THR:HG23	1.54	0.89
1:B:73:GLU:HG2	1:B:74:THR:HG23	1.56	0.87
1:D:77:VAL:HG22	1:D:86:LYS:HE3	1.57	0.87
1:D:93:ASN:HD21	1:D:95:ALA:HB3	1.37	0.87
1:B:232:VAL:HG11	1:B:243:LEU:HD23	1.58	0.86
1:D:73:GLU:HG2	1:D:74:THR:HG23	1.55	0.86
1:E:93:ASN:HD21	1:E:95:ALA:HB3	1.41	0.84
1:B:229:ALA:O	1:B:232:VAL:HG12	1.78	0.84
1:F:73:GLU:HG2	1:F:74:THR:HG23	1.60	0.82
1:B:93:ASN:ND2	1:B:95:ALA:HB3	1.94	0.81
1:D:232:VAL:HG11	1:D:243:LEU:HD23	1.63	0.81
1:C:229:ALA:O	1:C:232:VAL:HG12	1.81	0.81
1:A:93:ASN:ND2	1:A:95:ALA:HB3	1.97	0.80
1:B:93:ASN:HD21	1:B:95:ALA:HB3	1.46	0.79
1:A:251:PRO:HB2	1:D:251:PRO:HB2	1.65	0.79
1:B:195:SER:HB3	1:B:252:THR:O	1.83	0.78
1:F:172:ALA:HB3	1:F:173:PRO:HD3	1.63	0.78
1:A:171:LEU:HD11	1:A:260:LEU:HD22	1.67	0.77
1:D:229:ALA:O	1:D:232:VAL:HG12	1.84	0.76
1:B:251:PRO:HB2	1:C:251:PRO:HB2	1.64	0.76
1:A:328:LYS:HB2	1:D:189:LEU:HD23	1.66	0.76
1:A:172:ALA:HB3	1:A:173:PRO:HD3	1.68	0.75
1:F:229:ALA:O	1:F:232:VAL:HG12	1.87	0.75
1:D:93:ASN:ND2	1:D:95:ALA:HB3	2.01	0.75
1:E:5:VAL:HG12	1:E:106:TYR:HB2	1.69	0.74
1:D:172:ALA:HB3	1:D:173:PRO:HD3	1.71	0.73

