



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 07:36 AM GMT

PDB ID : 2F1O
Title : Crystal Structure of NQO1 with Dicoumarol
Authors : Shaul, Y.; Asher, G.; Dym, O.; Tsvetkov, P.; Adler, J.; Israel Structural Proteomics Center (ISPC)
Deposited on : 2005-11-15
Resolution : 2.75 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

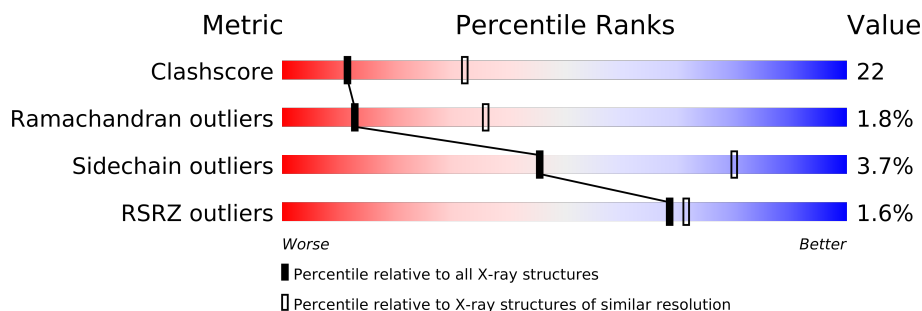
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.75 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	79885	2995 (2.80-2.72)
Ramachandran outliers	78287	2941 (2.80-2.72)
Sidechain outliers	78261	2944 (2.80-2.72)
RSRZ outliers	66119	2409 (2.80-2.72)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	273	
1	B	273	
1	C	273	
1	D	273	
1	E	273	
1	F	273	
1	G	273	
1	H	273	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	DTC	A	2280	-	X
2	DTC	B	3280	-	X
2	DTC	C	280	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
2	DTC	D	1280	-	X
2	DTC	E	4280	-	X
2	DTC	E	5280	-	X
2	DTC	H	6280	-	X

2 Entry composition

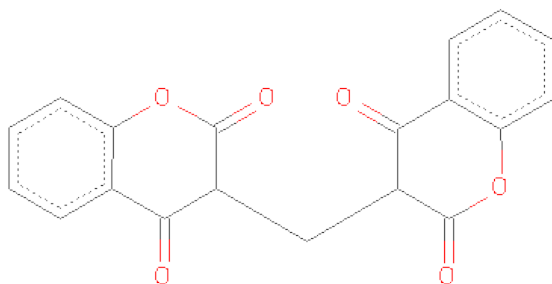
There are 4 unique types of molecules in this entry. The entry contains 18146 atoms, of which 0 are hydrogen and 0 are deuterium.

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 NAD(P)H dehydrogenase [quinone] 1.

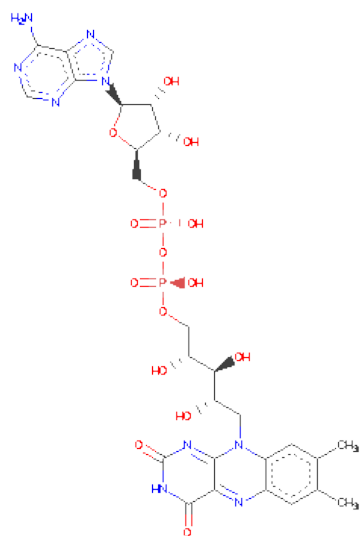
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	B	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	C	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	D	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	E	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	F	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	G	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			
1	H	273	Total	C	N	O	S	0	0	0
			2175	1414	365	389	7			

- Molecule 2 is BISHYDROXY[2H-1-BENZOPYRAN-2-ONE,1,2-BENZOPYRONE] (three-letter code: DTC) (formula: C₁₉H₁₂O₆).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			25	19	6		
2	B	1	Total	C	O	0	0
			25	19	6		
2	C	1	Total	C	O	0	0
			25	19	6		
2	D	1	Total	C	O	0	0
			25	19	6		
2	E	1	Total	C	O	0	0
			25	19	6		
2	E	1	Total	C	O	0	0
			25	19	6		
2	G	1	Total	C	O	0	0
			25	19	6		
2	H	1	Total	C	O	0	0
			25	19	6		

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	B	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	C	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	D	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	E	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	F	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	G	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
3	H	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	19	Total	O	0	0
			19	19		
4	B	23	Total	O	0	0
			23	23		
4	C	23	Total	O	0	0
			23	23		
4	D	13	Total	O	0	0
			13	13		

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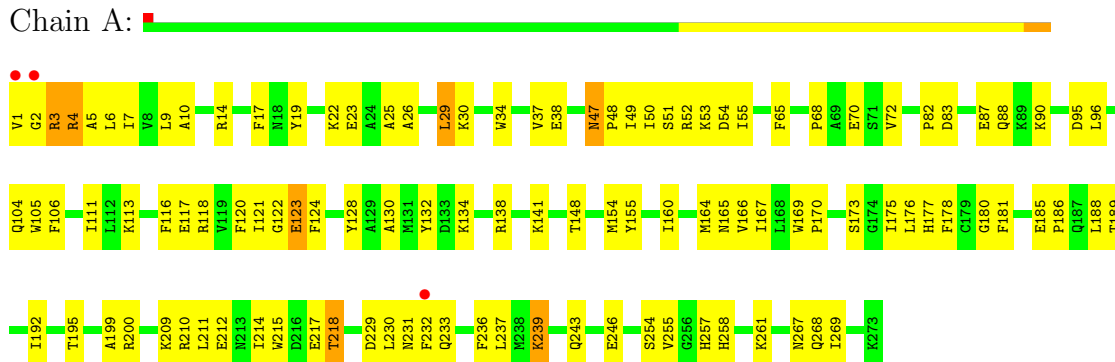
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	18	Total 18	O 18	0	0
4	F	10	Total 10	O 10	0	0
4	G	8	Total 8	O 8	0	0
4	H	8	Total 8	O 8	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

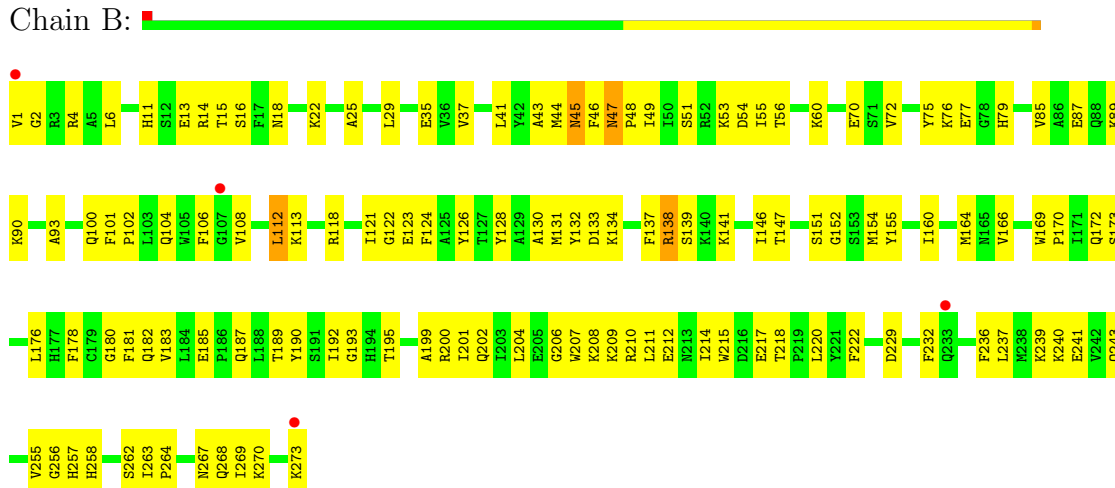
- Molecule 1: NAD(P)H dehydrogenase [quinone] 1

Chain A:



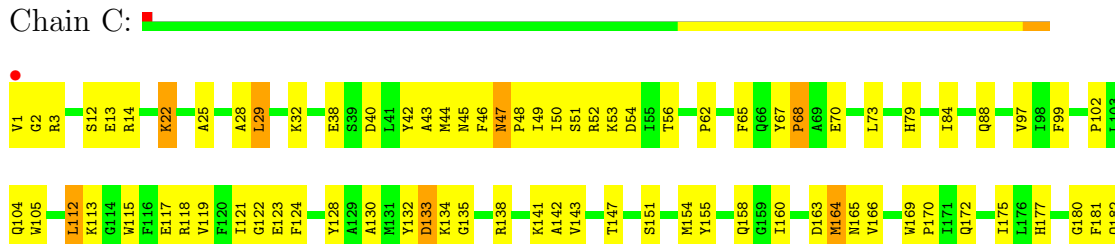
- Molecule 1: NAD(P)H dehydrogenase [quinone] 1

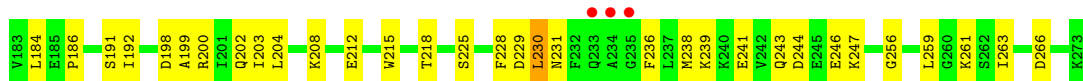
Chain B:



- Molecule 1: NAD(P)H dehydrogenase [quinone] 1

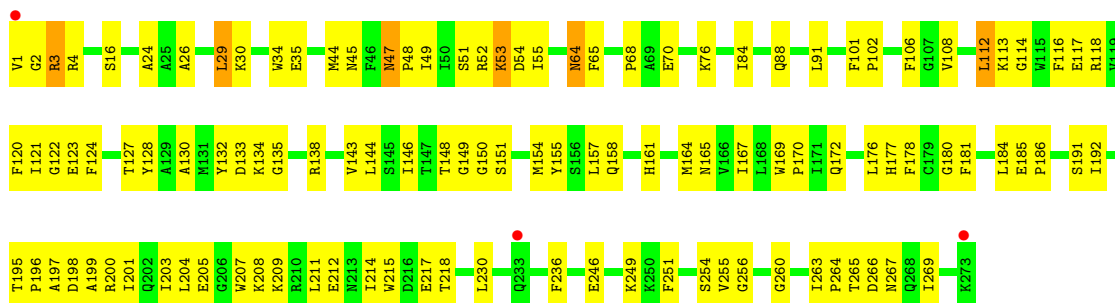
Chain C:





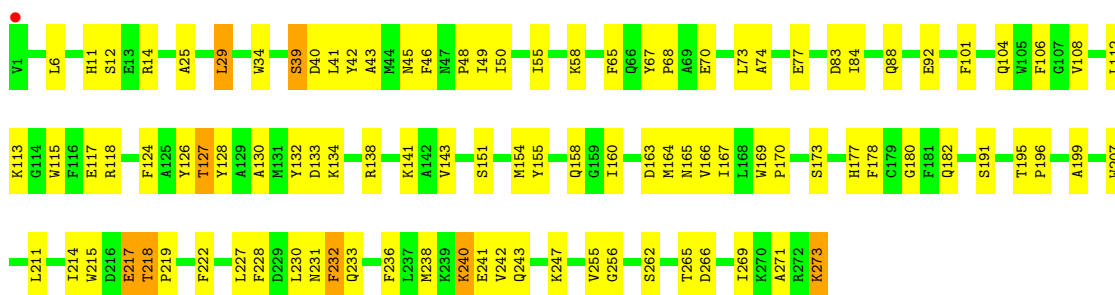
• Molecule 1: NAD(P)H dehydrogenase [quinone] 1

Chain D:



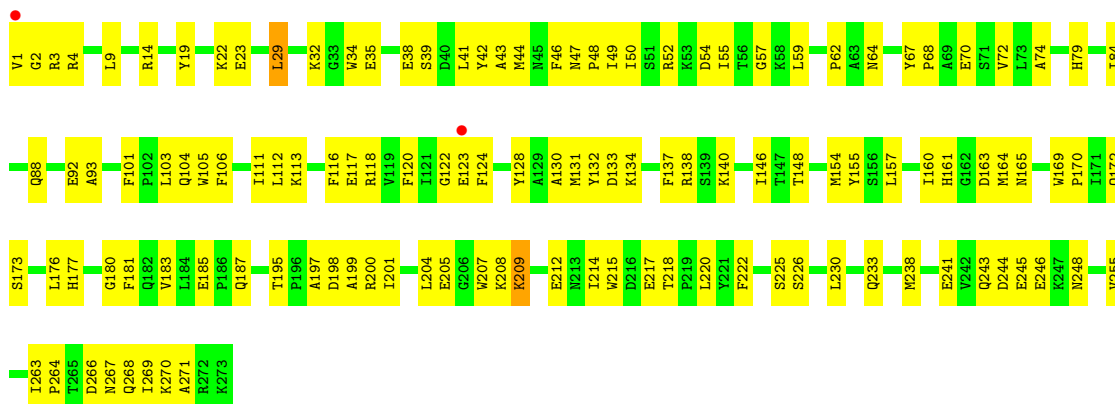
• Molecule 1: NAD(P)H dehydrogenase [quinone] 1

Chain E:



• Molecule 1: NAD(P)H dehydrogenase [quinone] 1

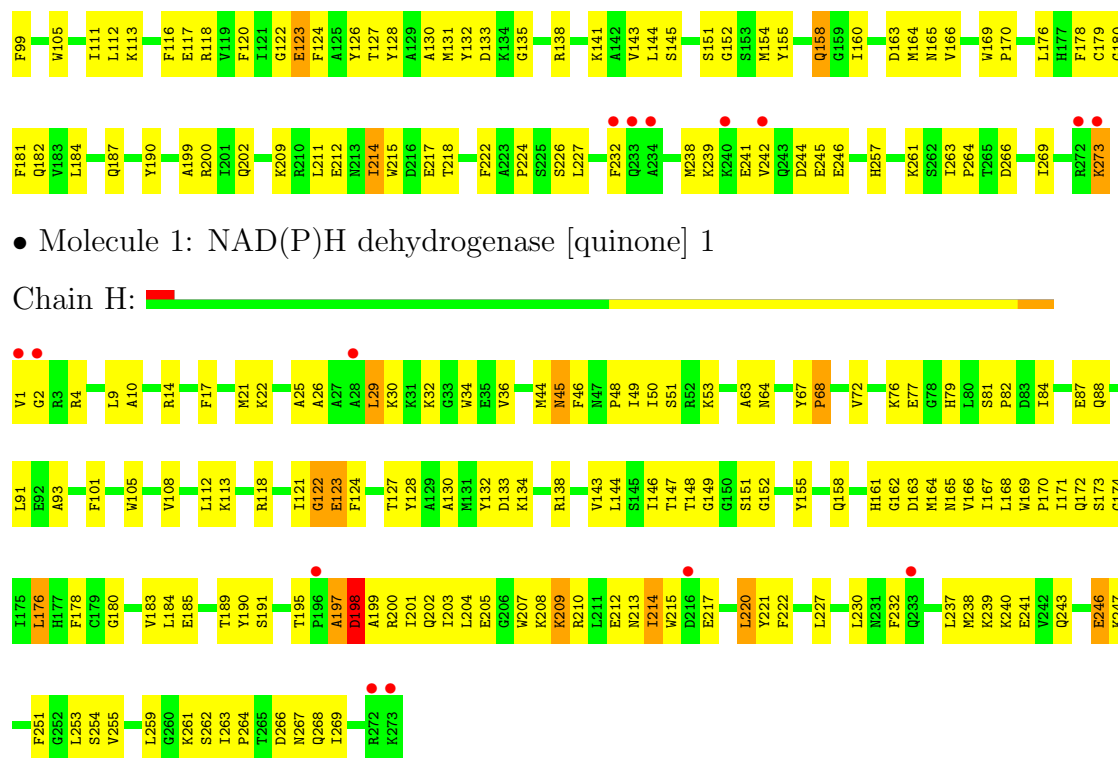
Chain F:



• Molecule 1: NAD(P)H dehydrogenase [quinone] 1

Chain G:





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	76.24Å 86.19Å 100.56Å 91.14° 107.91° 93.17°	Depositor
Resolution (Å)	38.66 – 2.75 38.66 – 2.70	Depositor EDS
% Data completeness (in resolution range)	(Not available) (38.66-2.75) 95.1 (38.66-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.02 (at 2.69Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.219 , 0.282 0.228 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	37.6	Xtriage
Anisotropy	0.311	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 13.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 63333 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	18146	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 11.12% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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	0/2233	0.65	0/3015
1	B	0.42	0/2233	0.67	0/3015
1	C	0.41	0/2233	0.64	1/3015 (0.0%)
1	D	0.40	0/2233	0.66	0/3015
1	E	0.45	0/2233	0.65	1/3015 (0.0%)
1	F	0.41	0/2233	0.62	0/3015
1	G	0.40	0/2233	0.64	0/3015
1	H	0.41	0/2233	0.64	0/3015
All	All	0.41	0/17864	0.65	2/24120 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	182	GLN	N-CA-C	-5.24	96.86	111.00
1	C	182	GLN	N-CA-C	-5.19	96.98	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2175	0	2179	94	0
1	B	2175	0	2179	125	0
1	C	2175	0	2179	100	0
1	D	2175	0	2179	116	0
1	E	2175	0	2179	76	0
1	F	2175	0	2179	110	0
1	G	2175	0	2179	97	0
1	H	2175	0	2179	129	0
2	A	25	0	10	1	0
2	B	25	0	10	1	0
2	C	25	0	10	2	0
2	D	25	0	10	1	0
2	E	50	0	20	3	0
2	G	25	0	10	5	0
2	H	25	0	10	3	0
3	A	53	0	31	4	0
3	B	53	0	31	5	0
3	C	53	0	31	6	0
3	D	53	0	31	4	0
3	E	53	0	31	2	0
3	F	53	0	31	2	0
3	G	53	0	31	2	0
3	H	53	0	31	5	0
4	A	19	0	0	1	0
4	B	23	0	0	2	0
4	C	23	0	0	4	0
4	D	13	0	0	1	0
4	E	18	0	0	1	0
4	F	10	0	0	2	0
4	G	8	0	0	0	0
4	H	8	0	0	2	0
All	All	18146	0	17760	788	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 22.