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:195:SER:HB3	1:C:252:THR:O	1.88	0.73
1:A:229:ALA:O	1:A:232:VAL:HG12	1.89	0.73
1:F:93:ASN:HD21	1:F:95:ALA:HB3	1.52	0.73
1:B:189:LEU:HD23	1:C:328:LYS:HB2	1.71	0.72
1:C:185:ILE:HD11	1:C:243:LEU:HD11	1.72	0.72
1:E:229:ALA:O	1:E:232:VAL:HG12	1.90	0.72
1:E:344:VAL:O	1:E:348:ARG:HG3	1.89	0.72
1:F:171:LEU:HD11	1:F:260:LEU:HD22	1.72	0.71
1:B:328:LYS:HB2	1:C:189:LEU:HD23	1.73	0.71
1:E:52:HIS:HB3	1:F:215:ARG:NH2	2.06	0.71
1:F:170:CYS:HA	1:F:308:SER:HB2	1.73	0.71
1:A:185:ILE:HD11	1:A:243:LEU:HD11	1.74	0.69
1:F:16:MET:HB3	1:F:340:SER:OG	1.92	0.69
1:F:77:VAL:HG22	1:F:86:LYS:HE3	1.73	0.69
1:F:232:VAL:HG11	1:F:243:LEU:HD23	1.75	0.69
1:B:73:GLU:H	1:B:73:GLU:CD	2.02	0.68
1:F:93:ASN:ND2	1:F:95:ALA:HB3	2.07	0.68
1:C:172:ALA:HB3	1:C:173:PRO:HD3	1.76	0.68
1:F:185:ILE:HD11	1:F:243:LEU:HD11	1.76	0.68
1:A:24:GLN:CB	1:A:26:LEU:HD13	2.23	0.67
1:A:189:LEU:HD23	1:D:328:LYS:HB2	1.75	0.67
1:D:195:SER:HB3	1:D:252:THR:O	1.95	0.67
1:E:207:SER:N	1:F:45:TYR:OH	2.28	0.67
1:D:175:VAL:O	1:D:179:THR:HG23	1.96	0.66
1:C:227:GLY:HA3	1:C:230:LYS:HE2	1.78	0.66
1:E:289:LEU:HD23	1:E:308:SER:O	1.95	0.66
1:F:201:LYS:HG2	1:F:205:GLY:HA3	1.78	0.66
1:B:227:GLY:HA3	1:B:230:LYS:HE2	1.77	0.66
1:F:69:SER:C	1:F:71:SER:H	2.03	0.65
1:D:24:GLN:HB3	1:D:26:LEU:HD13	1.77	0.64
1:A:232:VAL:HG11	1:A:243:LEU:HD23	1.80	0.64
1:E:307:SER:OG	1:E:342:ARG:HD2	1.98	0.64
1:E:320:LEU:HB2	1:E:323:GLU:HB2	1.78	0.64
1:E:195:SER:HB3	1:E:252:THR:O	1.98	0.64
1:D:5:VAL:HG12	1:D:106:TYR:HB2	1.80	0.64
1:C:169:ASN:O	1:C:307:SER:HB3	1.97	0.63
1:C:289:LEU:HD23	1:C:308:SER:O	1.98	0.63
1:D:69:SER:C	1:D:71:SER:H	2.07	0.63
1:A:290:GLY:HA3	1:A:306:ARG:NH1	2.14	0.63
1:D:117:LYS:HB3	1:D:139:GLY:HA3	1.81	0.63
1:F:35:ALA:HB2	1:F:86:LYS:HB2	1.79	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:232:VAL:HG11	1:C:243:LEU:HD23	1.80	0.62
1:B:204:ASP:OD1	1:B:215:ARG:HD2	1.99	0.62
1:A:171:LEU:CD1	1:A:260:LEU:HD22	2.29	0.62
1:C:302:ILE:O	1:C:303:ASN:HB2	1.98	0.62
1:D:16:MET:HB3	1:D:340:SER:OG	2.00	0.62
1:D:12:ARG:HH21	1:D:336:GLU:CD	2.08	0.61
1:D:171:LEU:HD11	1:D:260:LEU:HD22	1.83	0.61
1:F:190:MET:O	1:F:190:MET:HE3	1.99	0.61
1:C:92:ARG:HG2	2:C:363:TND:C5	2.30	0.61
1:F:287:GLY:O	1:F:306:ARG:HG3	2.01	0.61
1:C:35:ALA:HB2	1:C:86:LYS:HB2	1.81	0.61
1:D:86:LYS:HA	1:D:86:LYS:HE2	1.83	0.60
1:D:185:ILE:HD11	1:D:243:LEU:HD11	1.83	0.60
1:F:67:LYS:HB3	1:F:72:VAL:CG2	2.31	0.60
1:C:170:CYS:HA	1:C:308:SER:HB2	1.82	0.60
1:B:193:ILE:HB	1:B:257:VAL:HG12	1.81	0.60
1:B:15:ARG:O	1:B:19:GLN:HG3	2.01	0.60
1:F:258:VAL:HG23	1:F:333:TYR:HE1	1.67	0.60
1:A:99:TRP:NE1	1:A:123:HIS:ND1	2.46	0.60
1:B:215:ARG:NH2	1:C:300:ASP:OD1	2.33	0.59
1:B:232:VAL:HG11	1:B:243:LEU:CD2	2.30	0.59
1:F:24:GLN:CB	1:F:26:LEU:HD13	2.32	0.59
1:A:12:ARG:HH21	1:A:336:GLU:CD	2.10	0.59
1:B:169:ASN:O	1:B:307:SER:HB3	2.02	0.59
1:B:170:CYS:HA	1:B:308:SER:HB2	1.84	0.59
1:C:93:ASN:ND2	1:C:95:ALA:HB3	2.16	0.59
1:C:117:LYS:O	1:C:121:GLU:HG3	2.01	0.59
1:B:320:LEU:HB2	1:B:323:GLU:HB2	1.85	0.59
1:B:24:GLN:CB	1:B:26:LEU:HD13	2.33	0.59
1:A:117:LYS:HB3	1:A:139:GLY:HA3	1.84	0.59
1:D:117:LYS:O	1:D:121:GLU:HG3	2.03	0.59
1:E:201:LYS:N	1:E:201:LYS:HD2	2.18	0.59
1:A:12:ARG:HD3	1:B:204:ASP:O	2.03	0.59
1:D:227:GLY:HA3	1:D:230:LYS:HE2	1.85	0.58
1:A:69:SER:C	1:A:71:SER:H	2.10	0.58
1:A:93:ASN:HD21	1:A:95:ALA:HB3	1.68	0.58
1:B:185:ILE:HD11	1:B:243:LEU:HD11	1.85	0.58
1:D:320:LEU:HB2	1:D:323:GLU:HB2	1.85	0.58
1:F:169:ASN:O	1:F:307:SER:HB3	2.02	0.58
1:F:117:LYS:O	1:F:121:GLU:HG3	2.03	0.58
1:F:38:ASP:C	1:F:90:ALA:HB2	2.29	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:27:ILE:HG23	1:A:27:ILE:O	2.03	0.58
1:F:193:ILE:N	1:F:193:ILE:HD12	2.19	0.58
1:A:254:ASP:OD1	1:A:336:GLU:HG3	2.04	0.58
1:A:155:PRO:HG3	1:A:353:LYS:HG2	1.86	0.58
1:C:67:LYS:HB3	1:C:72:VAL:CG2	2.33	0.58
1:A:193:ILE:HB	1:A:257:VAL:HG12	1.86	0.57
1:A:195:SER:HB3	1:A:252:THR:O	2.03	0.57
1:E:67:LYS:HB3	1:E:72:VAL:HG22	1.85	0.57
1:F:297:VAL:O	1:F:298:SER:C	2.46	0.57
1:B:67:LYS:HD3	1:B:72:VAL:HG23	1.87	0.57
1:C:254:ASP:O	1:C:255:VAL:HB	2.04	0.57
1:E:16:MET:HE2	1:E:19:GLN:OE1	2.03	0.57
1:B:305:ASN:C	1:B:305:ASN:HD22	2.11	0.57
1:E:232:VAL:HG11	1:E:243:LEU:HD23	1.86	0.57
1:D:24:GLN:CB	1:D:26:LEU:HD13	2.34	0.57
1:B:69:SER:C	1:B:71:SER:H	2.12	0.57
1:A:24:GLN:HB2	1:A:26:LEU:HD13	1.85	0.56
1:B:73:GLU:CD	1:B:73:GLU:N	2.63	0.56
1:B:227:GLY:O	1:B:230:LYS:HG2	2.06	0.56
1:D:67:LYS:HB3	1:D:72:VAL:CG2	2.34	0.56
1:D:69:SER:C	1:D:71:SER:N	2.62	0.56
1:E:63:VAL:HG22	1:E:80:VAL:HG22	1.88	0.56
1:A:266:ARG:HG3	1:A:266:ARG:HH11	1.70	0.56
1:A:300:ASP:OD1	1:D:215:ARG:NH2	2.39	0.56
1:B:69:SER:C	1:B:71:SER:N	2.63	0.56
1:A:66:VAL:HG23	1:A:77:VAL:HB	1.86	0.56
1:D:67:LYS:HB3	1:D:72:VAL:HG22	1.88	0.56
1:F:227:GLY:HA3	1:F:230:LYS:HE2	1.88	0.56
1:C:12:ARG:HH21	1:C:336:GLU:CD	2.14	0.56
1:C:227:GLY:CA	1:C:230:LYS:HE2	2.36	0.56
1:B:12:ARG:HH21	1:B:336:GLU:CD	2.14	0.56
2:F:366:TND:N7A	2:F:366:TND:H1	2.20	0.56
1:F:69:SER:C	1:F:71:SER:N	2.63	0.55
1:A:215:ARG:NH2	1:B:52:HIS:HB3	2.22	0.55
1:A:17:VAL:HG11	1:A:108:ILE:HD13	1.88	0.55
1:A:24:GLN:HB3	1:A:26:LEU:HD13	1.87	0.55
1:A:106:TYR:OH	1:A:351:ALA:HA	2.07	0.55
1:B:73:GLU:CD	1:B:74:THR:H	2.14	0.55
1:F:86:LYS:HA	1:F:86:LYS:HE2	1.89	0.55
1:E:16:MET:HB3	1:E:340:SER:OG	2.06	0.55
1:F:232:VAL:HG11	1:F:243:LEU:CD2	2.36	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:349:TYR:OH	1:E:353:LYS:HE3	2.07	0.54
1:E:172:ALA:HB3	1:E:173:PRO:HD3	1.89	0.54
1:B:37:VAL:HG22	1:B:88:VAL:HB	1.89	0.54
1:B:16:MET:HB3	1:B:340:SER:OG	2.06	0.54
1:F:258:VAL:HG23	1:F:333:TYR:CE1	2.43	0.54
1:D:86:LYS:HE2	1:D:86:LYS:CA	2.38	0.54
1:A:155:PRO:CG	1:A:353:LYS:HG2	2.37	0.54
1:E:45:TYR:HE2	1:F:206:VAL:HG13	1.73	0.54
1:A:10:PHE:CE2	1:A:15:ARG:HG2	2.43	0.54
2:C:363:TND:H3B	1:D:208:LEU:HD12	1.89	0.54
1:D:7:ILE:CD1	1:D:108:ILE:HD12	2.38	0.54
1:F:24:GLN:HB2	1:F:26:LEU:HD13	1.90	0.54
1:C:24:GLN:CB	1:C:26:LEU:HD13	2.37	0.53
1:D:281:ALA:HB2	1:D:289:LEU:HD13	1.89	0.53
1:F:69:SER:O	1:F:71:SER:N	2.41	0.53
1:F:73:GLU:CD	1:F:73:GLU:H	2.15	0.53
1:F:161:VAL:HG12	1:F:162:SER:N	2.24	0.53
1:F:305:ASN:C	1:F:305:ASN:HD22	2.16	0.53
1:A:320:LEU:HB2	1:A:323:GLU:HB2	1.90	0.53
1:B:117:LYS:O	1:B:121:GLU:HG3	2.07	0.53
1:E:24:GLN:CB	1:E:26:LEU:HD13	2.38	0.53
1:E:92:ARG:HG2	2:E:365:TND:C5	2.39	0.53
1:F:227:GLY:CA	1:F:230:LYS:HE2	2.38	0.53
1:B:172:ALA:HB3	1:B:173:PRO:HD3	1.90	0.53
1:B:219:VAL:HG22	1:B:219:VAL:O	2.07	0.53
1:D:69:SER:O	1:D:71:SER:N	2.41	0.53
1:D:145:VAL:HG23	1:D:235:VAL:HG21	1.89	0.53
1:F:307:SER:OG	1:F:342:ARG:HD2	2.09	0.53
1:A:52:HIS:HB3	1:B:215:ARG:NH2	2.23	0.53
1:C:268:THR:O	1:C:324:LYS:HA	2.09	0.53
1:E:193:ILE:N	1:E:193:ILE:HD12	2.24	0.53
1:B:17:VAL:HG11	1:B:108:ILE:HD13	1.91	0.53
1:E:45:TYR:OH	1:F:207:SER:N	2.40	0.53
1:F:67:LYS:HB3	1:F:72:VAL:HG22	1.89	0.53
1:A:170:CYS:HA	1:A:308:SER:HB2	1.91	0.53
1:A:261:THR:HG21	1:D:261:THR:HG21	1.90	0.53
1:E:206:VAL:HG13	1:F:45:TYR:CE2	2.25	0.53
1:A:16:MET:HB3	1:A:340:SER:OG	2.09	0.53
1:D:18:PHE:HE2	1:D:50:MET:HE1	1.75	0.52
1:C:7:ILE:CD1	1:C:108:ILE:HD12	2.40	0.52
2:C:363:TND:H3B	1:D:208:LEU:CD1	2.39	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:15:ARG:O	1:E:19:GLN:HG3	2.09	0.52
1:F:86:LYS:HE2	1:F:86:LYS:CA	2.39	0.52
1:E:155:PRO:CG	1:E:353:LYS:HG2	2.39	0.52
1:E:254:ASP:O	1:E:255:VAL:HB	2.10	0.52
1:A:254:ASP:O	1:A:255:VAL:HB	2.09	0.52
1:B:145:VAL:O	1:B:146:MET:C	2.52	0.52
1:C:349:TYR:OH	1:C:353:LYS:HE3	2.08	0.52
1:A:69:SER:C	1:A:71:SER:N	2.67	0.52
1:A:163:ASN:OD1	1:A:343:VAL:HA	2.10	0.52
1:A:305:ASN:C	1:A:305:ASN:HD22	2.17	0.52
1:F:90:ALA:HB1	2:F:366:TND:H8	1.92	0.52
1:B:24:GLN:HB2	1:B:26:LEU:HD13	1.92	0.52
1:B:229:ALA:HB1	1:B:244:THR:HA	1.90	0.52
1:C:67:LYS:HB3	1:C:72:VAL:HG22	1.92	0.52
1:B:18:PHE:HE2	1:B:50:MET:HE1	1.75	0.52
1:B:185:ILE:HG23	1:B:185:ILE:O	2.09	0.51
1:C:290:GLY:O	1:C:309:VAL:HA	2.10	0.51
1:E:239:THR:HA	1:E:242:LYS:HD2	1.92	0.51
1:F:38:ASP:OD1	1:F:39:MET:N	2.42	0.51
1:B:227:GLY:CA	1:B:230:LYS:HE2	2.40	0.51
1:B:67:LYS:HB3	1:B:72:VAL:CG2	2.40	0.51
1:B:69:SER:O	1:B:71:SER:N	2.43	0.51
1:C:190:MET:HB3	1:C:260:LEU:HD13	1.92	0.51
1:F:153:TYR:CE1	1:F:158:HIS:HB2	2.45	0.51
1:A:297:VAL:O	1:A:298:SER:C	2.53	0.51
1:B:5:VAL:HG12	1:B:106:TYR:HB2	1.92	0.51
1:C:193:ILE:HB	1:C:257:VAL:CG1	2.41	0.51
1:C:200:GLN:C	1:C:201:LYS:HD2	2.35	0.51
1:B:27:ILE:HG23	1:B:27:ILE:O	2.11	0.51
1:A:69:SER:O	1:A:71:SER:N	2.44	0.51
1:E:219:VAL:HG22	1:E:219:VAL:O	2.11	0.51
1:C:73:GLU:CD	1:C:74:THR:H	2.17	0.51
1:F:18:PHE:HE2	1:F:50:MET:HE1	1.76	0.51
1:E:99:TRP:HA	1:E:99:TRP:CE3	2.46	0.51
1:E:227:GLY:HA3	1:E:230:LYS:HE2	1.92	0.51
1:F:106:TYR:OH	1:F:351:ALA:HA	2.11	0.51
1:B:200:GLN:OE1	1:B:249:ARG:NH1	2.44	0.50
1:C:227:GLY:O	1:C:230:LYS:HG2	2.11	0.50
1:F:18:PHE:CZ	1:F:80:VAL:HG21	2.46	0.50
2:C:363:TND:N7A	2:C:363:TND:H1	2.26	0.50
1:D:170:CYS:HA	1:D:308:SER:HB2	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:7:ILE:HD13	1:E:108:ILE:HB	1.93	0.50
1:E:193:ILE:HB	1:E:257:VAL:HG12	1.93	0.50
1:F:254:ASP:O	1:F:255:VAL:HB	2.11	0.50
1:F:320:LEU:HB2	1:F:323:GLU:HB2	1.93	0.50
1:B:302:ILE:O	1:B:303:ASN:HB2	2.11	0.50
1:E:12:ARG:HD3	1:F:204:ASP:O	2.10	0.50
1:F:280:ALA:O	1:F:285:MET:HB2	2.12	0.50
1:F:195:SER:HB3	1:F:252:THR:O	2.12	0.50
1:B:193:ILE:HD12	1:B:193:ILE:N	2.26	0.50
1:E:206:VAL:HG22	1:F:49:GLN:OE1	2.12	0.50
1:F:73:GLU:CD	1:F:74:THR:H	2.19	0.49
1:E:149:ASN:CG	1:E:235:VAL:HG13	2.37	0.49
1:F:12:ARG:HH21	1:F:336:GLU:CD	2.20	0.49
1:A:323:GLU:HG2	1:A:326:PHE:O	2.12	0.49
1:B:274:ASP:O	1:B:278:LYS:HG3	2.12	0.49
1:E:297:VAL:O	1:E:298:SER:C	2.55	0.49
1:F:35:ALA:HB1	1:F:88:VAL:HG23	1.95	0.49
1:D:77:VAL:CG2	1:D:86:LYS:HE3	2.36	0.49
1:F:84:ARG:C	1:F:85:ILE:HD12	2.38	0.49
1:F:266:ARG:HH11	1:F:266:ARG:HG3	1.78	0.49
1:C:268:THR:OG1	1:C:269:SER:N	2.43	0.49
1:B:66:VAL:HG23	1:B:77:VAL:HB	1.94	0.49
1:E:92:ARG:HE	2:E:365:TND:H5	1.78	0.49
1:E:168:THR:OG1	1:E:228:ALA:HA	2.13	0.49
1:F:219:VAL:O	1:F:219:VAL:HG22	2.13	0.49
1:F:124:ILE:HG23	1:F:128:ALA:O	2.13	0.49
1:F:27:ILE:HG23	1:F:27:ILE:O	2.13	0.48
1:F:334:ASP:O	1:F:335:ASN:C	2.55	0.48
1:A:295:GLU:HB3	1:D:212:ARG:HG3	1.96	0.48
1:D:35:ALA:HB2	1:D:86:LYS:HB2	1.95	0.48
1:D:169:ASN:O	1:D:307:SER:HB3	2.13	0.48
1:E:201:LYS:HB3	1:E:203:VAL:O	2.13	0.48
1:E:208:LEU:HD23	1:F:45:TYR:HB2	1.95	0.48
1:E:268:THR:O	1:E:324:LYS:HA	2.12	0.48
1:C:320:LEU:HB2	1:C:323:GLU:HB2	1.95	0.48
2:B:362:TND:N7A	2:B:362:TND:H1	2.29	0.48
1:E:180:LYS:C	1:E:182:ASN:H	2.20	0.48
1:C:93:ASN:HD21	1:C:95:ALA:HB3	1.78	0.48
1:D:85:ILE:HD12	1:D:85:ILE:N	2.29	0.48
1:F:118:LEU:N	1:F:118:LEU:HD12	2.28	0.48
1:F:210:ASP:OD2	1:F:213:GLY:HA3	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:204:ASP:O	1:F:12:ARG:HD3	2.12	0.48
1:E:243:LEU:O	1:E:244:THR:HB	2.14	0.48
1:A:73:GLU:CD	1:A:73:GLU:H	2.21	0.48
1:D:5:VAL:HA	1:D:106:TYR:O	2.13	0.48
1:D:24:GLN:HB3	1:D:26:LEU:CD1	2.43	0.48
1:A:193:ILE:N	1:A:193:ILE:HD12	2.27	0.48
1:B:356:ALA:C	1:B:358:SER:H	2.22	0.48
1:C:185:ILE:CD1	1:C:243:LEU:HD11	2.41	0.48
1:D:153:TYR:CE1	1:D:158:HIS:HB2	2.49	0.48
1:D:185:ILE:HG23	1:D:185:ILE:O	2.12	0.48
1:E:212:ARG:O	1:E:215:ARG:HG2	2.14	0.48
1:F:69:SER:O	1:F:72:VAL:HG22	2.14	0.48
1:B:216:ALA:HB1	1:B:219:VAL:HG12	1.95	0.48
1:D:67:LYS:HD3	1:D:72:VAL:O	2.13	0.48
1:F:18:PHE:CE2	1:F:50:MET:HE1	2.48	0.48
1:A:190:MET:O	1:A:190:MET:HG3	2.14	0.47
1:A:203:VAL:O	1:A:204:ASP:C	2.57	0.47
1:E:77:VAL:HG22	1:E:86:LYS:HE3	1.95	0.47
1:E:196:TYR:HA	1:E:200:GLN:OE1	2.14	0.47
1:B:229:ALA:CB	1:B:244:THR:HA	2.44	0.47
1:D:180:LYS:C	1:D:182:ASN:H	2.22	0.47
1:F:117:LYS:HB3	1:F:139:GLY:HA3	1.96	0.47
1:E:67:LYS:HB3	1:E:72:VAL:CG2	2.45	0.47
1:A:5:VAL:HA	1:A:106:TYR:O	2.15	0.47
1:A:212:ARG:HG2	1:D:295:GLU:HB3	1.96	0.47
1:B:144:ILE:CD1	1:B:153:TYR:HB2	2.45	0.47
1:B:61:TYR:HB3	1:B:81:ASN:HD21	1.79	0.47
1:B:229:ALA:HB1	1:B:244:THR:CA	2.45	0.47
1:C:10:PHE:CE1	1:C:36:VAL:HG11	2.50	0.47
1:D:227:GLY:O	1:D:230:LYS:HG2	2.15	0.47
1:F:73:GLU:CD	1:F:73:GLU:N	2.72	0.47
1:F:175:VAL:O	1:F:179:THR:HG23	2.14	0.47
1:B:92:ARG:HG2	2:B:362:TND:C5	2.45	0.47
1:B:258:VAL:HG23	1:B:333:TYR:HE1	1.79	0.47
1:D:254:ASP:O	1:D:255:VAL:HB	2.15	0.47
2:E:365:TND:C4B	1:F:206:VAL:HG11	2.45	0.47
1:A:189:LEU:HA	1:A:244:THR:O	2.15	0.47
1:A:254:ASP:O	1:A:255:VAL:CB	2.63	0.47
1:A:289:LEU:HD23	1:A:308:SER:O	2.14	0.47
1:B:254:ASP:O	1:B:255:VAL:HB	2.13	0.47
1:C:7:ILE:HD11	1:C:108:ILE:HD12	1.97	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:233:GLY:O	1:C:240:LYS:HE2	2.15	0.47
1:A:29:THR:OG1	1:A:30:GLU:N	2.47	0.46
1:A:45:TYR:O	1:A:48:TYR:HB3	2.14	0.46
1:B:155:PRO:CG	1:B:353:LYS:HG2	2.45	0.46
1:F:200:GLN:HE21	1:F:222:ILE:HD12	1.80	0.46
1:A:227:GLY:HA3	1:A:230:LYS:HE2	1.98	0.46
1:B:67:LYS:HB3	1:B:72:VAL:HG22	1.97	0.46
1:D:215:ARG:O	1:D:216:ALA:C	2.58	0.46
1:F:155:PRO:CG	1:F:353:LYS:HG2	2.45	0.46
1:F:204:ASP:OD1	1:F:215:ARG:HD2	2.16	0.46
1:A:24:GLN:HB3	1:A:26:LEU:CD1	2.45	0.46
1:A:116:ASP:O	1:A:117:LYS:C	2.58	0.46
1:C:338:ALA:O	1:C:339:TYR:C	2.58	0.46
1:D:92:ARG:HG2	2:D:364:TND:C5	2.45	0.46
1:B:220:ASN:OD1	1:C:299:ALA:HB2	2.15	0.46
1:E:85:ILE:N	1:E:85:ILE:HD12	2.31	0.46
1:E:118:LEU:HD12	1:E:118:LEU:N	2.31	0.46
1:C:145:VAL:O	1:C:146:MET:C	2.59	0.46
1:D:73:GLU:CD	1:D:73:GLU:H	2.23	0.46
1:C:85:ILE:N	1:C:85:ILE:HD12	2.29	0.46
1:F:5:VAL:HA	1:F:106:TYR:O	2.16	0.46
1:D:16:MET:HE2	1:D:19:GLN:OE1	2.16	0.46
1:C:305:ASN:C	1:C:305:ASN:HD22	2.24	0.46
1:E:58:ARG:HG3	1:E:59:PRO:HD2	1.98	0.46
1:E:229:ALA:HB1	1:E:244:THR:HA	1.98	0.46
1:A:9:GLY:HA3	1:A:111:THR:HG22	1.96	0.46
1:C:37:VAL:HG22	1:C:88:VAL:HB	1.98	0.46
1:C:297:VAL:O	1:C:298:SER:C	2.59	0.46
1:D:297:VAL:O	1:D:298:SER:C	2.57	0.46
1:F:149:ASN:CG	1:F:235:VAL:HG13	2.41	0.46
1:A:15:ARG:O	1:A:19:GLN:HG3	2.16	0.45
1:B:246:MET:HE3	1:B:246:MET:HB2	1.80	0.45
1:C:280:ALA:O	1:C:285:MET:HB2	2.17	0.45
1:D:305:ASN:C	1:D:305:ASN:HD22	2.24	0.45
1:F:173:PRO:O	1:F:177:VAL:HG13	2.15	0.45
1:F:289:LEU:HD23	1:F:308:SER:O	2.16	0.45
1:B:9:GLY:HA3	1:B:111:THR:HG22	1.98	0.45
1:D:285:MET:HB3	1:D:289:LEU:HB3	1.97	0.45
1:B:236:ILE:HG22	1:B:236:ILE:O	2.16	0.45
1:B:334:ASP:O	1:B:335:ASN:C	2.59	0.45
1:A:35:ALA:HB2	1:A:86:LYS:HB2	1.99	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:MET:HE2	1:C:19:GLN:OE1	2.17	0.45
1:D:178:LEU:O	1:D:183:PHE:HB2	2.16	0.45
1:D:200:GLN:OE1	1:D:249:ARG:NH1	2.50	0.45
1:E:201:LYS:HG2	1:E:205:GLY:HA3	1.99	0.45
2:E:365:TND:H1	2:E:365:TND:N7A	2.31	0.45
1:F:289:LEU:HD22	1:F:290:GLY:N	2.31	0.45
1:A:116:ASP:OD2	1:A:118:LEU:HB2	2.17	0.45
1:B:297:VAL:O	1:B:298:SER:C	2.59	0.45
1:C:11:GLY:O	1:C:12:ARG:C	2.58	0.45
1:C:54:THR:HG21	1:D:219:VAL:CG1	2.47	0.45
1:E:305:ASN:C	1:E:305:ASN:HD22	2.25	0.45
1:A:178:LEU:O	1:A:183:PHE:HB2	2.17	0.45
1:A:290:GLY:O	1:A:309:VAL:HA	2.17	0.45
1:B:144:ILE:HD11	1:B:153:TYR:HB2	1.98	0.45
1:C:229:ALA:CB	1:C:244:THR:HA	2.47	0.45
1:D:190:MET:HE3	1:D:190:MET:O	2.16	0.45
1:C:204:ASP:O	1:D:12:ARG:HD3	2.17	0.45
1:D:18:PHE:CE2	1:D:50:MET:HE1	2.51	0.45
1:E:12:ARG:HH21	1:E:336:GLU:CD	2.25	0.45
1:E:19:GLN:HG2	1:E:50:MET:HE3	1.98	0.45
1:A:117:LYS:O	1:A:121:GLU:HG3	2.17	0.45
1:D:124:ILE:HG23	1:D:128:ALA:O	2.17	0.45
1:E:155:PRO:HG2	1:E:353:LYS:HG2	1.98	0.45
1:E:215:ARG:NH1	1:F:54:THR:OG1	2.50	0.45
1:F:95:ALA:HA	1:F:122:GLY:O	2.16	0.45
1:C:16:MET:HB3	1:C:340:SER:OG	2.16	0.45
1:C:24:GLN:HB3	1:C:26:LEU:HD13	1.98	0.45
1:C:323:GLU:HG2	1:C:326:PHE:O	2.17	0.45
1:A:37:VAL:CG1	1:A:90:ALA:HA	2.47	0.45
1:E:117:LYS:O	1:E:121:GLU:HG3	2.17	0.45
1:E:24:GLN:HB2	1:E:26:LEU:HD13	1.98	0.44
1:E:203:VAL:O	1:E:205:GLY:N	2.51	0.44