All (788) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:255:VAL:HG23	1:B:267:ASN:HD22	1.05	1.17
1:D:151:SER:H	1:D:154:MET:HE3	1.07	1.15
1:D:47:ASN:HD22	1:D:48:PRO:N	1.51	1.08
1:G:1:VAL:HG12	1:G:2:GLY:H	1.17	1.06
1:A:48:PRO:HG3	1:C:49:ILE:HD11	1.37	1.06

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:48:PRO:HG3	1:D:49:ILE:HD11	1.41	1.03
1:G:128:TYR:OH	2:G:7280:DTC:O16	1.76	1.01
1:H:50:ILE:HG22	1:H:118:ARG:HG2	1.45	0.98
1:F:14:ARG:HH21	1:F:43:ALA:HB2	1.25	0.98
1:F:255:VAL:HG23	1:F:267:ASN:HD22	1.28	0.94
1:F:238:MET:HE3	1:F:243:GLN:HG2	1.49	0.92
1:H:1:VAL:HG22	1:H:2:GLY:H	1.36	0.91
1:B:1:VAL:HG12	1:B:2:GLY:H	1.34	0.91
1:D:47:ASN:ND2	1:D:49:ILE:H	1.67	0.91
1:B:108:VAL:HB	1:B:112:LEU:HD12	1.52	0.90
1:D:47:ASN:HD21	1:D:49:ILE:H	1.19	0.89
1:B:255:VAL:HG23	1:B:267:ASN:ND2	1.87	0.89
1:D:108:VAL:HB	1:D:112:LEU:HD12	1.53	0.87
1:A:255:VAL:HG23	1:A:267:ASN:HD22	1.41	0.85
1:C:143:VAL:HG22	1:C:184:LEU:HB2	1.57	0.85
1:A:51:SER:OG	1:A:53:LYS:HG2	1.76	0.84
1:F:14:ARG:NH2	1:F:43:ALA:HB2	1.93	0.83
1:D:47:ASN:HD22	1:D:47:ASN:C	1.78	0.83
1:E:160:ILE:HD12	1:F:230:LEU:HD21	1.60	0.82
1:C:200:ARG:HH11	3:C:2301:FAD:H1B	1.45	0.81
1:A:50:ILE:HG22	1:A:118:ARG:HG2	1.61	0.81
1:A:49:ILE:HD11	1:C:48:PRO:HG3	1.62	0.81
1:D:76:LYS:HE2	1:D:123:GLU:HG3	1.62	0.81
1:D:1:VAL:HG12	1:D:2:GLY:H	1.45	0.81
1:H:255:VAL:HG23	1:H:267:ASN:HD22	1.46	0.80
1:E:48:PRO:HG3	1:F:49:ILE:HD11	1.63	0.80
1:A:47:ASN:ND2	1:A:49:ILE:H	1.79	0.80
1:G:72:VAL:HG22	1:G:122:GLY:O	1.82	0.80
1:B:255:VAL:H	1:B:267:ASN:ND2	1.80	0.80
1:G:1:VAL:HG12	1:G:2:GLY:N	1.97	0.80
1:A:47:ASN:HD22	1:A:47:ASN:C	1.84	0.80
1:G:48:PRO:HG3	1:H:49:ILE:HD11	1.64	0.80
1:A:3:ARG:HE	1:A:3:ARG:HA	1.45	0.79
1:H:14:ARG:HD2	1:H:14:ARG:N	1.97	0.79
1:F:50:ILE:HG22	1:F:118:ARG:HG2	1.63	0.79
1:H:239:LYS:O	1:H:243:GLN:HG3	1.83	0.79
1:B:138:ARG:HA	1:B:180:GLY:O	1.83	0.78
1:B:49:ILE:HD11	1:D:48:PRO:HG3	1.64	0.78
1:E:231:ASN:OD1	1:E:233:GLN:HG3	1.84	0.78
1:G:227:LEU:HB3	1:G:242:VAL:HG11	1.65	0.78
1:F:163:ASP:OD2	1:F:165:ASN:HB2	1.84	0.78
1:H:32:LYS:HE3	1:H:212:GLU:HB3	1.65	0.77

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:151:SER:H	1:D:154:MET:CE	1.91	0.77
1:E:238:MET:HE3	1:E:243:GLN:HG2	1.65	0.77
1:D:151:SER:N	1:D:154:MET:HE3	1.93	0.77
1:G:128:TYR:OH	2:G:7280:DTC:C6	2.33	0.77
1:D:200:ARG:HH11	3:D:3301:FAD:H1B	1.50	0.76
1:D:143:VAL:HG22	1:D:184:LEU:HB2	1.67	0.75
1:C:151:SER:OG	1:C:154:MET:HG3	1.85	0.75
1:H:143:VAL:HG22	1:H:184:LEU:HB2	1.68	0.75
1:F:1:VAL:HG22	1:F:2:GLY:H	1.50	0.75
1:E:138:ARG:HA	1:E:180:GLY:O	1.86	0.75
1:H:243:GLN:O	1:H:247:LYS:HG3	1.87	0.74
1:C:138:ARG:HA	1:C:180:GLY:O	1.88	0.74
1:G:214:ILE:HD12	1:G:217:GLU:OE2	1.87	0.74
1:D:113:LYS:O	1:D:117:GLU:HG3	1.88	0.73
1:D:138:ARG:HA	1:D:180:GLY:O	1.87	0.73
1:D:150:GLY:HA2	1:D:154:MET:HE1	1.71	0.72
1:E:49:ILE:HD11	1:F:48:PRO:HG3	1.70	0.72
1:A:237:LEU:HD22	1:C:158:GLN:HB2	1.71	0.72
1:G:209:LYS:O	1:G:212:GLU:HB2	1.88	0.72
1:E:160:ILE:HD12	1:F:230:LEU:CD2	2.19	0.72
1:B:47:ASN:ND2	1:B:49:ILE:H	1.88	0.72
1:A:47:ASN:HD22	1:A:48:PRO:N	1.88	0.71
1:F:176:LEU:O	1:F:181:PHE:HB2	1.89	0.71
1:E:166:VAL:HG11	1:F:169:TRP:CD1	2.25	0.71
1:H:214:ILE:O	1:H:217:GLU:HB2	1.89	0.71
1:H:155:TYR:HB3	1:H:164:MET:HB2	1.73	0.71
1:B:237:LEU:HD22	1:D:158:GLN:HB2	1.73	0.71
1:A:26:ALA:HB1	1:A:30:LYS:NZ	2.05	0.71
1:H:209:LYS:HE3	1:H:212:GLU:OE1	1.91	0.71
1:F:54:ASP:OD2	1:F:118:ARG:HD2	1.92	0.70
1:E:240:LYS:H	1:E:240:LYS:HD2	1.55	0.70
1:H:128:TYR:CE1	4:H:7482:HOH:O	2.43	0.70
1:E:163:ASP:OD2	1:E:165:ASN:HB2	1.90	0.70
1:F:267:ASN:ND2	1:F:268:GLN:HE21	1.89	0.70
1:D:84:ILE:HD11	1:D:118:ARG:NH1	2.07	0.70
1:D:165:ASN:OD1	1:D:269:ILE:HG13	1.92	0.69
1:B:132:TYR:OH	1:D:161:HIS:HD2	1.75	0.69
1:F:169:TRP:HB3	1:F:170:PRO:HD3	1.74	0.69
1:C:200:ARG:NH1	3:C:2301:FAD:H1B	2.08	0.69
1:A:83:ASP:OD2	1:A:118:ARG:NH2	2.24	0.69
1:D:55:ILE:N	1:D:55:ILE:HD12	2.08	0.69
1:C:40:ASP:HB3	1:C:43:ALA:HB3	1.74	0.69

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:50:ILE:HG22	1:E:118:ARG:HG2	1.73	0.69
1:F:198:ASP:O	1:F:201:ILE:HB	1.92	0.68
1:H:202:GLN:O	1:H:205:GLU:HB2	1.93	0.68
1:A:176:LEU:O	1:A:181:PHE:HB2	1.93	0.68
1:D:51:SER:OG	1:D:53:LYS:HG2	1.94	0.68
1:H:77:GLU:OE1	1:H:79:HIS:CE1	2.46	0.68
1:A:155:TYR:HB3	1:A:164:MET:HB2	1.74	0.68
1:B:262:SER:HB2	1:D:260:GLY:O	1.93	0.68
1:H:1:VAL:HG22	1:H:2:GLY:N	2.07	0.68
1:B:60:LYS:O	1:B:60:LYS:HG2	1.94	0.68
1:D:201:ILE:O	1:D:205:GLU:HG2	1.93	0.68
1:H:195:THR:HG22	1:H:199:ALA:HB3	1.74	0.68
1:C:198:ASP:O	1:C:202:GLN:HG2	1.94	0.67
1:A:200:ARG:HH11	3:A:301:FAD:H1B	1.59	0.67
1:G:138:ARG:HA	1:G:180:GLY:O	1.95	0.67
1:B:49:ILE:O	1:B:118:ARG:HD3	1.94	0.67
1:A:47:ASN:ND2	1:A:47:ASN:C	2.48	0.67
1:C:132:TYR:O	1:C:134:LYS:N	2.28	0.66
1:H:128:TYR:CD1	4:H:7482:HOH:O	2.47	0.66
1:D:199:ALA:O	1:D:203:ILE:HG13	1.95	0.66
1:B:147:THR:HG22	1:B:189:THR:OG1	1.95	0.66
1:B:176:LEU:O	1:B:181:PHE:HB2	1.95	0.66
1:B:201:ILE:HD13	1:G:14:ARG:HD2	1.78	0.66
1:H:17:PHE:HB2	3:H:7301:FAD:H51A	1.77	0.66
1:H:32:LYS:HE3	1:H:212:GLU:CB	2.26	0.66
1:F:214:ILE:HD12	1:F:217:GLU:OE2	1.95	0.65
1:B:183:VAL:HG12	1:B:220:LEU:HD12	1.77	0.65
1:H:1:VAL:HA	1:H:215:TRP:NE1	2.10	0.65
1:F:59:LEU:HB2	1:F:62:PRO:HG3	1.78	0.65
1:C:32:LYS:HE3	1:C:212:GLU:HB3	1.79	0.65
1:H:144:LEU:HD21	1:H:176:LEU:HD11	1.79	0.65
1:H:201:ILE:O	1:H:205:GLU:HG2	1.98	0.64
1:A:214:ILE:HA	1:A:217:GLU:OE2	1.97	0.64
1:E:55:ILE:HG23	1:E:74:ALA:HB2	1.78	0.64
1:A:186:PRO:HB2	1:A:188:LEU:HD21	1.79	0.64
1:A:111:ILE:HB	1:C:49:ILE:HD12	1.80	0.64
1:B:76:LYS:HE3	1:B:123:GLU:HG3	1.79	0.64
1:F:185:GLU:OE2	1:F:270:LYS:HA	1.98	0.63
1:C:1:VAL:HG12	1:C:2:GLY:H	1.62	0.63
1:G:49:ILE:HD11	1:H:48:PRO:HG3	1.81	0.63
1:E:151:SER:H	1:E:154:MET:HE3	1.64	0.63
1:H:128:TYR:HD2	2:H:6280:DTC:C20	2.12	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:130:ALA:HB1	1:F:134:LYS:O	1.99	0.63
1:A:230:LEU:CD2	1:C:160:ILE:HD12	2.29	0.62
1:B:47:ASN:HD22	1:B:48:PRO:N	1.95	0.62
1:H:254:SER:HB2	1:H:267:ASN:HD21	1.63	0.62
1:B:1:VAL:HG12	1:B:2:GLY:N	2.11	0.62
1:F:225:SER:HB2	1:F:230:LEU:HD11	1.81	0.62
1:G:239:LYS:HB2	1:G:242:VAL:CG2	2.30	0.62
1:G:6:LEU:HD12	1:G:37:VAL:O	1.99	0.62
1:H:164:MET:HA	1:H:167:ILE:HD12	1.81	0.62
1:H:173:SER:HB2	1:H:222:PHE:CE1	2.35	0.62
1:A:54:ASP:OD1	1:A:118:ARG:NH1	2.33	0.62
1:C:84:ILE:O	1:C:88:GLN:HG3	2.00	0.62
1:B:29:LEU:HD13	1:B:211:LEU:HD13	1.82	0.61
1:G:127:THR:HB	1:G:130:ALA:HB3	1.81	0.61
1:C:50:ILE:HG22	1:C:118:ARG:HG2	1.82	0.61
1:E:130:ALA:HB1	1:E:134:LYS:O	2.00	0.61
1:G:75:TYR:CZ	1:G:124:PHE:HB2	2.34	0.61
1:G:239:LYS:HB2	1:G:242:VAL:HG23	1.82	0.61
1:C:1:VAL:HG12	1:C:2:GLY:N	2.15	0.61
1:H:163:ASP:OD2	1:H:165:ASN:HB2	2.01	0.61
1:C:155:TYR:HB3	1:C:164:MET:HB2	1.83	0.61
1:D:44:MET:O	1:D:45:ASN:HB3	2.01	0.61
1:H:72:VAL:HG22	1:H:122:GLY:HA3	1.82	0.61
1:H:84:ILE:O	1:H:88:GLN:HG3	2.00	0.61
1:H:128:TYR:CD2	2:H:6280:DTC:C20	2.83	0.60
1:C:104:GLN:HA	3:C:2301:FAD:N5	2.15	0.60
1:B:183:VAL:CG1	1:B:220:LEU:HD12	2.32	0.60
1:B:160:ILE:HD12	1:D:230:LEU:HD21	1.84	0.60
1:G:199:ALA:O	1:G:202:GLN:HB3	2.02	0.60
1:D:47:ASN:ND2	1:D:49:ILE:N	2.46	0.60
1:D:127:THR:OG1	1:D:130:ALA:HB3	2.01	0.60
1:B:201:ILE:CD1	1:G:14:ARG:HD2	2.31	0.60
1:E:151:SER:OG	1:E:154:MET:HG3	2.02	0.60
1:E:25:ALA:O	1:E:29:LEU:HD22	2.02	0.60
1:B:108:VAL:CB	1:B:112:LEU:HD12	2.29	0.60
1:D:108:VAL:CB	1:D:112:LEU:HD12	2.29	0.60
1:B:51:SER:O	1:B:54:ASP:HB2	2.02	0.60
1:F:42:TYR:HB2	4:F:7330:HOH:O	2.01	0.60
1:H:67:TYR:HB3	1:H:68:PRO:HD3	1.83	0.60
1:F:32:LYS:HE3	1:F:212:GLU:HB3	1.82	0.60
1:F:173:SER:HB2	1:F:222:PHE:CE1	2.37	0.60
1:G:128:TYR:HB3	2:G:7280:DTC:C16	2.32	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:267:ASN:ND2	1:A:268:GLN:HE21	2.00	0.59
1:H:14:ARG:CD	1:H:14:ARG:N	2.65	0.59
1:E:169:TRP:CZ2	1:E:256:GLY:HA3	2.36	0.59
1:G:238:MET:HB2	1:H:158:GLN:HB3	1.84	0.59
1:A:230:LEU:HD21	1:C:160:ILE:HD12	1.82	0.59
1:G:7:ILE:HG21	1:G:22:LYS:HG2	1.84	0.59
1:H:132:TYR:CD1	1:H:178:PHE:HA	2.37	0.59
1:G:151:SER:O	1:G:154:MET:HB2	2.01	0.59
1:G:152:GLY:HA2	1:G:190:TYR:CD1	2.38	0.59
1:B:255:VAL:N	1:B:267:ASN:ND2	2.50	0.59
1:G:166:VAL:HG11	1:H:169:TRP:CD1	2.38	0.59
1:A:160:ILE:HD12	1:C:230:LEU:HD21	1.85	0.59
1:E:155:TYR:HB3	1:E:164:MET:HB2	1.85	0.59
1:B:214:ILE:HG23	1:B:215:TRP:N	2.17	0.59
1:D:47:ASN:ND2	1:D:47:ASN:C	2.49	0.59
4:C:7378:HOH:O	1:D:53:LYS:HD3	2.03	0.59
1:A:132:TYR:CD1	1:A:178:PHE:HA	2.38	0.59
1:B:47:ASN:C	1:B:47:ASN:HD22	2.06	0.58
1:B:54:ASP:CG	1:B:118:ARG:HH11	2.06	0.58
1:D:200:ARG:NH1	3:D:3301:FAD:H1B	2.18	0.58
1:G:222:PHE:O	1:G:224:PRO:HD3	2.03	0.58
1:B:77:GLU:OE1	1:B:79:HIS:HE1	1.87	0.58
1:A:231:ASN:OD1	1:A:233:GLN:HB2	2.04	0.58
1:H:197:ALA:O	1:H:199:ALA:N	2.36	0.58
1:C:12:SER:HB3	1:C:42:TYR:CE1	2.39	0.58
1:G:65:PHE:CE1	1:G:70:GLU:HG3	2.39	0.58
1:C:115:TRP:O	1:C:119:VAL:HG23	2.03	0.58
1:G:122:GLY:O	1:G:123:GLU:CB	2.51	0.58
4:B:7390:HOH:O	1:G:15:THR:HB	2.02	0.58
1:A:229:ASP:O	1:A:236:PHE:HA	2.04	0.58
1:D:26:ALA:O	1:D:30:LYS:HG3	2.03	0.58
1:D:1:VAL:HA	1:D:215:TRP:CD1	2.39	0.57
1:D:47:ASN:ND2	1:D:48:PRO:N	2.37	0.57
1:A:6:LEU:HD12	1:A:37:VAL:O	2.04	0.57
1:C:132:TYR:HA	1:C:177:HIS:O	2.03	0.57
1:C:12:SER:HB3	1:C:42:TYR:CD1	2.40	0.57
1:C:122:GLY:O	1:C:123:GLU:HB2	2.04	0.57
1:B:169:TRP:HB3	1:B:170:PRO:HD3	1.86	0.57
1:A:132:TYR:O	1:A:180:GLY:HA2	2.04	0.57
1:H:26:ALA:O	1:H:30:LYS:HG3	2.05	0.57
1:F:214:ILE:HA	1:F:217:GLU:OE2	2.05	0.57
1:B:77:GLU:HB2	1:B:79:HIS:CE1	2.39	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:1:VAL:CG2	1:H:2:GLY:H	2.15	0.56
1:C:45:ASN:ND2	1:D:45:ASN:HD21	2.03	0.56
1:A:175:ILE:HG12	1:C:105:TRP:HB3	1.86	0.56
1:H:132:TYR:O	1:H:134:LYS:N	2.38	0.56
1:F:74:ALA:HA	1:F:79:HIS:CE1	2.40	0.56
1:A:55:ILE:CD1	1:A:70:GLU:HB3	2.35	0.56
1:F:241:GLU:H	1:F:241:GLU:CD	2.09	0.56
1:F:22:LYS:HD2	1:F:38:GLU:OE1	2.05	0.56
1:H:199:ALA:O	1:H:202:GLN:HB2	2.05	0.56
1:G:99:PHE:HB2	1:G:144:LEU:HD23	1.88	0.56
1:A:47:ASN:ND2	1:A:49:ILE:N	2.52	0.56
1:H:238:MET:HE1	1:H:259:LEU:HD21	1.87	0.56
1:D:169:TRP:HB3	1:D:170:PRO:HD3	1.88	0.56
1:D:84:ILE:O	1:D:88:GLN:HG3	2.06	0.56
1:B:232:PHE:HD1	1:B:232:PHE:H	1.54	0.56
1:C:1:VAL:HA	1:C:215:TRP:NE1	2.21	0.56
1:F:84:ILE:O	1:F:88:GLN:HG3	2.06	0.56
1:D:169:TRP:CZ2	1:D:256:GLY:HA3	2.41	0.56
1:C:25:ALA:O	1:C:29:LEU:HB2	2.06	0.55
1:A:209:LYS:O	1:A:212:GLU:HB2	2.06	0.55
1:F:267:ASN:HD21	1:F:268:GLN:HE21	1.53	0.55
1:G:151:SER:H	1:G:154:MET:HE3	1.71	0.55
1:A:258:HIS:CD2	1:C:263:ILE:HD12	2.41	0.55
1:D:172:GLN:HE22	1:D:186:PRO:HB3	1.71	0.55
1:C:47:ASN:ND2	1:C:49:ILE:H	2.04	0.55
1:D:54:ASP:OD1	1:D:118:ARG:NH1	2.39	0.55
1:B:128:TYR:HB3	2:B:3280:DTC:C16	2.36	0.55
1:E:240:LYS:N	1:E:240:LYS:HD2	2.21	0.55
1:D:101:PHE:CZ	1:D:146:ILE:HG12	2.41	0.55
1:G:6:LEU:HA	1:G:37:VAL:O	2.07	0.55
2:E:4280:DTC:C16	1:F:128:TYR:HB3	2.37	0.55
1:C:67:TYR:HB3	1:C:68:PRO:HD3	1.88	0.55
1:F:214:ILE:HG23	1:F:215:TRP:N	2.21	0.55
1:F:88:GLN:HB3	1:F:124:PHE:CZ	2.42	0.55
1:F:195:THR:CG2	1:F:199:ALA:HB3	2.37	0.55
1:B:106:PHE:HE2	1:B:155:TYR:HE1	1.55	0.55
1:B:269:ILE:HG22	1:B:270:LYS:HG2	1.88	0.55
1:B:54:ASP:OD2	1:B:118:ARG:HD2	2.07	0.54
1:D:76:LYS:HE2	1:D:123:GLU:CG	2.36	0.54
1:C:45:ASN:ND2	1:D:45:ASN:ND2	2.55	0.54
1:G:59:LEU:O	1:G:62:PRO:HD3	2.08	0.54
1:A:113:LYS:O	1:A:117:GLU:HG3	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:165:ASN:ND2	1:F:266:ASP:HA	2.22	0.54
1:E:11:HIS:O	1:E:14:ARG:NH2	2.39	0.54
1:A:246:GLU:O	1:A:261:LYS:NZ	2.40	0.54
1:B:255:VAL:CG2	1:B:267:ASN:HD22	1.98	0.54
1:G:128:TYR:O	1:G:131:MET:HG3	2.07	0.54
1:B:101:PHE:CE2	1:B:108:VAL:HG12	2.43	0.54
1:E:106:PHE:HD2	1:E:167:ILE:HD13	1.72	0.54
1:G:163:ASP:OD1	1:G:165:ASN:ND2	2.39	0.54
1:D:65:PHE:CD1	1:D:70:GLU:HG3	2.42	0.54
1:B:169:TRP:O	1:B:173:SER:HB3	2.08	0.54
1:H:29:LEU:O	1:H:34:TRP:HB2	2.08	0.54
1:D:255:VAL:HG23	1:D:267:ASN:HB3	1.90	0.54
1:E:218:THR:O	1:E:271:ALA:HB2	2.07	0.54
1:E:243:GLN:O	1:E:247:LYS:HG3	2.06	0.54
1:C:169:TRP:CZ2	1:C:256:GLY:HA3	2.43	0.54
1:F:197:ALA:HA	1:F:200:ARG:NE	2.23	0.54
1:B:172:GLN:HB3	1:B:183:VAL:HG11	1.90	0.54
1:D:130:ALA:HB1	1:D:134:LYS:O	2.08	0.54
1:D:255:VAL:H	1:D:267:ASN:HD22	1.56	0.54
1:A:17:PHE:CD2	1:A:192:ILE:HG12	2.43	0.54
1:C:241:GLU:H	1:C:241:GLU:CD	2.10	0.54
1:B:209:LYS:HD2	1:B:212:GLU:OE2	2.08	0.54
1:F:14:ARG:HD3	1:F:19:TYR:CE1	2.43	0.54
1:G:25:ALA:HA	1:G:211:LEU:HD13	1.90	0.54
1:E:101:PHE:CZ	1:E:108:VAL:HG12	2.43	0.54
1:B:267:ASN:ND2	1:B:268:GLN:HE21	2.07	0.53
1:C:133:ASP:OD1	1:C:225:SER:HB3	2.07	0.53
1:E:65:PHE:CD1	1:E:70:GLU:HG3	2.43	0.53
1:B:187:GLN:HG2	1:B:207:TRP:CE3	2.44	0.53
1:D:197:ALA:HA	1:D:200:ARG:NH2	2.22	0.53
1:F:197:ALA:HA	1:F:200:ARG:CZ	2.38	0.53
1:E:128:TYR:HB3	2:E:5280:DTC:C16	2.38	0.53
1:E:169:TRP:HB3	1:E:170:PRO:HD3	1.89	0.53
1:F:173:SER:HB2	1:F:222:PHE:HE1	1.74	0.53
1:B:169:TRP:CZ2	1:B:256:GLY:HA3	2.43	0.53
1:A:1:VAL:HG12	1:A:2:GLY:N	2.24	0.53
1:E:240:LYS:H	1:E:240:LYS:CD	2.20	0.53
1:B:122:GLY:O	1:B:123:GLU:HB2	2.09	0.53
1:H:4:ARG:HE	1:H:93:ALA:HB1	1.72	0.53
1:H:44:MET:HE1	1:H:87:GLU:OE2	2.08	0.53
1:A:47:ASN:HD21	1:A:49:ILE:H	1.52	0.53
1:H:227:LEU:O	1:H:239:LYS:HG3	2.08	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:151:SER:OG	1:B:154:MET:HG3	2.08	0.53
1:D:128:TYR:HB3	2:D:1280:DTC:C16	2.38	0.53
1:F:105:TRP:O	1:F:106:PHE:HB2	2.09	0.53
1:D:246:GLU:OE2	1:D:249:LYS:HG3	2.09	0.53
1:F:4:ARG:HE	1:F:93:ALA:HB1	1.74	0.53
1:D:197:ALA:HA	1:D:200:ARG:HH21	1.74	0.53
1:B:118:ARG:O	1:B:121:ILE:HD11	2.09	0.53
1:F:165:ASN:OD1	1:F:269:ILE:HG13	2.09	0.53
1:F:154:MET:O	1:F:161:HIS:HB2	2.08	0.53
1:D:47:ASN:HD21	1:D:49:ILE:N	1.98	0.53
1:G:1:VAL:CG1	1:G:2:GLY:H	2.02	0.53
1:E:151:SER:N	1:E:154:MET:HE3	2.23	0.53
1:G:246:GLU:O	1:G:261:LYS:NZ	2.42	0.53
1:F:165:ASN:HD21	1:F:266:ASP:HA	1.72	0.52
1:H:204:LEU:O	1:H:208:LYS:HG3	2.09	0.52
1:C:1:VAL:HA	1:C:215:TRP:CD1	2.44	0.52
1:F:255:VAL:H	1:F:267:ASN:ND2	2.08	0.52
1:G:14:ARG:HG2	1:G:19:TYR:CZ	2.44	0.52
1:F:88:GLN:O	1:F:92:GLU:HG3	2.09	0.52
1:E:14:ARG:NH1	1:E:40:ASP:OD2	2.41	0.52
1:E:126:TYR:CD2	1:E:178:PHE:HE2	2.27	0.52
1:B:46:PHE:CE2	1:B:47:ASN:O	2.62	0.52
1:B:72:VAL:HG22	1:B:122:GLY:HA3	1.91	0.52
1:H:173:SER:HB2	1:H:222:PHE:HE1	1.72	0.52
1:F:122:GLY:O	1:F:123:GLU:HB3	2.09	0.52
1:C:3:ARG:NH1	4:C:7428:HOH:O	2.41	0.52
1:H:151:SER:HA	1:H:190:TYR:HB3	1.91	0.52
1:F:214:ILE:CG2	1:F:215:TRP:N	2.73	0.52
1:H:167:ILE:O	1:H:170:PRO:HD2	2.09	0.52
1:E:104:GLN:HA	3:E:4301:FAD:C5X	2.40	0.52
1:A:106:PHE:HD2	1:A:167:ILE:CD1	2.23	0.52
1:H:138:ARG:HA	1:H:180:GLY:O	2.10	0.52
1:A:148:THR:HB	3:A:301:FAD:O2	2.09	0.52
1:E:29:LEU:HB3	1:E:34:TRP:HB2	1.92	0.52
1:A:25:ALA:O	1:A:29:LEU:HB2	2.10	0.52
1:E:65:PHE:CE1	1:E:70:GLU:HG3	2.45	0.52
1:B:6:LEU:HA	1:B:37:VAL:O	2.11	0.52
1:A:25:ALA:HA	1:A:211:LEU:CD1	2.40	0.51
1:E:46:PHE:CE2	1:E:115:TRP:HA	2.45	0.51
1:H:200:ARG:NH1	3:H:7301:FAD:H1B	2.26	0.51
1:H:46:PHE:O	1:H:48:PRO:HD3	2.10	0.51
1:B:229:ASP:O	1:B:236:PHE:HA	2.10	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:232:PHE:N	1:B:232:PHE:CD1	2.78	0.51
1:G:50:ILE:HG22	1:G:118:ARG:HG2	1.91	0.51
1:D:148:THR:HB	3:D:3301:FAD:O2	2.10	0.51
1:E:195:THR:HG22	1:E:199:ALA:HB3	1.91	0.51
1:B:18:ASN:OD1	1:B:100:GLN:NE2	2.40	0.51
1:H:50:ILE:O	1:H:50:ILE:HG13	2.09	0.51
1:G:158:GLN:HB2	1:H:237:LEU:HD22	1.92	0.51
1:A:243:GLN:OE1	1:C:158:GLN:HG2	2.11	0.51
1:A:130:ALA:HB1	1:A:134:LYS:O	2.10	0.51
1:H:128:TYR:CD2	2:H:6280:DTC:C19	2.93	0.51
1:B:76:LYS:CE	1:B:123:GLU:HG3	2.40	0.51
1:H:25:ALA:O	1:H:29:LEU:HB2	2.11	0.51
1:C:169:TRP:HB3	1:C:170:PRO:HD3	1.92	0.51
1:B:6:LEU:HD13	1:B:37:VAL:HG12	1.93	0.51
1:E:88:GLN:HG2	1:E:124:PHE:CE2	2.46	0.51
1:A:214:ILE:HD12	1:A:217:GLU:OE2	2.11	0.51
1:G:111:ILE:HB	1:H:49:ILE:HD12	1.93	0.50
1:H:204:LEU:HD11	3:H:7301:FAD:N1A	2.26	0.50
1:F:4:ARG:HG2	1:F:35:GLU:HB2	1.93	0.50
1:F:183:VAL:HG12	1:F:220:LEU:HD12	1.92	0.50
1:C:65:PHE:CE1	1:C:70:GLU:HG3	2.45	0.50
1:A:47:ASN:HD22	1:A:49:ILE:H	1.58	0.50
1:C:238:MET:HE3	1:C:243:GLN:HG2	1.93	0.50
1:E:167:ILE:O	1:E:170:PRO:HD2	2.12	0.50
1:A:7:ILE:HG21	1:A:22:LYS:HG2	1.92	0.50
1:B:204:LEU:O	1:B:208:LYS:HG3	2.11	0.50
1:G:244:ASP:C	1:G:246:GLU:H	2.13	0.50
1:E:173:SER:HB2	1:E:222:PHE:CE1	2.46	0.50
1:C:28:ALA:HB2	1:C:208:LYS:HE2	1.93	0.50
1:E:58:LYS:HA	4:E:7367:HOH:O	2.12	0.50
1:H:9:LEU:HD12	1:H:10:ALA:H	1.76	0.50
1:A:254:SER:HB2	1:A:267:ASN:HD21	1.77	0.50
1:G:214:ILE:HG23	1:G:215:TRP:N	2.27	0.50
1:A:186:PRO:HB2	1:A:188:LEU:CD2	2.42	0.50
1:H:130:ALA:HB1	1:H:134:LYS:O	2.12	0.50
1:B:200:ARG:NH1	3:B:1301:FAD:H1B	2.26	0.50
1:E:55:ILE:HG23	1:E:74:ALA:CB	2.40	0.50
1:A:128:TYR:HB3	2:A:2280:DTC:C16	2.42	0.50
1:F:55:ILE:HD13	1:F:70:GLU:HB3	1.93	0.50
1:B:55:ILE:HD13	1:B:70:GLU:HB3	1.93	0.50
1:H:1:VAL:HA	1:H:215:TRP:HE1	1.77	0.50
1:C:104:GLN:HA	3:C:2301:FAD:C5X	2.42	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:214:ILE:HD12	1:H:217:GLU:OE2	2.12	0.50
1:A:160:ILE:O	1:A:160:ILE:HG12	2.12	0.50
1:C:22:LYS:HD3	1:C:38:GLU:OE1	2.11	0.50
1:F:50:ILE:O	1:F:50:ILE:HG13	2.12	0.50
1:H:200:ARG:HD3	3:H:7301:FAD:N3A	2.27	0.50
1:B:4:ARG:HG2	1:B:35:GLU:OE1	2.12	0.50
1:C:53:LYS:HZ1	1:D:53:LYS:NZ	2.09	0.49
1:G:49:ILE:O	1:G:118:ARG:HD3	2.12	0.49
1:B:258:HIS:CD2	1:D:263:ILE:HD12	2.48	0.49
1:F:185:GLU:OE2	1:F:271:ALA:N	2.40	0.49
1:A:185:GLU:HG2	1:A:269:ILE:O	2.12	0.49
1:B:152:GLY:HA2	1:B:190:TYR:CD1	2.47	0.49
1:H:144:LEU:CD2	1:H:176:LEU:HD11	2.42	0.49
1:C:128:TYR:HB3	2:C:280:DTC:C16	2.42	0.49
1:D:106:PHE:HD2	1:D:167:ILE:HD13	1.76	0.49
1:A:26:ALA:HB1	1:A:30:LYS:HZ2	1.76	0.49
1:D:266:ASP:HB3	1:D:269:ILE:HB	1.94	0.49
1:A:169:TRP:HB3	1:A:170:PRO:HD3	1.95	0.49
1:B:255:VAL:H	1:B:267:ASN:HD22	1.60	0.49
1:D:1:VAL:HG12	1:D:2:GLY:N	2.20	0.49
1:H:208:LYS:O	1:H:212:GLU:HG3	2.13	0.49
1:C:246:GLU:O	1:C:261:LYS:NZ	2.46	0.49
1:F:50:ILE:HB	1:F:67:TYR:CE1	2.48	0.49
1:G:169:TRP:CD1	1:H:166:VAL:HG11	2.47	0.49
1:H:17:PHE:HE1	1:H:200:ARG:HB3	1.78	0.49
1:H:77:GLU:OE1	1:H:79:HIS:HE1	1.96	0.49
1:D:114:GLY:O	1:D:118:ARG:HG3	2.13	0.49
1:D:255:VAL:H	1:D:267:ASN:ND2	2.11	0.49
1:D:116:PHE:O	1:D:120:PHE:HB2	2.13	0.49
1:H:108:VAL:HB	1:H:112:LEU:HD23	1.95	0.49
1:D:29:LEU:HD12	1:D:34:TRP:CD1	2.48	0.49
1:H:255:VAL:HG23	1:H:267:ASN:ND2	2.23	0.49
1:H:17:PHE:CE1	1:H:200:ARG:HB3	2.48	0.49
1:G:160:ILE:CD1	1:H:230:LEU:HD21	2.42	0.49
1:D:197:ALA:CA	1:D:200:ARG:HH21	2.26	0.48
1:C:53:LYS:NZ	1:D:53:LYS:NZ	2.61	0.48
1:F:49:ILE:O	1:F:118:ARG:HD3	2.12	0.48
1:G:160:ILE:HD12	1:H:230:LEU:HD21	1.95	0.48
1:H:132:TYR:C	1:H:134:LYS:H	2.16	0.48
1:H:241:GLU:CD	1:H:241:GLU:H	2.16	0.48
1:A:87:GLU:O	1:A:90:LYS:N	2.44	0.48
1:A:3:ARG:HA	1:A:3:ARG:NE	2.22	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:104:GLN:HA	3:E:4301:FAD:N5	2.28	0.48
1:F:1:VAL:HG22	1:F:2:GLY:N	2.21	0.48
1:B:29:LEU:CD1	1:B:211:LEU:HB3	2.44	0.48
1:H:9:LEU:HD12	1:H:10:ALA:N	2.27	0.48
1:B:192:ILE:HD11	1:B:200:ARG:HG2	1.95	0.48
1:C:204:LEU:O	1:C:208:LYS:HG3	2.14	0.48
1:H:221:TYR:HE2	1:H:253:LEU:O	1.96	0.48
1:B:258:HIS:CE1	1:D:157:LEU:HD22	2.48	0.48
1:H:32:LYS:HE3	1:H:212:GLU:CG	2.44	0.48
1:D:200:ARG:HH11	3:D:3301:FAD:C1B	2.24	0.48
1:A:200:ARG:NH1	3:A:301:FAD:H1B	2.26	0.48
1:B:75:TYR:CZ	1:B:124:PHE:HB2	2.49	0.48
1:D:65:PHE:CE1	1:D:70:GLU:HG3	2.49	0.48