1:A:88:VAL:HG12	1:A:89:LYS:N	2.32	0.44
1:A:149:ASN:OD1	1:A:235:VAL:HG13	2.16	0.44
1:E:45:TYR:CE2	1:F:206:VAL:HG13	2.51	0.44
1:E:274:ASP:OD1	1:E:278:LYS:HE3	2.17	0.44
1:E:274:ASP:CG	1:E:278:LYS:HE3	2.42	0.44
1:C:208:LEU:HD12	2:D:364:TND:H1M3	2.00	0.44
1:E:349:TYR:CZ	1:E:353:LYS:HE2	2.52	0.44
1:B:59:PRO:HB2	1:B:61:TYR:CZ	2.53	0.44
1:C:15:ARG:O	1:C:19:GLN:HG3	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:190:MET:HE1	1:F:192:THR:HG22	1.99	0.44
1:A:85:ILE:HD12	1:A:85:ILE:N	2.32	0.44
1:F:26:LEU:HD23	1:F:31:ILE:HD12	1.99	0.44
1:A:320:LEU:HA	1:A:321:PRO:HD2	1.76	0.44
1:D:303:ASN:HA	1:D:337:TRP:CD1	2.53	0.44
1:F:86:LYS:HA	1:F:86:LYS:CE	2.48	0.44
1:A:37:VAL:HG22	1:A:88:VAL:HB	2.00	0.44
1:B:201:LYS:HD2	1:B:201:LYS:N	2.33	0.44
1:D:323:GLU:HG2	1:D:326:PHE:O	2.18	0.44
1:E:215:ARG:NH2	1:F:52:HIS:HB3	2.33	0.44
1:A:78:LEU:HD12	1:A:78:LEU:HA	1.85	0.44
1:F:77:VAL:HG13	1:F:85:ILE:O	2.18	0.44
1:F:123:HIS:C	1:F:128:ALA:HB3	2.43	0.44
1:B:18:PHE:CE2	1:B:50:MET:HE1	2.53	0.43
1:C:193:ILE:HB	1:C:257:VAL:HG12	2.00	0.43
1:C:356:ALA:C	1:C:358:SER:H	2.26	0.43
1:D:67:LYS:HD3	1:D:72:VAL:HG23	2.00	0.43
1:A:193:ILE:HB	1:A:257:VAL:CG1	2.48	0.43
1:D:21:ILE:HG23	1:D:31:ILE:HD12	1.99	0.43
1:E:66:VAL:HG23	1:E:77:VAL:HB	1.98	0.43
1:E:185:ILE:HG23	1:E:185:ILE:O	2.18	0.43
1:E:200:GLN:OE1	1:E:249:ARG:NH1	2.51	0.43
1:F:171:LEU:CD1	1:F:260:LEU:HD22	2.46	0.43
1:F:200:GLN:HB3	1:F:217:ALA:HB2	2.00	0.43
1:B:51:LYS:O	1:B:58:ARG:HG3	2.18	0.43
1:D:7:ILE:HD13	1:D:108:ILE:HB	2.00	0.43
1:E:310:TYR:CE1	1:E:329:VAL:HG13	2.53	0.43
1:D:231:ALA:C	1:D:233:GLY:N	2.74	0.43
1:E:49:GLN:OE1	1:F:206:VAL:HG22	2.17	0.43
1:E:222:ILE:HB	1:E:249:ARG:HB2	2.00	0.43
1:B:203:VAL:O	1:B:204:ASP:C	2.61	0.43
1:B:290:GLY:O	1:B:309:VAL:HA	2.19	0.43
1:F:274:ASP:HB2	1:F:316:LEU:HD21	1.99	0.43
1:F:309:VAL:HG13	1:F:332:TRP:HB2	1.99	0.43
1:A:266:ARG:HG3	1:A:266:ARG:NH1	2.32	0.43
1:B:79:VAL:HA	1:B:83:HIS:O	2.18	0.43
1:D:274:ASP:HB2	1:D:316:LEU:HD21	2.01	0.43
1:A:206:VAL:HG11	2:B:362:TND:C4B	2.48	0.43
1:D:168:THR:C	1:D:170:CYS:H	2.26	0.43
1:A:353:LYS:HE2	1:A:353:LYS:HB2	1.92	0.43
1:B:24:GLN:HB3	1:B:26:LEU:HD13	2.01	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:229:ALA:HB1	1:F:244:THR:HA	2.00	0.43
1:A:302:ILE:O	1:A:303:ASN:HB2	2.18	0.43
1:B:38:ASP:OD1	1:B:39:MET:N	2.52	0.43
1:C:12:ARG:NH2	1:C:336:GLU:OE1	2.52	0.43
1:D:280:ALA:O	1:D:285:MET:HB2	2.19	0.43
1:E:59:PRO:HB2	1:E:61:TYR:CZ	2.53	0.43
1:A:18:PHE:CE2	1:A:50:MET:HE1	2.53	0.43
1:A:173:PRO:O	1:A:177:VAL:HG13	2.19	0.43
1:D:195:SER:OG	1:D:255:VAL:O	2.37	0.43
1:F:55:VAL:HG11	1:F:254:ASP:CB	2.48	0.43
1:F:192:THR:HG22	1:F:246:MET:O	2.19	0.43
1:F:292:THR:HG21	1:F:296:LEU:HD12	2.00	0.43
1:A:67:LYS:HB3	1:A:72:VAL:HG22	2.01	0.42
1:A:232:VAL:HG11	1:A:243:LEU:CD2	2.46	0.42
1:C:18:PHE:HE2	1:C:50:MET:HE1	1.84	0.42
1:E:208:LEU:HD23	1:F:45:TYR:CG	2.54	0.42
1:E:210:ASP:OD2	1:E:213:GLY:HA3	2.19	0.42
1:F:18:PHE:CE2	1:F:80:VAL:HG21	2.54	0.42
1:F:85:ILE:HD12	1:F:85:ILE:N	2.34	0.42
1:D:118:LEU:N	1:D:118:LEU:HD12	2.34	0.42
1:D:145:VAL:CG2	1:D:235:VAL:HG21	2.48	0.42
1:E:190:MET:HE3	1:E:190:MET:O	2.19	0.42
1:C:98:PRO:HG2	1:C:102:LEU:CD1	2.48	0.42
1:F:203:VAL:O	1:F:204:ASP:C	2.62	0.42
1:F:274:ASP:O	1:F:278:LYS:HG3	2.19	0.42
1:F:299:ALA:O	1:F:302:ILE:HG13	2.20	0.42
1:F:229:ALA:CB	1:F:244:THR:HA	2.49	0.42
1:C:193:ILE:N	1:C:193:ILE:HD12	2.35	0.42
1:D:86:LYS:HA	1:D:86:LYS:CE	2.48	0.42
1:E:84:ARG:C	1:E:85:ILE:HD12	2.44	0.42
1:E:204:ASP:OD2	1:F:54:THR:N	2.44	0.42
1:F:5:VAL:HG12	1:F:106:TYR:HB2	2.01	0.42
1:B:200:GLN:C	1:B:201:LYS:HD2	2.45	0.42
1:A:67:LYS:HB3	1:A:72:VAL:CG2	2.49	0.42
1:C:99:TRP:HA	1:C:99:TRP:CE3	2.54	0.42
1:D:196:TYR:HA	1:D:200:GLN:OE1	2.20	0.42
1:A:185:ILE:CD1	1:A:243:LEU:HD11	2.46	0.42
1:B:67:LYS:HD3	1:B:72:VAL:O	2.19	0.42
1:B:281:ALA:HB2	1:B:289:LEU:HD13	2.01	0.42
1:A:200:GLN:OE1	1:A:249:ARG:NH1	2.52	0.42
1:E:7:ILE:HD13	1:E:108:ILE:HD12	2.02	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:17:VAL:HG11	1:E:108:ILE:HD13	2.02	0.42
1:F:155:PRO:HG3	1:F:353:LYS:HG2	2.01	0.42
1:F:229:ALA:HB1	1:F:244:THR:CA	2.49	0.42
1:A:313:LYS:HA	1:A:313:LYS:HD3	1.87	0.42
1:D:189:LEU:HA	1:D:244:THR:O	2.19	0.42
1:D:263:ARG:HA	1:D:325:ARG:O	2.20	0.42
1:D:338:ALA:O	1:D:339:TYR:C	2.63	0.42
1:E:27:ILE:O	1:E:27:ILE:HG23	2.20	0.42
1:E:232:VAL:HG11	1:E:243:LEU:CD2	2.48	0.42
1:B:231:ALA:C	1:B:233:GLY:N	2.77	0.41
1:B:289:LEU:HD22	1:B:290:GLY:N	2.35	0.41
1:C:32:ASP:C	1:C:32:ASP:OD1	2.63	0.41
1:C:243:LEU:O	1:C:244:THR:HB	2.19	0.41
1:E:309:VAL:HG13	1:E:309:VAL:O	2.20	0.41
1:F:7:ILE:HD13	1:F:108:ILE:HB	2.01	0.41
1:A:246:MET:HE3	1:A:246:MET:HB2	1.86	0.41
1:E:69:SER:C	1:E:71:SER:H	2.29	0.41
1:E:229:ALA:CB	1:E:244:THR:HA	2.51	0.41
1:B:250:VAL:HA	1:B:251:PRO:HD3	1.82	0.41
1:C:215:ARG:O	1:C:216:ALA:C	2.63	0.41
1:E:18:PHE:CE2	1:E:50:MET:HE1	2.55	0.41
1:F:17:VAL:HG11	1:F:108:ILE:HD13	2.01	0.41
1:F:80:VAL:O	1:F:81:ASN:C	2.63	0.41
1:A:227:GLY:O	1:A:230:LYS:HG2	2.20	0.41
1:B:85:ILE:N	1:B:85:ILE:HD12	2.35	0.41
1:C:246:MET:HE3	1:C:246:MET:HB2	1.93	0.41
1:D:189:LEU:HD12	1:D:244:THR:HG22	2.02	0.41
1:E:5:VAL:HA	1:E:106:TYR:O	2.20	0.41
1:E:99:TRP:HA	1:E:99:TRP:HE3	1.84	0.41
1:E:290:GLY:O	1:E:309:VAL:HA	2.20	0.41
1:B:12:ARG:HD2	1:B:12:ARG:HA	1.92	0.41
1:C:3:ILE:HD13	1:C:351:ALA:CB	2.50	0.41
1:E:13:ILE:H	1:E:13:ILE:HG12	1.56	0.41
1:E:149:ASN:OD1	1:E:235:VAL:HG13	2.19	0.41
1:E:349:TYR:CZ	1:E:353:LYS:CE	3.03	0.41
1:A:169:ASN:O	1:A:307:SER:HB3	2.21	0.41
1:B:215:ARG:NH2	1:C:300:ASP:CG	2.78	0.41
1:C:17:VAL:HG11	1:C:108:ILE:HD13	2.01	0.41
1:C:232:VAL:HG11	1:C:243:LEU:CD2	2.49	0.41
1:E:173:PRO:O	1:E:177:VAL:HG13	2.21	0.41
1:F:124:ILE:HA	1:F:128:ALA:O	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:277:ILE:HG23	1:F:289:LEU:HD11	2.03	0.41
1:B:118:LEU:HD12	1:B:118:LEU:N	2.35	0.41
1:D:64:GLU:HG2	1:D:65:ALA:N	2.34	0.41
1:D:200:GLN:HB3	1:D:217:ALA:HB2	2.03	0.41
1:E:170:CYS:HA	1:E:308:SER:HB2	2.03	0.41
1:E:227:GLY:O	1:E:230:LYS:HG2	2.20	0.41
1:A:180:LYS:C	1:A:182:ASN:H	2.28	0.41
1:A:190:MET:O	1:A:190:MET:HE3	2.20	0.41
1:A:261:THR:HG22	1:D:326:PHE:HZ	1.86	0.41
1:A:318:ASN:CG	1:D:246:MET:HB3	2.45	0.41
1:B:289:LEU:HD23	1:B:308:SER:O	2.21	0.41
1:B:356:ALA:C	1:B:358:SER:N	2.78	0.41
1:D:73:GLU:CD	1:D:74:THR:H	2.28	0.41
1:D:290:GLY:O	1:D:309:VAL:HA	2.21	0.41
1:E:178:LEU:O	1:E:183:PHE:HB2	2.21	0.41
1:F:24:GLN:HB3	1:F:26:LEU:HD13	2.02	0.41
1:F:130:LYS:HE3	1:F:354:ASP:CG	2.45	0.41
1:F:200:GLN:OE1	1:F:249:ARG:NH1	2.54	0.41
1:F:320:LEU:HA	1:F:321:PRO:HD2	1.78	0.41
1:E:178:LEU:HD23	1:E:178:LEU:HA	1.89	0.41
1:B:295:GLU:HB3	1:C:212:ARG:HG2	2.02	0.40
1:C:24:GLN:HB2	1:C:26:LEU:HD13	2.03	0.40
1:D:27:ILE:HG23	1:D:27:ILE:O	2.21	0.40
1:D:250:VAL:HA	1:D:251:PRO:HD3	1.85	0.40
1:E:69:SER:C	1:E:71:SER:N	2.80	0.40
1:E:266:ARG:HG3	1:E:266:ARG:HH11	1.86	0.40
1:F:335:ASN:OD1	1:F:335:ASN:N	2.53	0.40
1:D:88:VAL:HG12	1:D:89:LYS:N	2.36	0.40
1:E:170:CYS:O	1:E:173:PRO:HD2	2.21	0.40
1:D:268:THR:O	1:D:324:LYS:HA	2.21	0.40
1:A:149:ASN:HA	1:A:151:HIS:CE1	2.56	0.40
1:C:266:ARG:HH11	1:C:266:ARG:HG3	1.86	0.40
1:E:18:PHE:CD2	1:E:50:MET:HE1	2.56	0.40
1:C:283:THR:OG1	1:C:284:TYR:N	2.54	0.40
1:D:12:ARG:O	1:D:16:MET:HG2	2.21	0.40
1:D:124:ILE:HA	1:D:128:ALA:O	2.21	0.40
1:F:63:VAL:HG12	1:F:64:GLU:N	2.36	0.40
1:F:282:GLN:HE21	1:F:282:GLN:HB2	1.63	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	356/360 (99%)	311 (87%)	41 (12%)	4 (1%)	11	43
1	B	356/360 (99%)	320 (90%)	32 (9%)	4 (1%)	11	43
1	C	356/360 (99%)	314 (88%)	39 (11%)	3 (1%)	16	50
1	D	356/360 (99%)	317 (89%)	37 (10%)	2 (1%)	21	56
1	E	356/360 (99%)	313 (88%)	39 (11%)	4 (1%)	11	43
1	F	356/360 (99%)	315 (88%)	34 (10%)	7 (2%)	6	28
All	All	2136/2160 (99%)	1890 (88%)	222 (10%)	24 (1%)	11	43