1:A:1:VAL:HG12	1:A:2:GLY:H	1.79	0.48
1:H:251:PHE:HD1	1:H:262:SER:HB3	1.78	0.48
1:F:104:GLN:HA	3:F:5301:FAD:N5	2.29	0.48
1:G:232:PHE:H	1:G:232:PHE:HD1	1.60	0.48
1:E:207:TRP:CH2	1:E:211:LEU:HD21	2.48	0.48
1:H:210:ARG:NE	1:H:214:ILE:HD13	2.29	0.48
1:D:29:LEU:HB3	1:D:34:TRP:HB2	1.96	0.48
1:G:155:TYR:HB3	1:G:164:MET:HB2	1.96	0.48
1:C:192:ILE:CG2	3:C:2301:FAD:H5'1	2.44	0.47
1:H:198:ASP:O	1:H:202:GLN:HG2	2.14	0.47
1:B:76:LYS:HE2	1:B:123:GLU:OE1	2.14	0.47
1:H:72:VAL:HG13	1:H:123:GLU:HG2	1.96	0.47
1:B:4:ARG:NH1	1:B:93:ALA:O	2.45	0.47
1:B:47:ASN:C	1:B:47:ASN:ND2	2.66	0.47
1:H:165:ASN:HD21	1:H:266:ASP:HA	1.79	0.47
1:E:106:PHE:HD2	1:E:167:ILE:CD1	2.27	0.47
1:H:198:ASP:HA	1:H:201:ILE:HD12	1.95	0.47
1:E:265:THR:O	1:E:266:ASP:C	2.53	0.47
1:B:130:ALA:HB1	1:B:134:LYS:O	2.15	0.47
1:A:239:LYS:O	1:A:243:GLN:HG3	2.15	0.47
1:D:218:THR:HG23	1:D:218:THR:O	2.15	0.47
1:B:113:LYS:NZ	1:D:108:VAL:O	2.48	0.47
1:C:53:LYS:NZ	4:C:7378:HOH:O	2.48	0.47
1:B:257:HIS:HA	4:B:7430:HOH:O	2.15	0.47
1:A:68:PRO:O	1:A:72:VAL:HG23	2.15	0.47
1:E:227:LEU:HB3	1:E:242:VAL:HG11	1.96	0.47
1:H:185:GLU:O	1:H:210:ARG:NH2	2.41	0.47
1:C:45:ASN:CG	1:D:45:ASN:HD21	2.18	0.47
1:F:201:ILE:O	1:F:205:GLU:HG2	2.15	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:209:LYS:HA	1:D:212:GLU:OE2	2.15	0.47
1:D:130:ALA:O	1:D:135:GLY:HA2	2.15	0.46
1:F:101:PHE:O	1:F:146:ILE:HA	2.16	0.46
1:G:32:LYS:HE3	1:G:212:GLU:HG2	1.97	0.46
1:C:53:LYS:HZ1	1:D:53:LYS:HZ2	1.62	0.46
1:F:104:GLN:HA	3:F:5301:FAD:C5X	2.44	0.46
1:B:13:GLU:C	1:B:15:THR:H	2.19	0.46
1:H:246:GLU:O	1:H:261:LYS:NZ	2.48	0.46
1:B:102:PRO:HG2	1:B:102:PRO:O	2.15	0.46
1:D:4:ARG:HG2	1:D:35:GLU:OE2	2.15	0.46
1:B:137:PHE:C	1:B:139:SER:H	2.18	0.46
1:C:200:ARG:HD2	3:C:2301:FAD:N3A	2.30	0.46
1:F:50:ILE:CG2	1:F:118:ARG:HG2	2.41	0.46
1:G:88:GLN:HB3	1:G:124:PHE:CZ	2.51	0.46
1:D:209:LYS:O	1:D:212:GLU:HB2	2.16	0.46
1:A:116:PHE:O	1:A:120:PHE:HB2	2.16	0.46
1:G:113:LYS:O	1:G:117:GLU:HG3	2.16	0.46
1:A:23:GLU:HA	1:A:23:GLU:OE1	2.15	0.46
1:C:62:PRO:HG2	1:G:202:GLN:OE1	2.15	0.46
1:G:169:TRP:HB3	1:G:170:PRO:HD3	1.96	0.46
1:G:257:HIS:CD2	1:H:162:GLY:HA2	2.51	0.46
1:H:172:GLN:HB3	1:H:183:VAL:HG11	1.96	0.46
1:G:128:TYR:HH	2:G:7280:DTC:C6	2.16	0.46
1:D:55:ILE:CD1	1:D:55:ILE:N	2.78	0.46
1:H:197:ALA:O	1:H:198:ASP:C	2.54	0.46
1:F:132:TYR:HA	1:F:177:HIS:O	2.15	0.46
1:F:128:TYR:O	1:F:131:MET:HG3	2.16	0.46
1:G:17:PHE:HB2	3:G:6301:FAD:H51A	1.97	0.46
1:A:9:LEU:HD21	1:A:19:TYR:HD1	1.81	0.46
1:G:132:TYR:CD1	1:G:178:PHE:HA	2.49	0.46
1:B:1:VAL:CG1	1:B:2:GLY:H	2.16	0.46
1:C:46:PHE:CE2	1:C:115:TRP:HA	2.51	0.46
1:C:236:PHE:CZ	2:C:280:DTC:H16	2.51	0.46
1:D:204:LEU:O	1:D:208:LYS:HG3	2.16	0.46
1:C:51:SER:C	1:C:53:LYS:H	2.20	0.46
1:A:121:ILE:O	1:A:124:PHE:HB3	2.15	0.46
1:B:11:HIS:CE1	1:B:16:SER:HB3	2.51	0.46
1:A:88:GLN:HB3	1:A:124:PHE:CZ	2.51	0.46
1:B:106:PHE:CE2	1:B:155:TYR:HE1	2.33	0.46
1:H:22:LYS:O	1:H:25:ALA:HB3	2.15	0.46
1:H:168:LEU:O	1:H:172:GLN:HG3	2.16	0.46
1:G:266:ASP:HB3	1:G:269:ILE:HB	1.98	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:166:VAL:CG1	1:F:169:TRP:CD1	2.98	0.45
1:E:127:THR:HG22	1:E:130:ALA:N	2.31	0.45
1:A:55:ILE:HD13	1:A:70:GLU:HB3	1.96	0.45
1:D:254:SER:HB2	1:D:267:ASN:HD21	1.81	0.45
1:B:195:THR:CG2	1:B:199:ALA:HB3	2.46	0.45
1:D:149:GLY:O	1:D:191:SER:HA	2.16	0.45
1:H:209:LYS:O	1:H:212:GLU:HG3	2.17	0.45
1:E:166:VAL:O	1:E:170:PRO:HD3	2.16	0.45
1:A:104:GLN:HA	3:A:301:FAD:C5X	2.46	0.45
1:B:25:ALA:HA	1:B:211:LEU:CD1	2.47	0.45
1:C:73:LEU:HD23	4:C:7335:HOH:O	2.15	0.45
1:F:246:GLU:HG3	4:F:7318:HOH:O	2.16	0.45
1:G:6:LEU:CD1	1:G:37:VAL:HG12	2.47	0.45
1:C:45:ASN:CG	1:D:45:ASN:ND2	2.69	0.45
1:G:55:ILE:CD1	1:G:70:GLU:HB3	2.45	0.45
1:G:55:ILE:HG12	1:G:74:ALA:HB2	1.99	0.45
1:H:163:ASP:CG	1:H:165:ASN:HB2	2.36	0.45
1:G:244:ASP:C	1:G:246:GLU:N	2.69	0.45
1:D:155:TYR:HB3	1:D:164:MET:HB2	1.97	0.45
1:F:23:GLU:HA	1:F:23:GLU:OE1	2.17	0.45
1:E:40:ASP:HB3	1:E:43:ALA:HB3	1.98	0.45
1:B:141:LYS:HD2	1:B:215:TRP:CZ3	2.51	0.45
1:B:214:ILE:HD12	1:B:217:GLU:OE2	2.17	0.45
1:E:195:THR:HA	1:E:196:PRO:HD3	1.76	0.45
1:H:221:TYR:OH	1:H:253:LEU:HD22	2.17	0.45
1:B:239:LYS:O	1:B:243:GLN:HG3	2.16	0.45
1:F:116:PHE:O	1:F:120:PHE:HB2	2.16	0.45
1:H:1:VAL:HA	1:H:215:TRP:CD1	2.52	0.45
1:B:104:GLN:HA	3:B:1301:FAD:N5	2.31	0.45
1:A:165:ASN:ND2	1:A:269:ILE:HD12	2.31	0.45
1:F:263:ILE:O	1:F:264:PRO:C	2.54	0.45
1:D:214:ILE:HD12	1:D:217:GLU:OE2	2.16	0.45
1:H:146:ILE:HG22	1:H:147:THR:N	2.32	0.45
1:C:47:ASN:C	1:C:47:ASN:HD22	2.20	0.45
1:F:9:LEU:HD22	1:F:22:LYS:HD3	1.98	0.45
1:E:236:PHE:HB2	1:F:154:MET:HG2	1.97	0.45
1:F:72:VAL:HG22	1:F:122:GLY:HA3	1.99	0.45
1:E:12:SER:HB3	1:E:42:TYR:CE1	2.52	0.45
1:F:67:TYR:HB3	1:F:68:PRO:HD3	1.98	0.45
1:B:132:TYR:OH	1:D:161:HIS:CD2	2.64	0.45
1:D:144:LEU:HD12	1:D:172:GLN:NE2	2.32	0.45
1:H:108:VAL:HG13	1:H:171:ILE:HD13	1.99	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:218:THR:HG23	4:A:7406:HOH:O	2.16	0.45
1:C:244:ASP:O	1:C:247:LYS:HG3	2.17	0.45
1:C:113:LYS:O	1:C:117:GLU:HG3	2.16	0.45
1:B:200:ARG:HD2	3:B:1301:FAD:N3A	2.31	0.45
1:F:245:GLU:HA	1:F:245:GLU:OE1	2.16	0.45
1:H:105:TRP:CD1	3:H:7301:FAD:H6	2.52	0.44
1:A:166:VAL:HG13	1:C:166:VAL:HG13	1.99	0.44
1:A:122:GLY:O	1:A:123:GLU:CB	2.65	0.44
1:D:122:GLY:O	1:D:124:PHE:N	2.45	0.44
1:A:138:ARG:HA	1:A:180:GLY:O	2.16	0.44
1:H:251:PHE:HD1	1:H:262:SER:CB	2.30	0.44
1:E:207:TRP:O	1:E:211:LEU:HG	2.18	0.44
1:G:11:HIS:NE2	3:G:6301:FAD:O2P	2.38	0.44
1:G:141:LYS:HD3	1:G:184:LEU:HD21	1.98	0.44
1:D:132:TYR:HA	1:D:177:HIS:O	2.17	0.44
1:H:238:MET:HE1	1:H:259:LEU:CD2	2.48	0.44
1:B:155:TYR:HB3	1:B:164:MET:HB2	2.00	0.44
1:E:266:ASP:HB3	1:E:269:ILE:HB	1.98	0.44
1:G:87:GLU:O	1:G:90:LYS:HB2	2.16	0.44
1:H:21:MET:SD	1:H:204:LEU:HD23	2.57	0.44
1:F:132:TYR:O	1:F:180:GLY:HA2	2.18	0.44
1:D:132:TYR:CD1	1:D:178:PHE:HA	2.53	0.44
1:E:141:LYS:NZ	1:E:215:TRP:O	2.50	0.44
1:D:123:GLU:OE2	1:D:123:GLU:HA	2.18	0.44
1:H:174:GLY:O	1:H:178:PHE:HB2	2.18	0.44
1:F:106:PHE:N	1:F:106:PHE:CD1	2.86	0.44
1:A:22:LYS:NZ	1:A:38:GLU:OE1	2.49	0.44
1:C:56:THR:O	1:C:79:HIS:HB3	2.18	0.44
1:F:157:LEU:HD23	1:F:163:ASP:HB2	1.99	0.44
1:C:102:PRO:HA	1:C:147:THR:OG1	2.17	0.44
1:H:51:SER:OG	1:H:53:LYS:HB3	2.18	0.44
1:E:273:LYS:HD3	1:E:273:LYS:C	2.38	0.44
1:H:121:ILE:HG22	1:H:122:GLY:N	2.32	0.44
1:B:56:THR:O	1:B:79:HIS:CD2	2.71	0.44
1:B:15:THR:HG21	1:G:200:ARG:HH12	1.82	0.44
1:G:126:TYR:CD2	1:G:178:PHE:HE2	2.36	0.44
1:H:101:PHE:CZ	1:H:146:ILE:HG12	2.53	0.44
1:C:199:ALA:O	1:C:203:ILE:HG13	2.17	0.44
1:F:155:TYR:HB3	1:F:164:MET:HB2	1.98	0.44
1:A:254:SER:OG	1:A:257:HIS:HB2	2.17	0.44
1:D:121:ILE:HG22	1:D:122:GLY:N	2.33	0.44
1:G:214:ILE:CD1	1:G:217:GLU:OE2	2.62	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:H:266:ASP:HB3	1:H:269:ILE:HB	1.99	0.44
1:B:141:LYS:HG2	1:B:182:GLN:HB2	2.00	0.44
1:G:25:ALA:HA	1:G:211:LEU:CD1	2.48	0.44
1:F:41:LEU:O	1:F:44:MET:HB2	2.18	0.44
1:G:176:LEU:O	1:G:181:PHE:HB2	2.18	0.44
1:A:195:THR:CG2	1:A:199:ALA:HB3	2.48	0.44
1:F:111:ILE:HG23	1:F:112:LEU:N	2.33	0.44
1:F:1:VAL:HA	1:F:215:TRP:NE1	2.33	0.43
1:E:166:VAL:O	1:E:169:TRP:HB3	2.18	0.43
1:F:238:MET:CE	1:F:243:GLN:HG2	2.34	0.43
1:B:214:ILE:CG2	1:B:215:TRP:N	2.80	0.43
1:F:122:GLY:O	1:F:123:GLU:CB	2.66	0.43
1:A:106:PHE:HD2	1:A:167:ILE:HD11	1.83	0.43
1:A:65:PHE:HB3	1:C:13:GLU:OE1	2.19	0.43
1:C:118:ARG:O	1:C:121:ILE:HD11	2.18	0.43
1:B:101:PHE:CZ	1:B:108:VAL:HG12	2.53	0.43
1:C:122:GLY:C	1:C:124:PHE:H	2.21	0.43
1:A:105:TRP:HB3	1:C:175:ILE:HG12	2.00	0.43
1:E:6:LEU:HD11	1:E:39:SER:HB2	1.99	0.43
1:A:50:ILE:O	1:A:50:ILE:HG13	2.18	0.43
1:H:200:ARG:O	1:H:203:ILE:N	2.52	0.43
1:E:166:VAL:HA	1:E:255:VAL:HG11	2.01	0.43
1:H:155:TYR:HD2	1:H:190:TYR:CE1	2.36	0.43
1:E:73:LEU:HD11	1:E:77:GLU:CD	2.39	0.43
1:D:47:ASN:HD22	1:D:48:PRO:CD	2.28	0.43
1:G:163:ASP:HB3	1:G:166:VAL:HG23	2.00	0.43
1:D:24:ALA:O	1:D:208:LYS:HE3	2.18	0.43
1:F:137:PHE:HB3	1:F:140:LYS:HD2	2.00	0.43
1:D:192:ILE:O	1:D:192:ILE:HG13	2.18	0.43
1:A:4:ARG:NH1	1:A:4:ARG:HG3	2.33	0.43
1:B:146:ILE:HG22	1:B:147:THR:N	2.34	0.43
1:B:152:GLY:HA2	1:B:190:TYR:CE1	2.53	0.43
1:G:160:ILE:HG12	1:G:160:ILE:O	2.18	0.43
1:G:17:PHE:O	1:G:20:ALA:HB3	2.19	0.43
1:C:165:ASN:OD1	1:C:266:ASP:HA	2.19	0.43
1:H:169:TRP:HB3	1:H:170:PRO:HD3	1.99	0.43
1:A:95:ASP:HB3	1:A:215:TRP:CH2	2.53	0.43
1:A:5:ALA:HB2	1:A:34:TRP:CE3	2.53	0.43
1:G:273:LYS:O	1:G:273:LYS:HD3	2.18	0.43
1:C:14:ARG:HA	1:C:14:ARG:HD3	1.88	0.43
1:B:85:VAL:CG1	1:B:89:LYS:HE3	2.49	0.43
1:F:1:VAL:HA	1:F:215:TRP:CD1	2.53	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:263:ILE:H	1:B:263:ILE:HG13	1.66	0.43
1:G:135:GLY:HA3	1:G:179:CYS:O	2.19	0.43
1:B:77:GLU:OE1	1:B:79:HIS:CE1	2.70	0.43
1:E:40:ASP:O	1:E:41:LEU:C	2.57	0.43
1:H:213:ASN:O	1:H:215:TRP:N	2.52	0.43
1:A:52:ARG:C	1:A:54:ASP:H	2.22	0.43
1:H:152:GLY:O	1:H:155:TYR:N	2.49	0.43
1:C:132:TYR:O	1:C:135:GLY:N	2.51	0.43
1:G:55:ILE:HD13	1:G:70:GLU:HB3	2.00	0.43
3:B:1301:FAD:C8M	1:D:68:PRO:HG3	2.49	0.43
1:B:44:MET:O	1:B:45:ASN:HB3	2.19	0.43
1:D:64:ASN:HD22	1:D:64:ASN:HA	1.50	0.43
1:D:196:PRO:O	1:D:199:ALA:N	2.52	0.42
1:F:132:TYR:C	1:F:134:LYS:H	2.22	0.42
1:F:233:GLN:HA	1:F:233:GLN:NE2	2.34	0.42
1:E:132:TYR:HA	1:E:177:HIS:O	2.19	0.42
1:B:195:THR:HG22	1:B:199:ALA:HB3	2.00	0.42
1:C:142:ALA:HB2	1:C:181:PHE:CE1	2.54	0.42
1:E:67:TYR:HB3	1:E:68:PRO:HD3	2.00	0.42
1:D:251:PHE:HB3	1:D:264:PRO:HG3	2.02	0.42
1:E:241:GLU:H	1:E:241:GLU:CD	2.23	0.42
1:H:165:ASN:ND2	1:H:266:ASP:HA	2.34	0.42
1:E:132:TYR:OH	1:F:161:HIS:HD2	2.02	0.42
1:B:263:ILE:HD11	1:D:263:ILE:HD11	2.01	0.42
1:B:263:ILE:HA	1:B:264:PRO:HD3	1.89	0.42
1:A:47:ASN:HD21	1:A:49:ILE:N	2.15	0.42
1:B:72:VAL:O	1:B:75:TYR:HB3	2.18	0.42
1:F:9:LEU:HD22	1:F:22:LYS:HB2	2.01	0.42
1:E:126:TYR:CG	1:E:178:PHE:HE2	2.37	0.42
1:C:238:MET:CE	1:C:259:LEU:HD21	2.49	0.42
1:C:97:VAL:HG12	1:C:99:PHE:CE1	2.55	0.42
1:F:204:LEU:O	1:F:208:LYS:HG3	2.20	0.42
1:D:185:GLU:HG3	4:D:7305:HOH:O	2.19	0.42
1:A:52:ARG:C	1:A:54:ASP:N	2.73	0.42
1:B:166:VAL:HG11	1:D:169:TRP:CD1	2.53	0.42
1:B:199:ALA:O	1:B:202:GLN:HB3	2.19	0.42
1:G:128:TYR:CD1	2:G:7280:DTC:C19	3.03	0.42
1:E:163:ASP:CG	1:E:165:ASN:HB2	2.40	0.42
1:D:165:ASN:OD1	1:D:266:ASP:HA	2.19	0.42
1:E:84:ILE:HD11	1:E:118:ARG:NH1	2.34	0.42
1:C:45:ASN:HD21	1:D:45:ASN:HD21	1.66	0.42
1:G:244:ASP:O	1:G:246:GLU:N	2.53	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:172:GLN:HB3	1:F:183:VAL:HG11	2.01	0.42
1:F:187:GLN:HA	1:F:187:GLN:OE1	2.19	0.42
1:F:52:ARG:HG2	1:F:52:ARG:H	1.70	0.42
1:G:32:LYS:CE	1:G:212:GLU:HG2	2.49	0.42
1:F:195:THR:HG23	1:F:199:ALA:HB3	2.01	0.42
1:G:67:TYR:HB3	1:G:68:PRO:HD3	2.02	0.42
1:D:102:PRO:HG2	1:D:102:PRO:O	2.20	0.42
1:G:54:ASP:OD2	1:G:118:ARG:HD2	2.20	0.42
1:C:229:ASP:O	1:C:231:ASN:N	2.40	0.42
1:B:126:TYR:CD2	1:B:178:PHE:HE2	2.38	0.42
1:F:160:ILE:O	1:F:160:ILE:HG12	2.20	0.42
1:C:112:LEU:HD22	1:C:112:LEU:O	2.19	0.42
1:A:122:GLY:O	1:A:123:GLU:HB3	2.19	0.42
1:C:143:VAL:CG2	1:C:184:LEU:HB2	2.38	0.42
1:G:6:LEU:HD13	1:G:37:VAL:HG12	2.02	0.42
1:C:62:PRO:HD2	1:G:202:GLN:NE2	2.34	0.42
1:D:52:ARG:C	1:D:54:ASP:H	2.24	0.41
1:E:50:ILE:CG2	1:E:118:ARG:HG2	2.44	0.41
1:F:209:LYS:O	1:F:212:GLU:HG3	2.20	0.41
1:D:176:LEU:O	1:D:181:PHE:HB2	2.20	0.41
1:F:9:LEU:CD2	1:F:22:LYS:HD3	2.51	0.41
1:A:9:LEU:HD12	1:A:10:ALA:N	2.35	0.41
1:G:91:LEU:HA	1:G:91:LEU:HD23	1.88	0.41
1:F:64:ASN:HA	1:F:64:ASN:HD22	1.61	0.41
1:D:112:LEU:HD22	1:D:112:LEU:O	2.21	0.41
1:A:1:VAL:HA	1:A:215:TRP:NE1	2.35	0.41
1:B:87:GLU:O	1:B:90:LYS:HB2	2.20	0.41
1:G:141:LYS:HG2	1:G:182:GLN:HB2	2.01	0.41
1:B:14:ARG:HH21	1:B:43:ALA:CB	2.34	0.41
1:C:54:ASP:OD1	1:C:118:ARG:NH1	2.54	0.41
1:F:46:PHE:O	1:F:48:PRO:HD3	2.20	0.41
1:D:195:THR:CG2	1:D:199:ALA:HB3	2.51	0.41
1:B:185:GLU:O	1:B:210:ARG:NH2	2.47	0.41
1:H:155:TYR:CE1	1:H:161:HIS:CD2	3.09	0.41
1:G:22:LYS:HB3	1:G:22:LYS:HE3	1.94	0.41
1:B:206:GLY:O	1:B:209:LYS:HB3	2.20	0.41
1:B:137:PHE:O	1:B:139:SER:N	2.54	0.41
1:D:207:TRP:O	1:D:211:LEU:HG	2.21	0.41
1:G:116:PHE:O	1:G:120:PHE:HB2	2.20	0.41
1:F:3:ARG:HG2	1:F:3:ARG:NH1	2.35	0.41
1:C:47:ASN:O	1:C:118:ARG:NE	2.52	0.41
1:D:3:ARG:HE	1:D:3:ARG:HA	1.85	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:96:LEU:HA	1:A:141:LYS:O	2.21	0.41
1:C:47:ASN:C	1:C:47:ASN:ND2	2.74	0.41
1:C:54:ASP:CG	1:C:118:ARG:HH11	2.24	0.41
1:H:122:GLY:O	1:H:124:PHE:N	2.53	0.41
1:B:192:ILE:HG23	1:B:193:GLY:N	2.36	0.41
1:A:185:GLU:O	1:A:210:ARG:NH2	2.33	0.41
1:F:29:LEU:O	1:F:34:TRP:HB2	2.21	0.41
1:E:228:PHE:CD1	1:E:228:PHE:N	2.88	0.41
1:G:96:LEU:HD11	1:G:143:VAL:HG23	2.02	0.41
1:C:141:LYS:HD3	1:C:184:LEU:HD21	2.01	0.41
1:D:122:GLY:O	1:D:123:GLU:HB2	2.21	0.41
1:G:122:GLY:O	1:G:123:GLU:HB2	2.20	0.41
1:H:17:PHE:CE1	1:H:204:LEU:HD21	2.56	0.41
1:D:265:THR:O	1:D:266:ASP:C	2.59	0.41
1:C:1:VAL:CG1	1:C:2:GLY:H	2.33	0.41
1:B:185:GLU:OE2	1:B:270:LYS:HA	2.21	0.41
2:E:5280:DTC:HC3	1:F:105:TRP:CZ2	2.56	0.41
1:H:44:MET:O	1:H:45:ASN:C	2.59	0.41
1:E:132:TYR:HD1	1:E:177:HIS:CD2	2.38	0.41
1:B:6:LEU:HD22	1:B:90:LYS:HB3	2.03	0.41
1:A:154:MET:HG2	1:C:236:PHE:HB2	2.02	0.41
1:F:244:ASP:C	1:F:246:GLU:H	2.23	0.41
1:C:142:ALA:HB2	1:C:181:PHE:CD1	2.56	0.41
1:F:103:LEU:CB	1:F:148:THR:HG22	2.51	0.41
1:E:214:ILE:HD12	1:E:217:GLU:OE2	2.20	0.41
1:H:149:GLY:O	1:H:191:SER:HA	2.21	0.41
1:G:263:ILE:HA	1:G:264:PRO:HD3	1.95	0.41
1:H:263:ILE:HA	1:H:264:PRO:HD2	1.89	0.41
1:F:113:LYS:O	1:F:117:GLU:HG3	2.20	0.41
1:C:172:GLN:HE22	1:C:186:PRO:HB3	1.85	0.41
1:F:14:ARG:HH21	1:F:43:ALA:CB	2.12	0.41
1:H:195:THR:CG2	1:H:199:ALA:HB3	2.46	0.41
1:H:72:VAL:HG12	1:H:76:LYS:HE3	2.03	0.41
1:G:65:PHE:CD1	1:G:70:GLU:HG3	2.56	0.41
1:B:173:SER:HB2	1:B:222:PHE:HE1	1.85	0.41
1:A:173:SER:HA	1:A:177:HIS:HB3	2.03	0.41
1:B:72:VAL:HG22	1:B:122:GLY:CA	2.52	0.40
1:C:45:ASN:CG	1:C:45:ASN:O	2.59	0.40
1:B:169:TRP:CE2	1:B:256:GLY:HA3	2.57	0.40
1:F:57:GLY:HA3	1:F:79:HIS:CD2	2.56	0.40
1:H:238:MET:CE	1:H:259:LEU:HD21	2.49	0.40
1:D:101:PHE:CE1	1:D:146:ILE:HG12	2.55	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:65:PHE:CD1	1:C:70:GLU:HG3	2.56	0.40
1:H:147:THR:HA	1:H:189:THR:OG1	2.21	0.40
1:B:240:LYS:HG2	1:B:241:GLU:OE2	2.21	0.40
1:G:105:TRP:HB2	1:H:113:LYS:HE3	2.03	0.40
1:B:53:LYS:HG2	1:B:53:LYS:O	2.22	0.40
1:G:145:SER:HA	1:G:187:GLN:HB3	2.03	0.40
1:G:226:SER:O	1:G:239:LYS:HE3	2.21	0.40
1:E:83:ASP:OD2	1:E:118:ARG:NH2	2.46	0.40
1:C:130:ALA:HB1	1:C:134:LYS:O	2.20	0.40
1:D:230:LEU:HA	1:D:236:PHE:CD2	2.56	0.40
1:A:160:ILE:HA	1:C:228:PHE:CE2	2.57	0.40
1:C:163:ASP:OD2	1:C:165:ASN:HB2	2.22	0.40
1:F:103:LEU:HB3	1:F:148:THR:HG22	2.02	0.40
1:B:25:ALA:HA	1:B:211:LEU:HD12	2.03	0.40
1:C:44:MET:O	1:C:45:ASN:HB3	2.21	0.40
1:H:174:GLY:O	1:H:178:PHE:CB	2.70	0.40
1:H:26:ALA:CB	1:H:36:VAL:HG11	2.50	0.40
1:H:183:VAL:HG12	1:H:220:LEU:HD12	2.03	0.40
1:F:246:GLU:C	1:F:248:ASN:H	2.23	0.40
1:H:255:VAL:HG21	1:H:268:GLN:HG2	2.02	0.40
1:F:138:ARG:HA	1:F:180:GLY:O	2.22	0.40
1:B:200:ARG:NH1	3:B:1301:FAD:N3A	2.56	0.40
1:E:113:LYS:O	1:E:117:GLU:HG3	2.22	0.40
1:B:49:ILE:C	1:B:118:ARG:HD3	2.40	0.40
1:G:130:ALA:O	1:G:135:GLY:HA2	2.22	0.40
1:E:46:PHE:HE2	1:E:115:TRP:HA	1.86	0.40
1:B:137:PHE:C	1:B:139:SER:N	2.75	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	271/273 (99%)	247 (91%)	21 (8%)	3 (1%)	21 53

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	271/273 (99%)	246 (91%)	21 (8%)	4 (2%)	15	43
1	C	271/273 (99%)	246 (91%)	18 (7%)	7 (3%)	8	23
1	D	271/273 (99%)	239 (88%)	29 (11%)	3 (1%)	21	53
1	E	271/273 (99%)	242 (89%)	23 (8%)	6 (2%)	10	29
1	F	271/273 (99%)	241 (89%)	29 (11%)	1 (0%)	43	79
1	G	271/273 (99%)	245 (90%)	21 (8%)	5 (2%)	13	36
1	H	271/273 (99%)	235 (87%)	25 (9%)	11 (4%)	4	12
All	All	2168/2184 (99%)	1941 (90%)	187 (9%)	40 (2%)	13	36

All (40) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	133	ASP
1	C	230	LEU
1	H	63	ALA
1	H	133	ASP
1	H	197	ALA
1	H	198	ASP
1	H	214	ILE
1	A	239	LYS
1	D	16	SER
1	D	133	ASP
1	F	133	ASP
1	G	123	GLU
1	G	133	ASP
1	B	41	LEU
1	B	133	ASP
1	E	133	ASP
1	E	232	PHE
1	G	32	LYS
1	A	123	GLU
1	A	232	PHE
1	B	131	MET
1	B	138	ARG
1	C	164	MET
1	C	191	SER
1	C	239	LYS
1	H	123	GLU
1	H	220	LEU
1	C	52	ARG