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	204	ASP
1	A	255	VAL
1	B	251	PRO
1	B	255	VAL
1	A	335	ASN
1	C	255	VAL
1	D	251	PRO
1	D	255	VAL
1	E	255	VAL
1	F	204	ASP
1	F	255	VAL
1	F	298	SER
1	A	204	ASP
1	B	216	ALA
1	C	204	ASP
1	E	185	ILE
1	E	244	THR
1	F	251	PRO
1	F	335	ASN
1	C	185	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	185	ILE
1	F	70	PRO
1	F	219	VAL
1	A	70	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	294/296 (99%)	283 (96%)	11 (4%)	30	64
1	B	294/296 (99%)	283 (96%)	11 (4%)	30	64
1	C	294/296 (99%)	280 (95%)	14 (5%)	23	57
1	D	294/296 (99%)	283 (96%)	11 (4%)	30	64
1	E	294/296 (99%)	282 (96%)	12 (4%)	27	61
1	F	294/296 (99%)	283 (96%)	11 (4%)	30	64
All	All	1764/1776 (99%)	1694 (96%)	70 (4%)	28	62

All (70) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	58	ARG
1	A	71	SER
1	A	73	GLU
1	A	78	LEU
1	A	86	LYS
1	A	177	VAL
1	A	190	MET
1	A	215	ARG
1	A	289	LEU
1	A	305	ASN
1	A	309	VAL
1	B	58	ARG
1	B	71	SER
1	B	73	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	78	LEU
1	B	177	VAL
1	B	190	MET
1	B	215	ARG
1	B	243	LEU
1	B	289	LEU
1	B	305	ASN
1	B	309	VAL
1	C	5	VAL
1	C	58	ARG
1	C	71	SER
1	C	73	GLU
1	C	78	LEU
1	C	86	LYS
1	C	177	VAL
1	C	190	MET
1	C	215	ARG
1	C	243	LEU
1	C	289	LEU
1	C	305	ASN
1	C	309	VAL
1	C	335	ASN
1	D	58	ARG
1	D	73	GLU
1	D	78	LEU
1	D	86	LYS
1	D	177	VAL
1	D	201	LYS
1	D	215	ARG
1	D	243	LEU
1	D	289	LEU
1	D	305	ASN
1	D	309	VAL
1	E	13	ILE
1	E	58	ARG
1	E	71	SER
1	E	86	LYS
1	E	177	VAL
1	E	190	MET
1	E	201	LYS
1	E	215	ARG
1	E	243	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	289	LEU
1	E	305	ASN
1	E	335	ASN
1	F	58	ARG
1	F	73	GLU
1	F	78	LEU
1	F	86	LYS
1	F	166	CYS
1	F	177	VAL
1	F	190	MET
1	F	289	LEU
1	F	305	ASN
1	F	309	VAL
1	F	335	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	83	HIS
1	A	93	ASN
1	A	176	HIS
1	A	282	GLN
1	A	305	ASN
1	A	341	HIS
1	B	81	ASN
1	B	93	ASN
1	B	163	ASN
1	B	176	HIS
1	B	282	GLN
1	B	305	ASN
1	C	49	GLN
1	C	159	HIS
1	C	163	ASN
1	C	176	HIS
1	C	282	GLN
1	C	303	ASN
1	C	305	ASN
1	D	49	GLN
1	D	83	HIS
1	D	163	ASN
1	D	282	GLN
1	D	305	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	341	HIS
1	E	52	HIS
1	E	93	ASN
1	E	176	HIS
1	E	282	GLN
1	E	305	ASN
1	F	52	HIS
1	F	93	ASN
1	F	176	HIS
1	F	282	GLN
1	F	305	ASN

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](#)

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	TND	C	363	-	46,46,46	3.10	15 (32%)	61,66,66	0.94	2 (3%)
2	TND	F	366	-	46,46,46	3.34	15 (32%)	61,66,66	0.93	2 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	TND	A	361	-	46,46,46	3.09	17 (36%)	61,66,66	1.04	3 (4%)
2	TND	E	365	-	46,46,46	3.21	15 (32%)	61,66,66	0.91	2 (3%)
2	TND	B	362	-	46,46,46	3.19	15 (32%)	61,66,66	0.85	1 (1%)
2	TND	D	364	-	46,46,46	3.14	15 (32%)	61,66,66	0.88	1 (1%)

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
2	TND	C	363	-	-	5/22/48/48	0/6/6/6
2	TND	F	366	-	-	5/22/48/48	0/6/6/6
2	TND	A	361	-	-	5/22/48/48	0/6/6/6
2	TND	E	365	-	-	5/22/48/48	0/6/6/6
2	TND	B	362	-	-	5/22/48/48	0/6/6/6
2	TND	D	364	-	-	5/22/48/48	0/6/6/6

All (92) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	363	TND	C8-C9	10.14	1.52	1.39
2	F	366	TND	C8-C9	10.10	1.52	1.39
2	B	362	TND	C8-C9	10.03	1.51	1.39
2	D	364	TND	C8-C9	9.84	1.51	1.39
2	E	365	TND	C8-C9	9.80	1.51	1.39
2	A	361	TND	C8-C9	9.60	1.51	1.39
2	D	364	TND	C10-C9	8.00	1.53	1.40
2	B	362	TND	C5-C10	7.97	1.52	1.39
2	F	366	TND	C10-C9	7.90	1.53	1.40
2	E	365	TND	C5-C10	7.62	1.52	1.39
2	B	362	TND	C10-C9	7.57	1.52	1.40
2	F	366	TND	C5-C10	7.55	1.51	1.39
2	E	365	TND	C10-C9	7.50	1.52	1.40
2	C	363	TND	C10-C9	7.46	1.52	1.40
2	F	366	TND	C7-C8	7.33	1.51	1.38
2	F	366	TND	C6-C5	7.31	1.51	1.38
2	C	363	TND	C6-C5	7.25	1.51	1.38
2	B	362	TND	C6-C5	7.24	1.51	1.38
2	A	361	TND	C5-C10	7.19	1.51	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	363	TND	C5-C10	7.08	1.51	1.39
2	A	361	TND	C6-C5	7.06	1.51	1.38
2	E	365	TND	C7-C8	7.05	1.51	1.38
2	B	362	TND	C7-C8	7.00	1.50	1.38
2	D	364	TND	C5-C10	6.96	1.50	1.39
2	D	364	TND	C7-C8	6.92	1.50	1.38
2	E	365	TND	C6-C5	6.88	1.50	1.38
2	A	361	TND	C7-C8	6.87	1.50	1.38
2	C	363	TND	C7-C8	6.83	1.50	1.38
2	D	364	TND	C6-C5	6.80	1.50	1.38
2	A	361	TND	C10-C9	6.57	1.50	1.40
2	A	361	TND	C6-C7	5.76	1.50	1.38
2	F	366	TND	C6-C7	5.75	1.50	1.38
2	C	363	TND	C6-C7	5.63	1.50	1.38
2	B	362	TND	C6-C7	5.60	1.50	1.38
2	D	364	TND	C6-C7	5.56	1.50	1.38
2	E	365	TND	C6-C7	5.52	1.50	1.38
2	B	362	TND	C3B-C2B	4.52	1.46	1.39
2	F	366	TND	C3B-C2B	4.43	1.46	1.39
2	E	365	TND	C3B-C2B	4.28	1.46	1.39
2	F	366	TND	C5B-C4B	4.21	1.45	1.39
2	D	364	TND	C9-C1	4.18	1.56	1.52
2	A	361	TND	C3B-C2B	4.17	1.45	1.39
2	D	364	TND	C3B-C2B	4.17	1.45	1.39
2	C	363	TND	C3B-C2B	4.14	1.45	1.39
2	F	366	TND	C1B-C6B	3.92	1.45	1.39
2	E	365	TND	C5B-C4B	3.84	1.45	1.39
2	A	361	TND	C5B-C4B	3.75	1.45	1.39
2	F	366	TND	C3B-C4B	3.63	1.45	1.39
2	E	365	TND	C3B-C4B	3.54	1.44	1.39
2	F	366	TND	C5B-C6B	3.53	1.44	1.39
2	C	363	TND	C3B-C4B	3.50	1.44	1.39
2	E	365	TND	C9-C1	3.49	1.55	1.52
2	E	365	TND	C1B-C2B	3.49	1.44	1.39
2	E	365	TND	C1B-C6B	3.49	1.44	1.39
2	F	366	TND	C9-C1	3.44	1.55	1.52
2	F	366	TND	C1B-C2B	3.44	1.44	1.39
2	A	361	TND	C1B-C6B	3.37	1.44	1.39
2	C	363	TND	C5B-C4B	3.33	1.44	1.39
2	B	362	TND	C3B-C4B	3.28	1.44	1.39
2	D	364	TND	C3B-C4B	3.26	1.44	1.39
2	D	364	TND	C1B-C6B	3.25	1.44	1.39

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	364	TND	C1B-C2B	3.16	1.44	1.39
2	A	361	TND	C3B-C4B	3.16	1.44	1.39
2	D	364	TND	C5B-C4B	3.08	1.44	1.39
2	A	361	TND	C5B-C6B	3.05	1.44	1.39
2	B	362	TND	C1B-C6B	3.03	1.44	1.39
2	C	363	TND	C1B-C6B	3.02	1.44	1.39
2	B	362	TND	C5B-C4B	2.97	1.43	1.39
2	B	362	TND	C1B-C2B	2.97	1.43	1.39
2	B	362	TND	C9-C1	2.96	1.54	1.52
2	C	363	TND	C5B-C6B	2.90	1.43	1.39
2	A	361	TND	C1B-C2B	2.87	1.43	1.39
2	B	362	TND	C4-C10	2.87	1.56	1.51
2	F	366	TND	C4-C10	2.82	1.55	1.51
2	E	365	TND	C4-C10	2.81	1.55	1.51
2	B	362	TND	C5B-C6B	2.76	1.43	1.39
2	E	365	TND	C5B-C6B	2.76	1.43	1.39
2	B	362	TND	C6A-N1A	2.75	1.39	1.35
2	C	363	TND	C1B-C2B	2.70	1.43	1.39
2	D	364	TND	C5B-C6B	2.68	1.43	1.39
2	C	363	TND	C4-C10	2.67	1.55	1.51
2	D	364	TND	C4-C10	2.65	1.55	1.51
2	A	361	TND	C9-C1	2.53	1.54	1.52
2	E	365	TND	C6A-N1A	2.51	1.38	1.35
2	A	361	TND	C2-C1	2.26	1.56	1.53
2	F	366	TND	C6A-N1A	2.23	1.38	1.35
2	A	361	TND	C6A-N1A	2.19	1.38	1.35
2	C	363	TND	C9-C1	2.18	1.54	1.52
2	D	364	TND	C6A-N1A	2.14	1.38	1.35
2	A	361	TND	C3-C2	2.13	1.58	1.53
2	A	361	TND	C1-N6A	2.11	1.48	1.45
2	C	363	TND	C6A-N1A	2.03	1.38	1.35

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	361	TND	C10-C9-C1	-2.95	117.84	121.38
2	C	363	TND	C2B-C3B-C4B	2.28	121.76	118.48
2	F	366	TND	C2B-C3B-C4B	2.23	121.69	118.48
2	A	361	TND	C2B-C3B-C4B	2.21	121.67	118.48
2	B	362	TND	C2B-C3B-C4B	2.21	121.66	118.48
2	E	365	TND	C2B-C3B-C4B	2.20	121.65	118.48
2	F	366	TND	C10-C9-C1	-2.15	118.80	121.38

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	361	TND	C2-C3-C4	2.13	116.42	110.69
2	C	363	TND	C3B-C4B-C5B	-2.10	117.79	120.98
2	D	364	TND	C2B-C3B-C4B	2.08	121.48	118.48
2	E	365	TND	C2'-N2'-C7B	2.01	125.56	122.42

There are no chirality outliers.

All (30) torsion outliers are listed below:

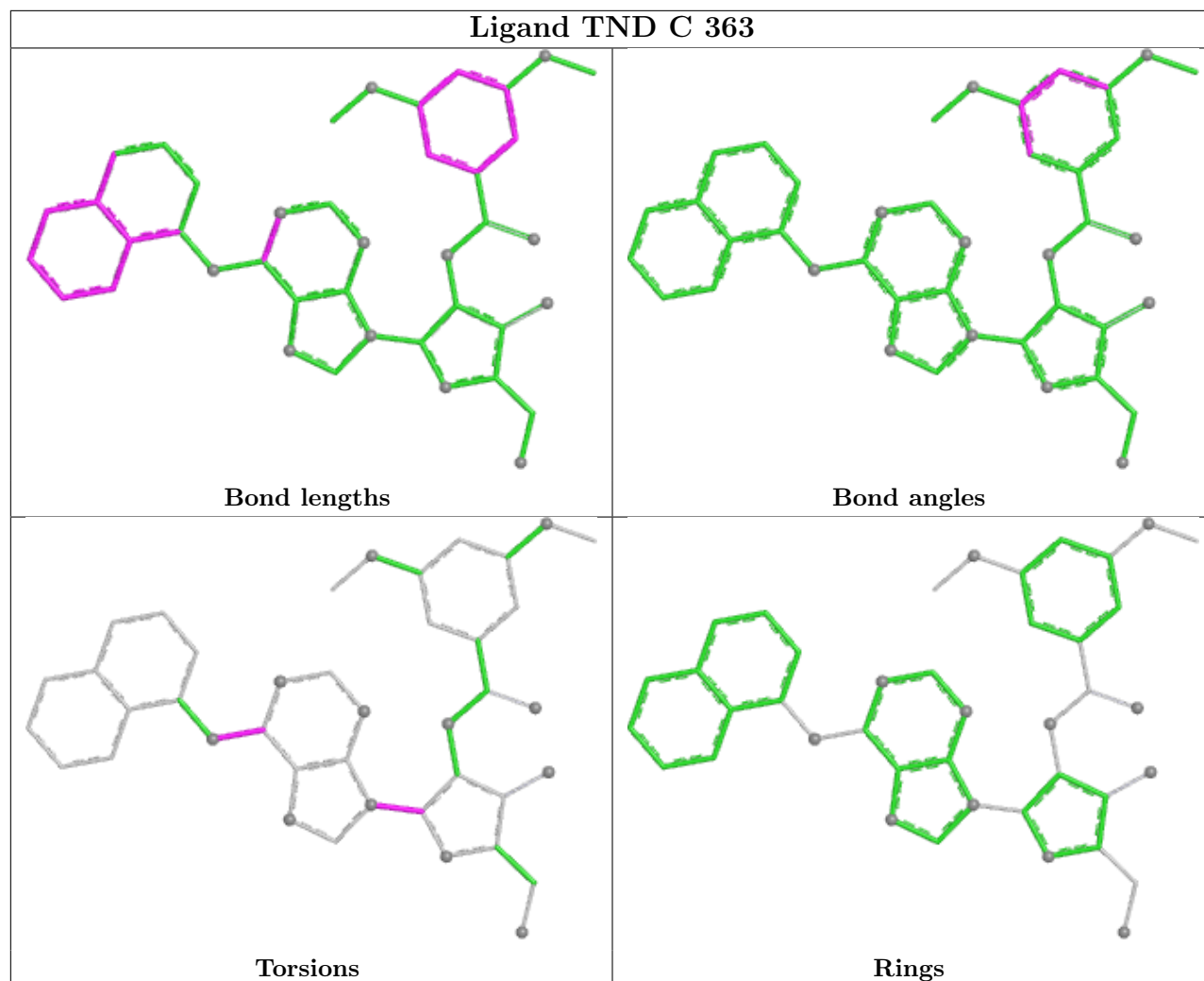
Mol	Chain	Res	Type	Atoms
2	A	361	TND	C5A-C6A-N6A-C1
2	B	362	TND	C5A-C6A-N6A-C1
2	E	365	TND	C5A-C6A-N6A-C1
2	A	361	TND	N1A-C6A-N6A-C1
2	B	362	TND	N1A-C6A-N6A-C1
2	D	364	TND	N1A-C6A-N6A-C1
2	E	365	TND	N1A-C6A-N6A-C1
2	F	366	TND	N1A-C6A-N6A-C1
2	B	362	TND	C2'-C1'-N9A-C8A
2	C	363	TND	C2'-C1'-N9A-C8A
2	E	365	TND	C2'-C1'-N9A-C8A
2	F	366	TND	C2'-C1'-N9A-C8A
2	C	363	TND	C5A-C6A-N6A-C1
2	D	364	TND	C5A-C6A-N6A-C1
2	F	366	TND	C5A-C6A-N6A-C1
2	C	363	TND	N1A-C6A-N6A-C1
2	A	361	TND	C2'-C1'-N9A-C8A
2	D	364	TND	C2'-C1'-N9A-C8A
2	B	362	TND	C2'-C1'-N9A-C4A
2	C	363	TND	C2'-C1'-N9A-C4A
2	E	365	TND	C2'-C1'-N9A-C4A
2	F	366	TND	C2'-C1'-N9A-C4A
2	A	361	TND	O4'-C1'-N9A-C8A
2	D	364	TND	C2'-C1'-N9A-C4A
2	D	364	TND	O4'-C1'-N9A-C8A
2	F	366	TND	O4'-C1'-N9A-C8A
2	C	363	TND	O4'-C1'-N9A-C8A
2	A	361	TND	C2'-C1'-N9A-C4A
2	B	362	TND	O4'-C1'-N9A-C8A
2	E	365	TND	O4'-C1'-N9A-C8A