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Mol	Chain	Res	Type
1	D	53	LYS
1	E	191	SER
1	E	217	GLU
1	E	230	LEU
1	G	245	GLU
1	H	45	ASN
1	H	176	LEU
1	E	219	PRO
1	C	68	PRO
1	G	214	ILE
1	H	68	PRO
1	H	122	GLY

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	227/227 (100%)	219 (96%)	8 (4%)	48	81
1	B	227/227 (100%)	221 (97%)	6 (3%)	59	89
1	C	227/227 (100%)	222 (98%)	5 (2%)	64	92
1	D	227/227 (100%)	220 (97%)	7 (3%)	52	85
1	E	227/227 (100%)	214 (94%)	13 (6%)	29	61
1	F	227/227 (100%)	220 (97%)	7 (3%)	52	85
1	G	227/227 (100%)	218 (96%)	9 (4%)	42	77
1	H	227/227 (100%)	214 (94%)	13 (6%)	29	61
All	All	1816/1816 (100%)	1748 (96%)	68 (4%)	45	80

All (68) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	4	ARG
1	A	14	ARG
1	A	29	LEU
1	A	47	ASN

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Mol	Chain	Res	Type
1	A	82	PRO
1	A	189	THR
1	A	218	THR
1	B	22	LYS
1	B	45	ASN
1	B	47	ASN
1	B	112	LEU
1	B	218	THR
1	B	273	LYS
1	C	22	LYS
1	C	29	LEU
1	C	47	ASN
1	C	112	LEU
1	C	218	THR
1	D	3	ARG
1	D	29	LEU
1	D	47	ASN
1	D	64	ASN
1	D	91	LEU
1	D	112	LEU
1	D	198	ASP
1	E	29	LEU
1	E	39	SER
1	E	45	ASN
1	E	92	GLU
1	E	112	LEU
1	E	127	THR
1	E	143	VAL
1	E	158	GLN
1	E	218	THR
1	E	232	PHE
1	E	240	LYS
1	E	262	SER
1	E	273	LYS
1	F	29	LEU
1	F	39	SER
1	F	47	ASN
1	F	207	TRP
1	F	209	LYS
1	F	218	THR
1	F	226	SER
1	G	22	LYS

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Mol	Chain	Res	Type
1	G	29	LEU
1	G	48	PRO
1	G	52	ARG
1	G	112	LEU
1	G	158	GLN
1	G	218	THR
1	G	241	GLU
1	G	273	LYS
1	H	29	LEU
1	H	64	ASN
1	H	81	SER
1	H	82	PRO
1	H	91	LEU
1	H	127	THR
1	H	148	THR
1	H	198	ASP
1	H	207	TRP
1	H	209	LYS
1	H	232	PHE
1	H	240	LYS
1	H	246	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	47	ASN
1	A	66	GLN
1	A	104	GLN
1	A	158	GLN
1	A	172	GLN
1	A	267	ASN
1	B	45	ASN
1	B	47	ASN
1	B	79	HIS
1	B	172	GLN
1	B	267	ASN
1	C	45	ASN
1	C	47	ASN
1	C	104	GLN
1	C	172	GLN
1	C	267	ASN
1	D	45	ASN

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Mol	Chain	Res	Type
1	D	47	ASN
1	D	64	ASN
1	D	79	HIS
1	D	161	HIS
1	D	172	GLN
1	D	267	ASN
1	E	45	ASN
1	E	66	GLN
1	E	158	GLN
1	E	194	HIS
1	F	45	ASN
1	F	47	ASN
1	F	64	ASN
1	F	79	HIS
1	F	104	GLN
1	F	161	HIS
1	F	233	GLN
1	F	267	ASN
1	G	45	ASN
1	G	172	GLN
1	G	177	HIS
1	G	268	GLN
1	H	47	ASN
1	H	64	ASN
1	H	79	HIS
1	H	88	GLN
1	H	172	GLN
1	H	233	GLN
1	H	267	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

16 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	DTC	A	2280	-	28,28,28	5.05	24 (85%)	41,41,41	2.57	11 (26%)
3	FAD	A	301	-	58,58,58	11.78	18 (31%)	85,89,89	2.62	19 (22%)
3	FAD	B	1301	-	58,58,58	12.29	17 (29%)	85,89,89	2.53	14 (16%)
2	DTC	B	3280	-	28,28,28	5.02	23 (82%)	41,41,41	2.64	12 (29%)
3	FAD	C	2301	-	58,58,58	12.39	14 (24%)	85,89,89	2.51	18 (21%)
2	DTC	C	280	-	28,28,28	5.16	24 (85%)	41,41,41	2.52	11 (26%)
2	DTC	D	1280	-	28,28,28	5.13	23 (82%)	41,41,41	2.59	12 (29%)
3	FAD	D	3301	-	58,58,58	12.14	17 (29%)	85,89,89	2.50	18 (21%)
2	DTC	E	4280	-	28,28,28	5.09	24 (85%)	41,41,41	2.54	11 (26%)
3	FAD	E	4301	-	58,58,58	13.00	14 (24%)	85,89,89	2.53	19 (22%)
2	DTC	E	5280	-	28,28,28	5.06	23 (82%)	41,41,41	2.60	11 (26%)
3	FAD	F	5301	-	58,58,58	11.94	18 (31%)	85,89,89	2.48	17 (20%)
3	FAD	G	6301	-	58,58,58	11.69	16 (27%)	85,89,89	2.57	18 (21%)
2	DTC	G	7280	-	28,28,28	5.09	24 (85%)	41,41,41	2.61	10 (24%)
2	DTC	H	6280	-	28,28,28	5.06	24 (85%)	41,41,41	2.59	12 (29%)
3	FAD	H	7301	-	58,58,58	11.55	16 (27%)	85,89,89	2.57	14 (16%)

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	DTC	A	2280	-	2/2/6/6	0/4/36/36	0/0/4/4
3	FAD	A	301	-	-	0/34/50/50	0/1/6/6
3	FAD	B	1301	-	-	0/34/50/50	0/1/6/6
2	DTC	B	3280	-	2/2/6/6	0/4/36/36	0/0/4/4

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	FAD	C	2301	-	-	0/34/50/50	0/1/6/6
2	DTC	C	280	-	2/2/6/6	0/4/36/36	0/0/4/4
2	DTC	D	1280	-	2/2/6/6	0/4/36/36	0/0/4/4
3	FAD	D	3301	-	-	0/34/50/50	0/1/6/6
2	DTC	E	4280	-	2/2/6/6	0/4/36/36	0/0/4/4
3	FAD	E	4301	-	-	0/34/50/50	0/1/6/6
2	DTC	E	5280	-	2/2/6/6	0/4/36/36	0/0/4/4
3	FAD	F	5301	-	-	0/34/50/50	0/1/6/6
3	FAD	G	6301	-	-	0/34/50/50	0/1/6/6
2	DTC	G	7280	-	2/2/6/6	0/4/36/36	0/0/4/4
2	DTC	H	6280	-	2/2/6/6	0/4/36/36	0/0/4/4
3	FAD	H	7301	-	-	0/34/50/50	0/1/6/6