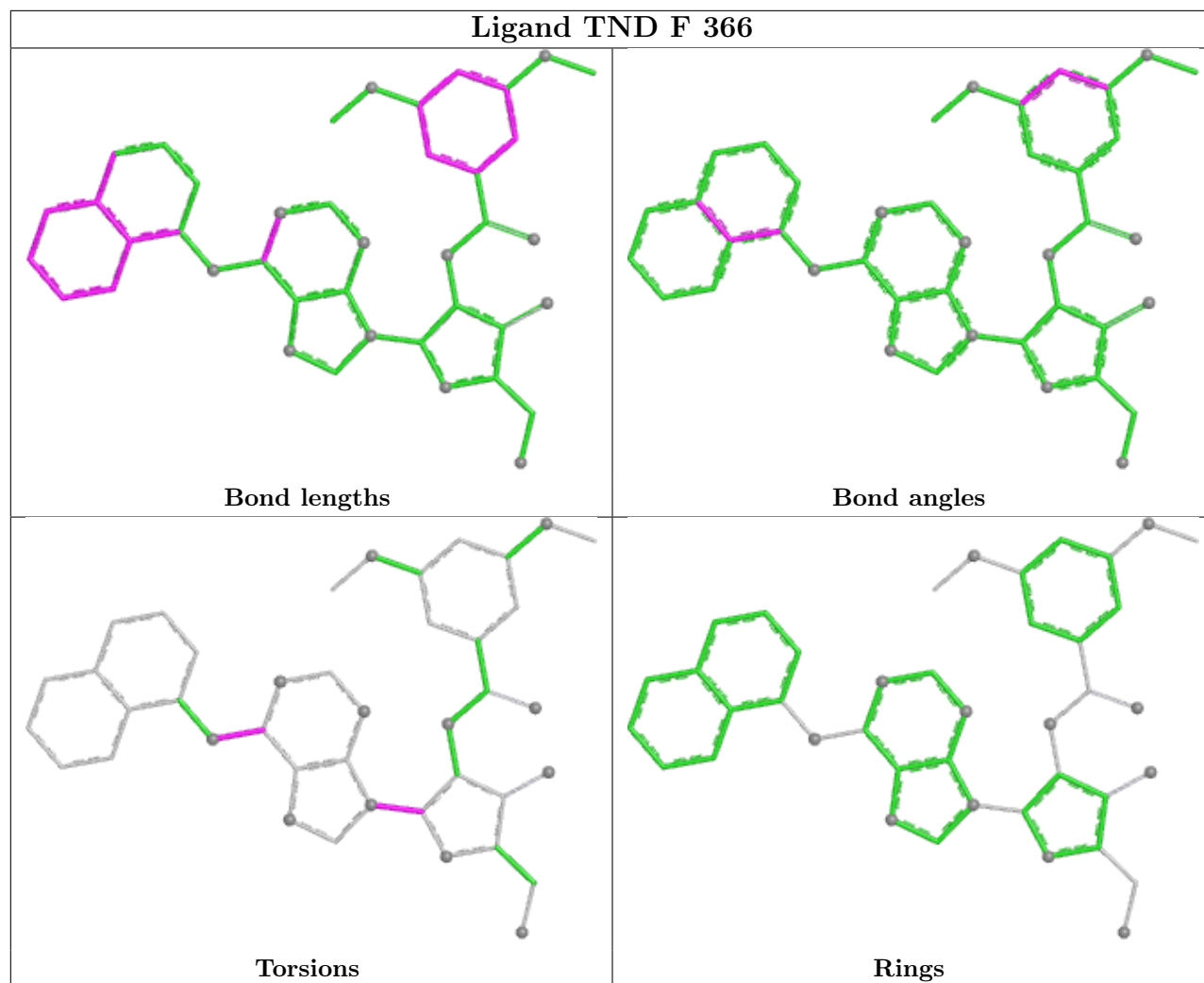
There are no ring outliers.

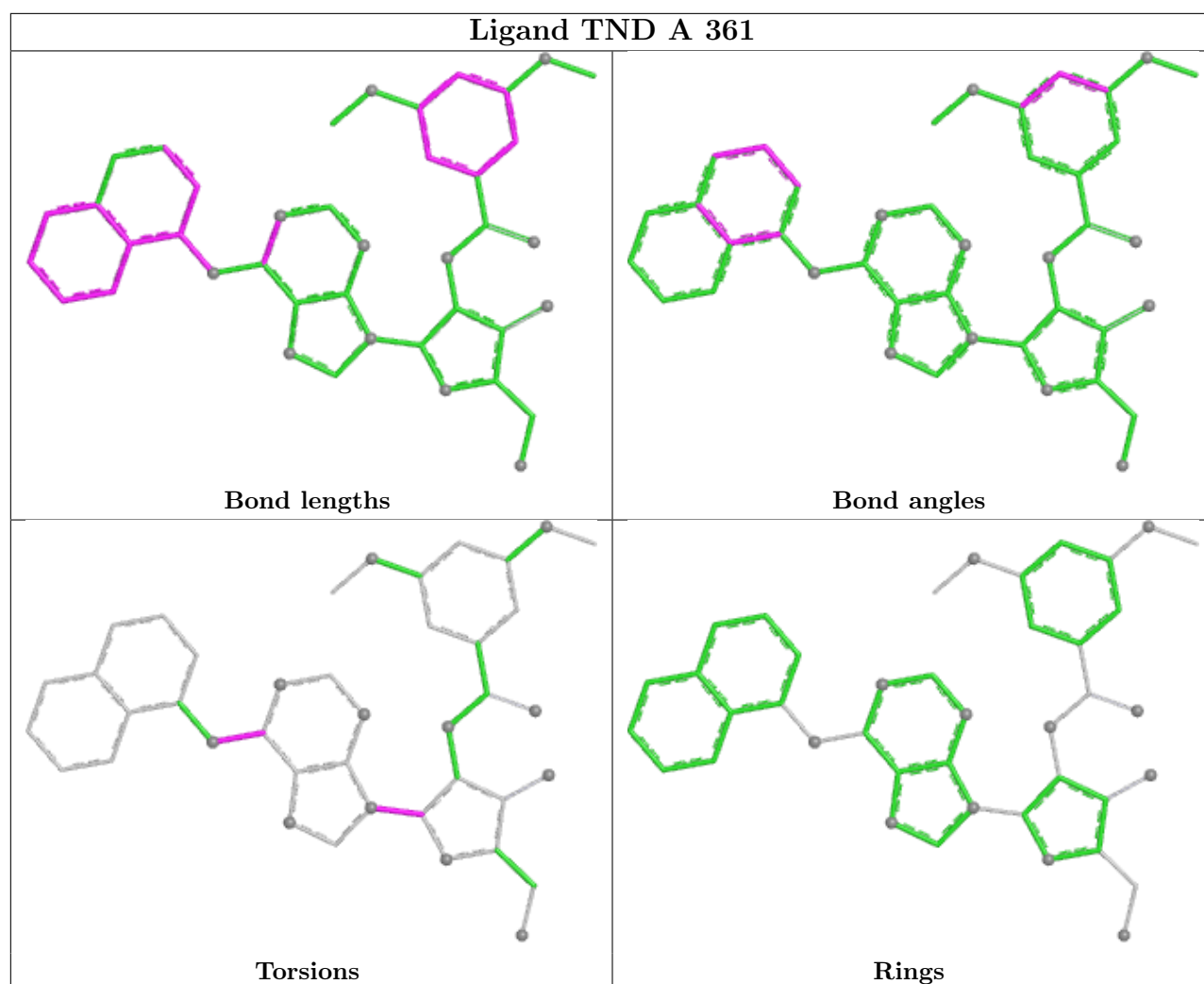
5 monomers are involved in 15 short contacts:

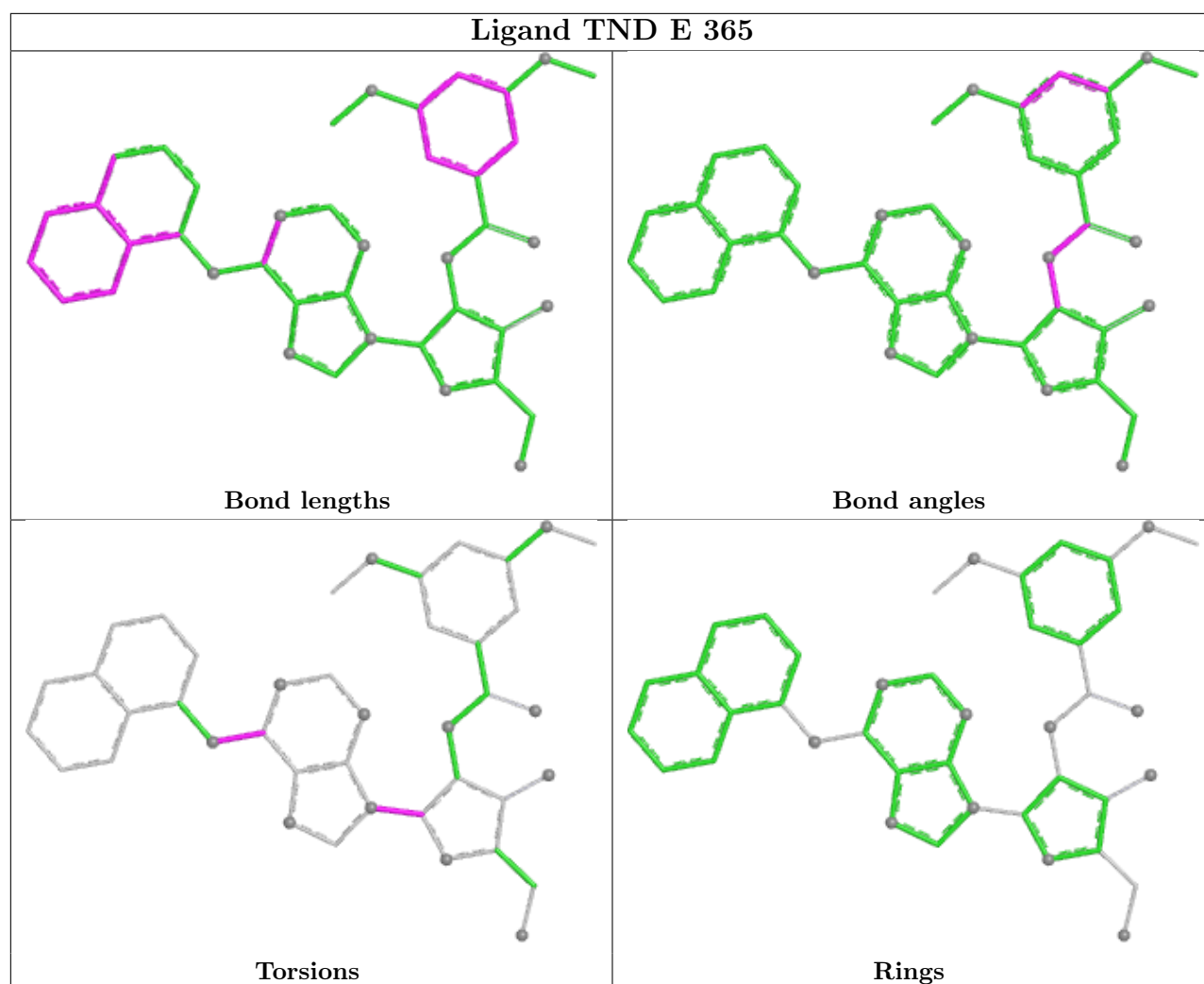
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	363	TND	4	0
2	F	366	TND	2	0
2	E	365	TND	4	0
2	B	362	TND	3	0
2	D	364	TND	2	0

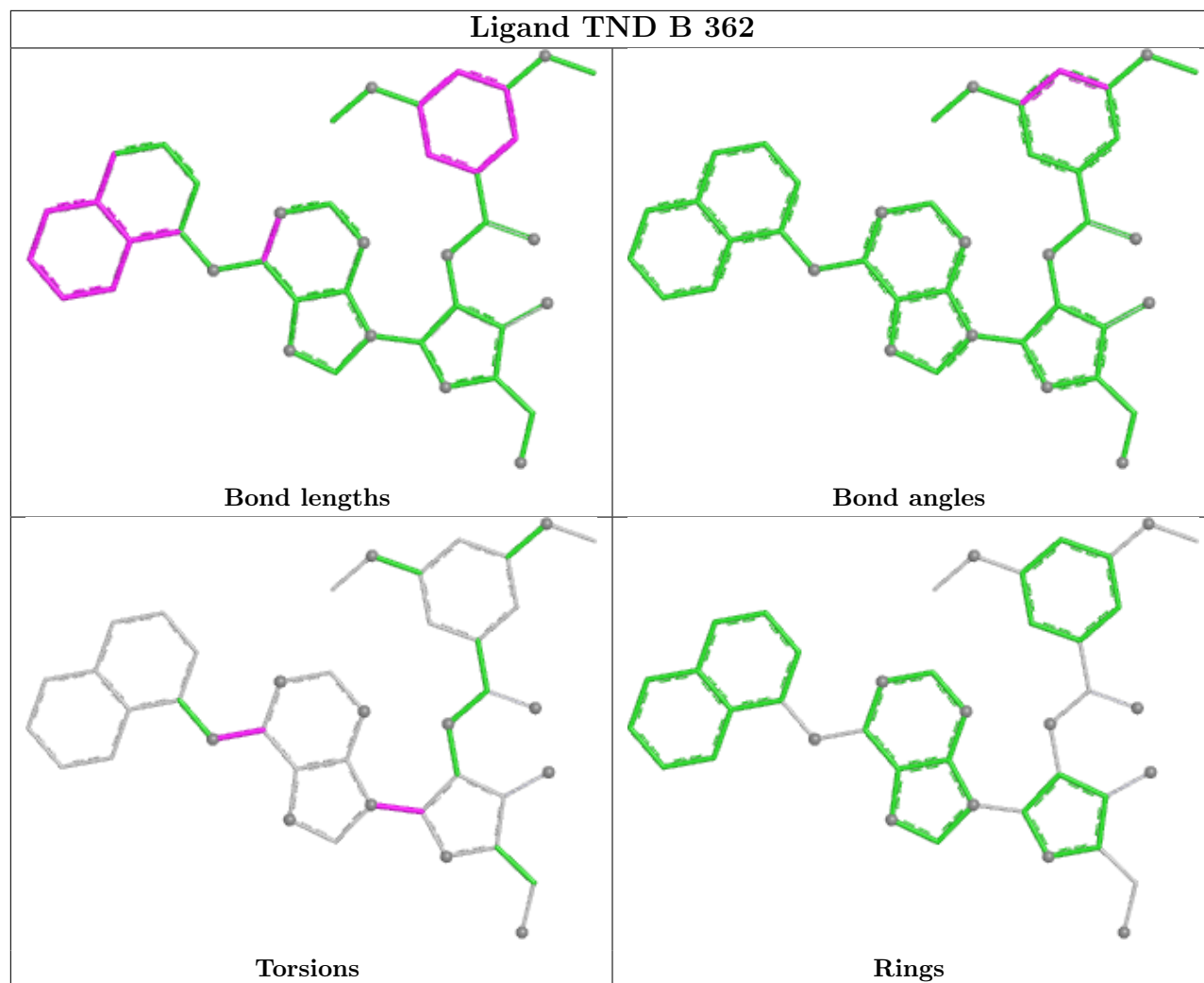
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

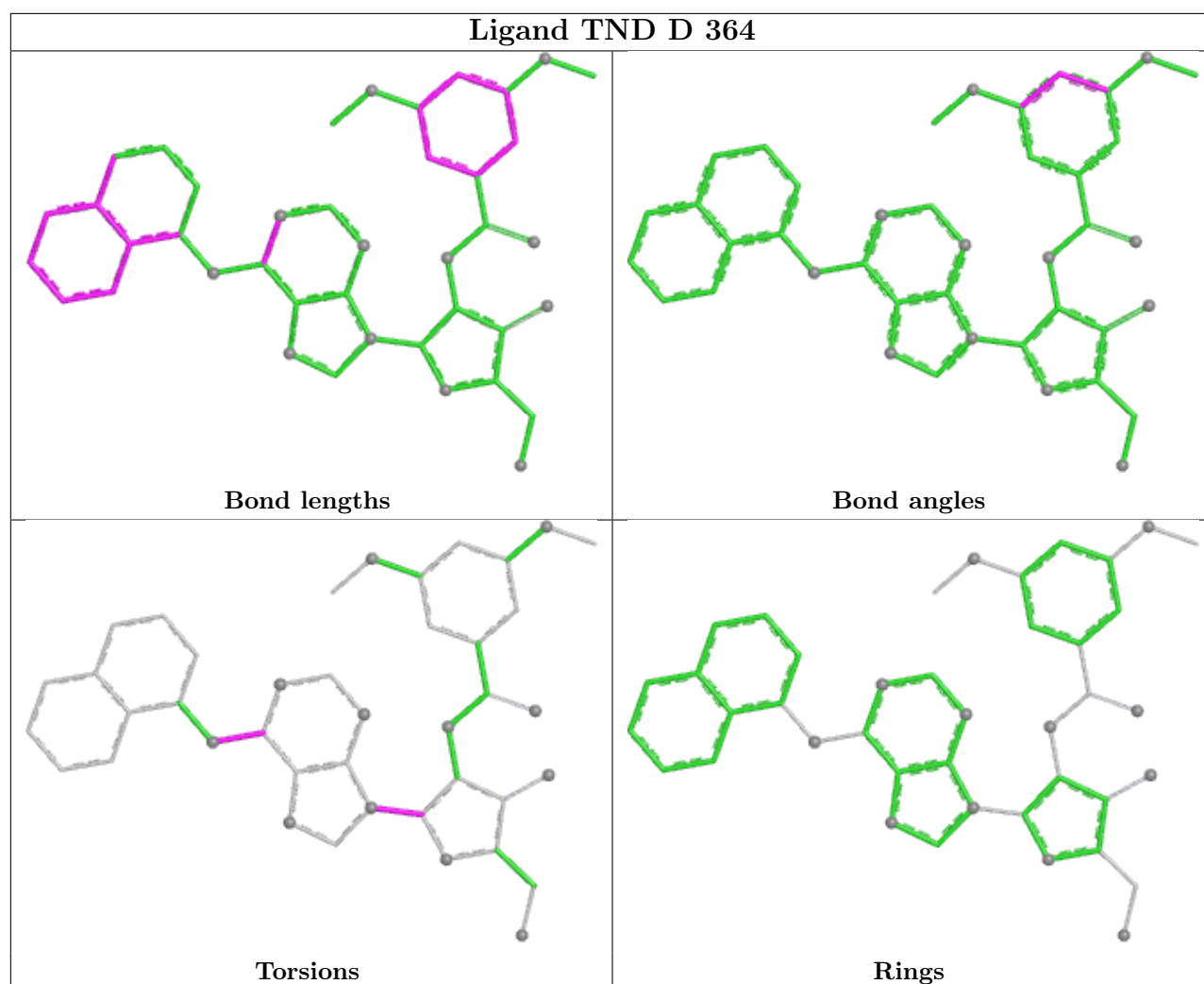












5.7 Other polymers [i](#)

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.