All (319) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	E	4301	FAD	PA-O2A	97.71	5.91	1.55
3	C	2301	FAD	PA-O2A	92.88	5.69	1.55
3	B	1301	FAD	PA-O2A	92.19	5.66	1.55
3	D	3301	FAD	PA-O2A	91.25	5.62	1.55
3	F	5301	FAD	PA-O2A	89.46	5.54	1.55
3	A	301	FAD	PA-O2A	88.22	5.48	1.55
3	G	6301	FAD	PA-O2A	87.51	5.45	1.55
3	H	7301	FAD	PA-O2A	86.39	5.40	1.55
2	C	280	DTC	O17-C8	12.96	1.41	1.22
2	H	6280	DTC	O17-C8	12.92	1.41	1.22
2	G	7280	DTC	O17-C8	12.77	1.40	1.22
2	A	2280	DTC	O17-C8	12.71	1.40	1.22
2	D	1280	DTC	O17-C8	12.69	1.40	1.22
2	B	3280	DTC	O17-C8	12.46	1.40	1.22
2	E	5280	DTC	O17-C8	12.43	1.40	1.22
2	E	4280	DTC	O17-C8	12.41	1.40	1.22
2	E	4280	DTC	O38-C14	11.86	1.39	1.22
2	C	280	DTC	O38-C14	11.81	1.39	1.22
2	H	6280	DTC	O38-C14	11.64	1.39	1.22
2	D	1280	DTC	O38-C14	11.64	1.39	1.22
2	E	5280	DTC	O38-C14	11.58	1.39	1.22
2	G	7280	DTC	O38-C14	11.43	1.39	1.22
2	A	2280	DTC	O38-C14	11.31	1.38	1.22
2	B	3280	DTC	O38-C14	11.14	1.38	1.22
2	C	280	DTC	C15-C13	-10.86	1.31	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	1280	DTC	C15-C13	-10.58	1.31	1.53
2	E	5280	DTC	C15-C13	-10.35	1.32	1.53
2	A	2280	DTC	C15-C13	-10.33	1.32	1.53
2	H	6280	DTC	C15-C13	-10.16	1.32	1.53
2	E	4280	DTC	C15-C13	-10.10	1.32	1.53
2	B	3280	DTC	C15-C13	-10.00	1.32	1.53
2	G	7280	DTC	C15-C13	-9.91	1.32	1.53
2	E	4280	DTC	O32-C12	8.35	1.42	1.21
2	A	2280	DTC	O32-C12	8.27	1.42	1.21
2	G	7280	DTC	O32-C12	8.26	1.42	1.21
2	C	280	DTC	O32-C12	8.25	1.42	1.21
2	E	5280	DTC	O32-C12	8.18	1.42	1.21
2	B	3280	DTC	O32-C12	8.18	1.42	1.21
2	D	1280	DTC	O32-C12	8.18	1.42	1.21
2	H	6280	DTC	O32-C12	8.12	1.41	1.21
3	H	7301	FAD	P-O3P	-7.89	1.45	1.59
2	G	7280	DTC	O16-C6	7.47	1.40	1.21
3	B	1301	FAD	P-O3P	-7.45	1.46	1.59
2	D	1280	DTC	O16-C6	7.42	1.40	1.21
2	E	4280	DTC	O16-C6	7.33	1.39	1.21
2	E	5280	DTC	O16-C6	7.31	1.39	1.21
2	C	280	DTC	O16-C6	7.27	1.39	1.21
2	B	3280	DTC	O16-C6	7.22	1.39	1.21
3	G	6301	FAD	P-O3P	-7.20	1.46	1.59
2	A	2280	DTC	O16-C6	7.19	1.39	1.21
3	C	2301	FAD	P-O3P	-7.15	1.46	1.59
3	F	5301	FAD	P-O3P	-7.14	1.46	1.59
3	A	301	FAD	P-O3P	-7.14	1.46	1.59
2	H	6280	DTC	O16-C6	7.08	1.39	1.21
3	E	4301	FAD	P-O3P	-6.77	1.47	1.59
3	C	2301	FAD	C9A-N10	6.70	1.48	1.38
3	E	4301	FAD	C9A-N10	6.42	1.48	1.38
3	D	3301	FAD	P-O3P	-5.87	1.49	1.59
3	G	6301	FAD	C9A-N10	5.82	1.47	1.38
3	A	301	FAD	C9A-N10	5.74	1.47	1.38
2	C	280	DTC	C9-C10	5.67	1.51	1.40
2	G	7280	DTC	C9-C10	5.50	1.51	1.40
2	H	6280	DTC	C9-C10	5.49	1.51	1.40
2	E	4280	DTC	C9-C10	5.48	1.51	1.40
3	H	7301	FAD	C9A-N10	5.46	1.46	1.38
2	B	3280	DTC	C9-C10	5.37	1.50	1.40
2	D	1280	DTC	C9-C10	5.30	1.50	1.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2280	DTC	C9-C10	5.25	1.50	1.40
3	B	1301	FAD	C9A-N10	5.24	1.46	1.38
3	F	5301	FAD	C9A-N10	5.20	1.46	1.38
2	E	5280	DTC	C9-C10	5.16	1.50	1.40
3	A	301	FAD	C1'-C2'	4.91	1.56	1.51
3	G	6301	FAD	C1'-C2'	4.61	1.56	1.51
3	E	4301	FAD	C4-C4X	4.49	1.48	1.41
3	H	7301	FAD	C1'-C2'	4.43	1.55	1.51
3	F	5301	FAD	O4B-C1B	4.42	1.48	1.41
3	C	2301	FAD	C1'-C2'	4.35	1.55	1.51
3	F	5301	FAD	C1'-C2'	4.34	1.55	1.51
2	B	3280	DTC	C18-C19	4.25	1.48	1.39
3	G	6301	FAD	O4B-C1B	4.21	1.47	1.41
3	A	301	FAD	O4B-C1B	4.20	1.47	1.41
2	A	2280	DTC	O21-C19	4.17	1.45	1.38
3	C	2301	FAD	C4X-C10	4.17	1.48	1.40
2	D	1280	DTC	O21-C19	4.15	1.45	1.38
2	E	4280	DTC	C18-C19	4.15	1.48	1.39
2	G	7280	DTC	O21-C19	4.13	1.45	1.38
3	F	5301	FAD	C4X-C10	4.08	1.48	1.40
3	E	4301	FAD	C1'-C2'	4.07	1.55	1.51
2	E	4280	DTC	O21-C19	4.06	1.45	1.38
2	A	2280	DTC	C18-C19	4.05	1.48	1.39
2	B	3280	DTC	C5-C20	4.05	1.46	1.39
3	B	1301	FAD	C4X-C10	4.02	1.47	1.40
3	H	7301	FAD	C4X-C10	3.98	1.47	1.40
2	G	7280	DTC	C18-C19	3.97	1.48	1.39
2	E	5280	DTC	C5-C20	3.96	1.46	1.39
2	G	7280	DTC	C5-C20	3.95	1.46	1.39
3	A	301	FAD	C4X-C10	3.95	1.47	1.40
2	H	6280	DTC	C5-C20	3.95	1.46	1.39
3	D	3301	FAD	O4B-C1B	3.95	1.47	1.41
3	C	2301	FAD	C4-C4X	3.94	1.47	1.41
2	D	1280	DTC	C18-C19	3.94	1.48	1.39
2	C	280	DTC	C18-C19	3.93	1.48	1.39
2	E	5280	DTC	C18-C19	3.93	1.48	1.39
2	B	3280	DTC	O21-C19	3.91	1.44	1.38
2	C	280	DTC	O21-C19	3.90	1.44	1.38
3	H	7301	FAD	O4B-C1B	3.89	1.47	1.41
3	C	2301	FAD	O4B-C1B	3.89	1.47	1.41
2	D	1280	DTC	C5-C20	3.88	1.46	1.39
3	D	3301	FAD	C4-C4X	3.85	1.47	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	5280	DTC	C13-C12	-3.82	1.44	1.52
2	E	4280	DTC	O21-C12	3.81	1.44	1.36
2	E	4280	DTC	C5-C20	3.80	1.46	1.39
3	D	3301	FAD	C9A-N10	3.80	1.44	1.38
3	E	4301	FAD	O5'-C5'	3.79	1.60	1.44
2	D	1280	DTC	C13-C12	-3.79	1.44	1.52
3	B	1301	FAD	C2-N3	3.79	1.44	1.37
3	E	4301	FAD	C4X-C10	3.77	1.47	1.40
3	F	5301	FAD	C2-N3	3.77	1.44	1.37
3	D	3301	FAD	C4X-C10	3.76	1.47	1.40
3	E	4301	FAD	C2-N3	3.72	1.44	1.37
2	H	6280	DTC	C18-C19	3.70	1.47	1.39
3	B	1301	FAD	O4B-C1B	3.70	1.47	1.41
3	H	7301	FAD	O5'-C5'	3.68	1.60	1.44
3	H	7301	FAD	C4-C4X	3.67	1.47	1.41
3	F	5301	FAD	C4-C4X	3.67	1.47	1.41
2	E	5280	DTC	O21-C19	3.66	1.44	1.38
3	G	6301	FAD	C4-C4X	3.66	1.47	1.41
3	G	6301	FAD	C4X-C10	3.65	1.47	1.40
3	A	301	FAD	O5'-C5'	3.64	1.59	1.44
2	C	280	DTC	C13-C12	-3.63	1.45	1.52
2	G	7280	DTC	O21-C12	3.61	1.43	1.36
2	A	2280	DTC	C5-C20	3.61	1.46	1.39
2	C	280	DTC	C5-C20	3.60	1.46	1.39
3	C	2301	FAD	O5'-C5'	3.59	1.59	1.44
3	C	2301	FAD	P-O2P	-3.58	1.39	1.55
3	D	3301	FAD	C2-N3	3.57	1.44	1.37
3	E	4301	FAD	O4B-C1B	3.55	1.46	1.41
3	B	1301	FAD	C4-C4X	3.55	1.47	1.41
3	C	2301	FAD	C2-N3	3.54	1.44	1.37
2	H	6280	DTC	O21-C19	3.54	1.44	1.38
2	G	7280	DTC	O5-C6	3.54	1.43	1.36
2	A	2280	DTC	O21-C12	3.54	1.43	1.36
2	D	1280	DTC	O5-C6	3.53	1.43	1.36
3	A	301	FAD	O5B-C5B	-3.53	1.30	1.44
3	B	1301	FAD	O5B-C5B	-3.52	1.30	1.44
2	H	6280	DTC	O21-C12	3.51	1.43	1.36
2	B	3280	DTC	C13-C12	-3.51	1.45	1.52
2	H	6280	DTC	C13-C12	-3.50	1.45	1.52
3	D	3301	FAD	O5'-C5'	3.50	1.59	1.44
2	B	3280	DTC	O5-C6	3.49	1.43	1.36
2	D	1280	DTC	O21-C12	3.48	1.43	1.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1301	FAD	P-O2P	-3.48	1.39	1.55
2	E	5280	DTC	O21-C12	3.48	1.43	1.36
2	B	3280	DTC	O21-C12	3.46	1.43	1.36
3	C	2301	FAD	O5B-C5B	-3.45	1.30	1.44
2	C	280	DTC	O5-C6	3.44	1.43	1.36
2	E	4280	DTC	O5-C6	3.44	1.43	1.36
3	F	5301	FAD	P-O2P	-3.43	1.39	1.55
2	D	1280	DTC	O5-C10	3.43	1.44	1.38
3	G	6301	FAD	O5B-C5B	-3.39	1.30	1.44
3	G	6301	FAD	P-O2P	-3.38	1.39	1.55
2	G	7280	DTC	C13-C12	-3.37	1.45	1.52
2	H	6280	DTC	O5-C6	3.36	1.43	1.36
3	D	3301	FAD	P-O2P	-3.35	1.40	1.55
2	C	280	DTC	O21-C12	3.33	1.43	1.36
2	E	5280	DTC	O5-C6	3.31	1.43	1.36
3	A	301	FAD	P-O2P	-3.29	1.40	1.55
3	F	5301	FAD	O5B-C5B	-3.29	1.31	1.44
3	A	301	FAD	C4-C4X	3.29	1.46	1.41
2	H	6280	DTC	O5-C10	3.28	1.43	1.38
3	E	4301	FAD	O5B-C5B	-3.28	1.31	1.44
3	G	6301	FAD	O5'-C5'	3.26	1.58	1.44
3	H	7301	FAD	O5B-C5B	-3.26	1.31	1.44
2	E	4280	DTC	C20-C19	3.23	1.46	1.40
3	F	5301	FAD	O5'-C5'	3.19	1.58	1.44
3	E	4301	FAD	P-O2P	-3.19	1.40	1.55
2	A	2280	DTC	C13-C12	-3.18	1.46	1.52
3	G	6301	FAD	C2-N3	3.16	1.43	1.37
2	E	4280	DTC	C13-C12	-3.16	1.46	1.52
2	G	7280	DTC	O5-C10	3.16	1.43	1.38
2	A	2280	DTC	O5-C6	3.13	1.42	1.36
2	C	280	DTC	C20-C19	3.13	1.46	1.40
3	D	3301	FAD	C1'-C2'	3.13	1.54	1.51
3	A	301	FAD	C2-N3	3.12	1.43	1.37
2	A	2280	DTC	C20-C19	3.10	1.46	1.40
3	B	1301	FAD	C1'-C2'	3.10	1.54	1.51
3	D	3301	FAD	O5B-C5B	-3.10	1.32	1.44
2	B	3280	DTC	C16-C5	3.10	1.46	1.39
3	H	7301	FAD	P-O2P	-3.09	1.41	1.55
2	E	5280	DTC	O5-C10	3.05	1.43	1.38
2	B	3280	DTC	C20-C19	3.04	1.46	1.40
2	G	7280	DTC	C20-C19	3.01	1.46	1.40
2	E	5280	DTC	C16-C17	2.99	1.46	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2280	DTC	C16-C17	2.97	1.46	1.37
2	E	5280	DTC	C7-C8	-2.97	1.46	1.52
2	E	4280	DTC	C16-C5	2.96	1.45	1.39
2	C	280	DTC	O5-C10	2.95	1.43	1.38
2	A	2280	DTC	O5-C10	2.93	1.43	1.38
2	A	2280	DTC	C16-C5	2.92	1.45	1.39
2	B	3280	DTC	O5-C10	2.92	1.43	1.38
2	G	7280	DTC	C16-C5	2.92	1.45	1.39
2	D	1280	DTC	C16-C17	2.92	1.46	1.37
2	E	4280	DTC	C16-C17	2.91	1.46	1.37
2	C	280	DTC	C16-C17	2.91	1.46	1.37
3	H	7301	FAD	C2-N3	2.91	1.43	1.37
2	G	7280	DTC	C16-C17	2.90	1.46	1.37
2	E	5280	DTC	C16-C5	2.90	1.45	1.39
3	H	7301	FAD	PA-O5B	-2.89	1.46	1.59
2	E	5280	DTC	C20-C19	2.89	1.46	1.40
2	H	6280	DTC	C16-C17	2.86	1.46	1.37
2	D	1280	DTC	C1-C9	2.84	1.44	1.39
2	B	3280	DTC	C16-C17	2.84	1.46	1.37
2	E	4280	DTC	O5-C10	2.84	1.43	1.38
2	G	7280	DTC	C7-C8	-2.84	1.46	1.52
2	C	280	DTC	C7-C8	-2.83	1.46	1.52
3	B	1301	FAD	C5X-N5	2.83	1.39	1.35
2	E	5280	DTC	C9-C8	-2.82	1.43	1.48
2	B	3280	DTC	C7-C8	-2.82	1.46	1.52
2	B	3280	DTC	C15-C7	2.81	1.59	1.53
2	H	6280	DTC	C20-C19	2.81	1.46	1.40
2	D	1280	DTC	C7-C8	-2.80	1.46	1.52
2	C	280	DTC	C16-C5	2.78	1.45	1.39
3	B	1301	FAD	O5'-C5'	2.77	1.56	1.44
2	D	1280	DTC	C16-C5	2.72	1.45	1.39
2	A	2280	DTC	C7-C8	-2.72	1.46	1.52
2	D	1280	DTC	C20-C19	2.71	1.45	1.40
2	H	6280	DTC	C1-C9	2.70	1.44	1.39
2	E	4280	DTC	C1-C9	2.70	1.44	1.39
3	B	1301	FAD	C2B-C1B	-2.69	1.49	1.53
3	B	1301	FAD	PA-O5B	-2.69	1.47	1.59
2	D	1280	DTC	C17-C18	2.69	1.45	1.39
2	H	6280	DTC	C17-C18	2.67	1.45	1.39
2	H	6280	DTC	C16-C5	2.66	1.45	1.39
3	D	3301	FAD	C5X-N5	2.65	1.39	1.35
3	A	301	FAD	PA-O5B	-2.65	1.47	1.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	7280	DTC	C1-C9	2.63	1.44	1.39
2	B	3280	DTC	C1-C9	2.62	1.44	1.39
2	A	2280	DTC	C17-C18	2.62	1.45	1.39
2	B	3280	DTC	C2-C1	2.62	1.45	1.39
2	B	3280	DTC	C17-C18	2.60	1.45	1.39
2	E	5280	DTC	C1-C9	2.58	1.44	1.39
2	E	4280	DTC	C9-C8	-2.57	1.44	1.48
2	A	2280	DTC	C1-C9	2.56	1.44	1.39
2	E	4280	DTC	C7-C8	-2.56	1.47	1.52
2	G	7280	DTC	C3-C4	2.56	1.44	1.39
2	C	280	DTC	C9-C8	-2.56	1.44	1.48
2	E	5280	DTC	C17-C18	2.54	1.44	1.39
3	G	6301	FAD	PA-O5B	-2.53	1.47	1.59
3	C	2301	FAD	C5X-N5	2.53	1.39	1.35
2	H	6280	DTC	C3-C4	2.52	1.44	1.39
2	E	4280	DTC	C17-C18	2.51	1.44	1.39
2	D	1280	DTC	C3-C4	2.51	1.44	1.39
2	D	1280	DTC	C2-C1	2.51	1.44	1.39
3	H	7301	FAD	C8-C7	2.51	1.48	1.40
2	C	280	DTC	C3-C4	2.50	1.44	1.39
2	G	7280	DTC	C17-C18	2.50	1.44	1.39
2	E	4280	DTC	C15-C7	2.49	1.58	1.53
2	B	3280	DTC	C3-C4	2.48	1.44	1.39
2	G	7280	DTC	C9-C8	-2.44	1.44	1.48
2	E	5280	DTC	C3-C4	2.44	1.44	1.39
3	D	3301	FAD	C4A-N3A	2.44	1.39	1.35
2	A	2280	DTC	C2-C1	2.44	1.44	1.39
2	H	6280	DTC	C15-C7	2.43	1.58	1.53
2	H	6280	DTC	C2-C1	2.43	1.44	1.39
2	C	280	DTC	C1-C9	2.42	1.44	1.39
3	F	5301	FAD	PA-O5B	-2.41	1.48	1.59
3	G	6301	FAD	C5X-N5	2.40	1.39	1.35
2	A	2280	DTC	C9-C8	-2.40	1.44	1.48
3	F	5301	FAD	C5X-N5	2.40	1.39	1.35
2	E	4280	DTC	C2-C1	2.40	1.44	1.39
2	C	280	DTC	C17-C18	2.39	1.44	1.39
2	H	6280	DTC	C7-C8	-2.39	1.47	1.52
2	E	5280	DTC	C2-C1	2.39	1.44	1.39
3	C	2301	FAD	PA-O5B	-2.38	1.48	1.59
2	A	2280	DTC	C3-C4	2.36	1.44	1.39
3	D	3301	FAD	C2B-C1B	-2.36	1.50	1.53
2	G	7280	DTC	C15-C7	2.35	1.58	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	3301	FAD	PA-O5B	-2.33	1.48	1.59
2	E	5280	DTC	C3-C2	2.33	1.44	1.37
2	E	4280	DTC	C3-C4	2.32	1.44	1.39
2	D	1280	DTC	C3-C2	2.30	1.44	1.37
2	H	6280	DTC	C3-C2	2.30	1.44	1.37
3	B	1301	FAD	C5'-C4'	-2.30	1.48	1.51
2	C	280	DTC	C2-C1	2.30	1.44	1.39
2	C	280	DTC	C3-C2	2.30	1.44	1.37
2	G	7280	DTC	C2-C1	2.26	1.44	1.39
3	F	5301	FAD	C4A-N9A	2.25	1.41	1.37
3	F	5301	FAD	P-O5'	-2.25	1.49	1.59
2	G	7280	DTC	C3-C2	2.24	1.44	1.37
2	H	6280	DTC	C9-C8	-2.22	1.44	1.48
3	E	4301	FAD	PA-O5B	-2.22	1.49	1.59
3	B	1301	FAD	P-O5'	-2.21	1.49	1.59
2	B	3280	DTC	C3-C2	2.20	1.44	1.37
3	G	6301	FAD	C4A-N3A	2.20	1.39	1.35
3	E	4301	FAD	C1'-N10	2.17	1.50	1.48
2	E	4280	DTC	C3-C2	2.17	1.44	1.37
2	A	2280	DTC	C3-C2	2.16	1.44	1.37
3	C	2301	FAD	C2B-C1B	-2.16	1.50	1.53
3	A	301	FAD	C4A-N3A	2.15	1.38	1.35
3	A	301	FAD	C1'-N10	2.15	1.50	1.48
2	D	1280	DTC	C9-C8	-2.14	1.44	1.48
3	A	301	FAD	C5X-N5	2.13	1.38	1.35
3	F	5301	FAD	C8-C7	2.12	1.47	1.40
3	B	1301	FAD	C4A-N3A	2.10	1.38	1.35
3	H	7301	FAD	C5X-N5	2.09	1.38	1.35
3	F	5301	FAD	C2A-N3A	2.08	1.36	1.32
3	A	301	FAD	C2A-N3A	2.07	1.36	1.32
3	D	3301	FAD	C2A-N3A	2.07	1.36	1.32
3	H	7301	FAD	C1'-N10	2.06	1.50	1.48
3	A	301	FAD	P-O5'	-2.05	1.49	1.59
3	G	6301	FAD	P-O5'	-2.05	1.49	1.59
3	F	5301	FAD	C4A-N3A	2.04	1.38	1.35
3	G	6301	FAD	C1'-N10	2.03	1.50	1.48
3	E	4301	FAD	C2B-C1B	-2.03	1.50	1.53
2	A	2280	DTC	C15-C7	2.03	1.57	1.53
2	C	280	DTC	C15-C7	2.01	1.57	1.53
3	A	301	FAD	C8-C7	2.01	1.46	1.40
3	H	7301	FAD	O2-C2	-2.00	1.19	1.23
3	D	3301	FAD	C2A-N1A	2.00	1.37	1.33

All (227) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	4301	FAD	O2A-PA-O5B	-13.90	38.45	108.51
3	C	2301	FAD	O2A-PA-O5B	-13.30	41.43	108.51
3	B	1301	FAD	O2A-PA-O5B	-13.07	42.59	108.51
3	D	3301	FAD	O2A-PA-O5B	-12.95	43.20	108.51
3	F	5301	FAD	O2A-PA-O5B	-12.88	43.58	108.51
3	A	301	FAD	O2A-PA-O5B	-12.66	44.70	108.51
3	G	6301	FAD	O2A-PA-O5B	-12.54	45.27	108.51
3	H	7301	FAD	O2A-PA-O5B	-12.04	47.80	108.51
2	G	7280	DTC	C15-C13-C14	11.44	128.53	111.77
2	B	3280	DTC	C15-C13-C14	11.24	128.24	111.77
2	E	5280	DTC	C15-C13-C14	11.18	128.15	111.77
2	A	2280	DTC	C15-C13-C14	11.14	128.09	111.77
2	D	1280	DTC	C15-C13-C14	11.09	128.02	111.77
2	H	6280	DTC	C15-C13-C14	11.07	127.98	111.77
2	E	4280	DTC	C15-C13-C14	10.94	127.79	111.77
2	C	280	DTC	C15-C13-C14	10.77	127.55	111.77
3	H	7301	FAD	O2A-PA-O3P	9.76	151.44	105.14
3	G	6301	FAD	O2A-PA-O3P	9.64	150.90	105.14
3	A	301	FAD	O2A-PA-O3P	9.45	149.96	105.14
3	F	5301	FAD	O2A-PA-O3P	8.83	147.05	105.14
3	D	3301	FAD	O2A-PA-O3P	8.55	145.73	105.14
3	B	1301	FAD	O2A-PA-O3P	8.52	145.58	105.14
3	C	2301	FAD	O2A-PA-O3P	8.27	144.37	105.14
3	A	301	FAD	O4B-C1B-N9A	-7.73	101.25	108.44
3	H	7301	FAD	O5B-PA-O1A	-7.59	79.66	109.37
3	E	4301	FAD	O2A-PA-O3P	7.51	140.75	105.14
3	A	301	FAD	O5B-PA-O1A	-7.42	80.30	109.37
3	H	7301	FAD	O2A-PA-O1A	-7.40	70.85	112.21
3	G	6301	FAD	O5B-PA-O1A	-7.34	80.63	109.37
3	B	1301	FAD	O5B-PA-O1A	-7.06	81.71	109.37
3	H	7301	FAD	O4B-C1B-N9A	-7.01	101.92	108.44
3	F	5301	FAD	O5B-PA-O1A	-6.83	82.61	109.37
3	D	3301	FAD	O5B-PA-O1A	-6.76	82.90	109.37
3	E	4301	FAD	O5B-PA-O1A	-6.64	83.36	109.37
3	B	1301	FAD	O4B-C1B-N9A	-6.63	102.27	108.44
3	A	301	FAD	O2A-PA-O1A	-6.56	75.58	112.21
3	C	2301	FAD	O5B-PA-O1A	-6.52	83.83	109.37
3	D	3301	FAD	O4B-C1B-N9A	-6.31	102.58	108.44
3	G	6301	FAD	O4B-C1B-N9A	-6.17	102.70	108.44
3	B	1301	FAD	C2-N1-C10	6.03	121.05	114.98
3	E	4301	FAD	C2-N1-C10	5.97	121.00	114.98
3	G	6301	FAD	O2A-PA-O1A	-5.93	79.07	112.21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3301	FAD	C2-N1-C10	5.93	120.95	114.98
3	C	2301	FAD	O4B-C1B-N9A	-5.89	102.96	108.44
3	F	5301	FAD	C2-N1-C10	5.85	120.87	114.98
3	G	6301	FAD	C2-N1-C10	5.83	120.85	114.98
3	F	5301	FAD	O2A-PA-O1A	-5.79	79.86	112.21
3	C	2301	FAD	C2-N1-C10	5.72	120.74	114.98
3	B	1301	FAD	O2A-PA-O1A	-5.71	80.30	112.21
2	B	3280	DTC	C15-C7-C6	5.70	123.72	112.46
3	A	301	FAD	C2-N1-C10	5.69	120.71	114.98
3	H	7301	FAD	C2-N1-C10	5.61	120.64	114.98
2	G	7280	DTC	C15-C7-C6	5.58	123.49	112.46
3	F	5301	FAD	O4B-C1B-N9A	-5.56	103.27	108.44
3	E	4301	FAD	O4B-C1B-N9A	-5.44	103.38	108.44
2	C	280	DTC	C15-C7-C6	5.42	123.16	112.46
2	E	5280	DTC	C15-C7-C6	5.39	123.11	112.46
2	H	6280	DTC	C15-C7-C6	5.37	123.08	112.46
2	A	2280	DTC	C15-C7-C6	5.37	123.06	112.46
2	E	4280	DTC	C15-C7-C6	5.34	123.02	112.46
2	D	1280	DTC	C15-C7-C6	5.34	123.01	112.46
3	D	3301	FAD	O2A-PA-O1A	-5.20	83.18	112.21
2	E	4280	DTC	C15-C7-C8	5.07	119.19	111.77
2	H	6280	DTC	C15-C7-C8	5.04	119.15	111.77
2	A	2280	DTC	C15-C7-C8	4.95	119.01	111.77
2	D	1280	DTC	C15-C7-C8	4.82	118.83	111.77
2	E	5280	DTC	C15-C7-C8	4.82	118.83	111.77
2	B	3280	DTC	C15-C7-C8	4.78	118.77	111.77
2	C	280	DTC	C15-C7-C8	4.76	118.75	111.77
2	E	5280	DTC	C9-C8-C7	4.74	121.82	116.54
2	B	3280	DTC	C9-C8-C7	4.69	121.76	116.54
3	C	2301	FAD	O2A-PA-O1A	-4.69	86.02	112.21
2	G	7280	DTC	C15-C7-C8	4.68	118.63	111.77
3	E	4301	FAD	O2A-PA-O1A	-4.65	86.21	112.21
2	G	7280	DTC	C9-C8-C7	4.63	121.69	116.54
2	D	1280	DTC	C9-C8-C7	4.57	121.63	116.54
3	E	4301	FAD	C4B-O4B-C1B	-4.56	104.79	109.75
2	H	6280	DTC	C9-C8-C7	4.49	121.54	116.54
2	A	2280	DTC	C9-C8-C7	4.47	121.52	116.54
2	E	4280	DTC	C9-C8-C7	4.45	121.49	116.54
3	C	2301	FAD	C4B-O4B-C1B	-4.36	105.01	109.75
2	C	280	DTC	C9-C8-C7	4.34	121.36	116.54
3	D	3301	FAD	C4B-O4B-C1B	-4.28	105.10	109.75
3	C	2301	FAD	C2'-C1'-N10	-4.26	106.80	112.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	5301	FAD	O4B-C1B-C2B	-4.01	100.62	106.77
3	B	1301	FAD	C4B-O4B-C1B	-3.87	105.55	109.75
3	H	7301	FAD	PA-O5B-C5B	3.77	149.15	122.03
3	F	5301	FAD	C4B-O4B-C1B	-3.76	105.66	109.75
3	B	1301	FAD	N3A-C2A-N1A	-3.66	125.65	128.71
3	D	3301	FAD	PA-O5B-C5B	3.56	147.65	122.03
3	A	301	FAD	PA-O5B-C5B	3.52	147.36	122.03
3	E	4301	FAD	PA-O5B-C5B	3.52	147.31	122.03
3	B	1301	FAD	PA-O5B-C5B	3.52	147.31	122.03
2	B	3280	DTC	O21-C12-C13	3.51	120.20	116.92
3	G	6301	FAD	PA-O5B-C5B	3.51	147.26	122.03
3	G	6301	FAD	O4B-C1B-C2B	-3.49	101.42	106.77
3	G	6301	FAD	C4B-O4B-C1B	-3.49	105.96	109.75
2	H	6280	DTC	O21-C12-C13	3.46	120.14	116.92
2	E	4280	DTC	O21-C12-C13	3.46	120.14	116.92
2	D	1280	DTC	C20-C14-C13	3.45	120.38	116.54
2	G	7280	DTC	O21-C12-C13	3.45	120.14	116.92
3	D	3301	FAD	N3A-C2A-N1A	-3.44	125.83	128.71
2	G	7280	DTC	C20-C14-C13	3.43	120.36	116.54
3	F	5301	FAD	PA-O5B-C5B	3.43	146.68	122.03
2	A	2280	DTC	C20-C14-C13	3.42	120.34	116.54
3	C	2301	FAD	PA-O5B-C5B	3.41	146.55	122.03
2	B	3280	DTC	C20-C14-C13	3.38	120.31	116.54
3	D	3301	FAD	O4B-C1B-C2B	-3.38	101.59	106.77
2	E	5280	DTC	O21-C12-C13	3.38	120.07	116.92
2	E	5280	DTC	C20-C14-C13	3.37	120.29	116.54
3	C	2301	FAD	O4B-C1B-C2B	-3.36	101.62	106.77
2	H	6280	DTC	C20-C14-C13	3.35	120.27	116.54
3	H	7301	FAD	O4B-C1B-C2B	-3.33	101.67	106.77
2	C	280	DTC	O21-C12-C13	3.29	119.99	116.92
3	G	6301	FAD	N3A-C2A-N1A	-3.29	125.96	128.71
2	A	2280	DTC	O21-C12-C13	3.29	119.98	116.92
3	E	4301	FAD	O4B-C1B-C2B	-3.26	101.78	106.77
2	E	4280	DTC	C20-C14-C13	3.18	120.08	116.54
2	C	280	DTC	C20-C14-C13	3.16	120.06	116.54
2	D	1280	DTC	O21-C12-C13	3.14	119.84	116.92
3	H	7301	FAD	C4B-O4B-C1B	-3.09	106.39	109.75
3	E	4301	FAD	C4X-C10-N10	-3.07	118.98	120.51
3	A	301	FAD	C4X-C10-N1	-3.03	119.70	122.73
3	A	301	FAD	N3A-C2A-N1A	-3.03	126.17	128.71
3	H	7301	FAD	N3A-C2A-N1A	-3.01	126.19	128.71
3	E	4301	FAD	N3A-C2A-N1A	-2.99	126.21	128.71

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	4301	FAD	P-O3P-PA	2.97	140.39	131.68
3	E	4301	FAD	C2'-C1'-N10	-2.95	108.53	112.45
3	A	301	FAD	O4B-C1B-C2B	-2.92	102.29	106.77
3	F	5301	FAD	N3A-C2A-N1A	-2.90	126.28	128.71
3	C	2301	FAD	N3A-C2A-N1A	-2.90	126.28	128.71
3	B	1301	FAD	C2'-C1'-N10	-2.81	108.72	112.45
3	B	1301	FAD	P-O3P-PA	2.78	139.85	131.68
3	A	301	FAD	C4B-O4B-C1B	-2.77	106.74	109.75
2	H	6280	DTC	O5-C6-C7	2.76	119.49	116.92
2	B	3280	DTC	O5-C6-C7	2.76	119.49	116.92
2	C	280	DTC	O5-C6-C7	2.75	119.49	116.92
3	G	6301	FAD	N3A-C4A-N9A	2.75	130.40	125.43
2	E	4280	DTC	O5-C6-C7	2.69	119.43	116.92
2	A	2280	DTC	O5-C6-C7	2.67	119.41	116.92
3	F	5301	FAD	N3A-C4A-N9A	2.67	130.25	125.43
3	G	6301	FAD	C5A-C4A-N9A	-2.58	103.43	107.16
3	D	3301	FAD	P-O3P-PA	2.57	139.23	131.68
3	G	6301	FAD	P-O3P-PA	2.53	139.10	131.68
2	G	7280	DTC	O5-C6-C7	2.52	119.27	116.92
3	A	301	FAD	C2'-C1'-N10	-2.52	109.10	112.45
2	E	5280	DTC	C19-C20-C14	-2.52	118.58	120.40
2	D	1280	DTC	C13-C15-C7	2.51	120.51	114.77
3	G	6301	FAD	C4X-C10-N1	-2.51	120.23	122.73
2	D	1280	DTC	C19-C20-C14	-2.48	118.61	120.40
3	E	4301	FAD	C4X-N5-C5X	2.48	119.47	116.69
2	D	1280	DTC	O5-C6-C7	2.46	119.22	116.92
3	B	1301	FAD	O4B-C1B-C2B	-2.44	103.03	106.77
2	C	280	DTC	C19-C20-C14	-2.43	118.65	120.40
2	B	3280	DTC	C5-C20-C14	2.43	123.29	119.71
3	C	2301	FAD	C4X-C10-N10	-2.43	119.30	120.51
2	B	3280	DTC	C19-C20-C14	-2.41	118.66	120.40
3	F	5301	FAD	P-O3P-PA	2.38	138.66	131.68
2	H	6280	DTC	C19-C20-C14	-2.38	118.69	120.40
3	C	2301	FAD	C2A-N1A-C6A	2.37	123.05	118.77
2	E	5280	DTC	O5-C6-C7	2.37	119.13	116.92
2	E	5280	DTC	C5-C20-C14	2.35	123.17	119.71
2	H	6280	DTC	O5-C10-C4	2.34	119.60	116.26
3	B	1301	FAD	C2A-N1A-C6A	2.34	123.00	118.77
3	E	4301	FAD	C2A-N1A-C6A	2.31	122.95	118.77
2	E	5280	DTC	O5-C10-C4	2.31	119.55	116.26
3	H	7301	FAD	C2A-N1A-C6A	2.30	122.93	118.77
2	H	6280	DTC	C13-C15-C7	2.30	120.02	114.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1280	DTC	O5-C10-C4	2.29	119.52	116.26
3	E	4301	FAD	C4X-C10-N1	-2.27	120.46	122.73
3	H	7301	FAD	C4X-C10-N1	-2.27	120.46	122.73
3	G	6301	FAD	C4A-C5A-N7A	2.26	111.46	109.52
2	G	7280	DTC	C19-C20-C14	-2.26	118.77	120.40
3	D	3301	FAD	N3A-C4A-N9A	2.26	129.51	125.43
3	F	5301	FAD	C4A-C5A-N7A	2.25	111.45	109.52
3	F	5301	FAD	C5A-C4A-N9A	-2.24	103.93	107.16
3	A	301	FAD	N3A-C4A-N9A	2.24	129.47	125.43
2	D	1280	DTC	C1-C9-C8	2.23	122.98	119.71
2	B	3280	DTC	C1-C9-C8	2.22	122.98	119.71
3	D	3301	FAD	C5A-C4A-N9A	-2.21	103.97	107.16
2	C	280	DTC	C5-C20-C14	2.20	122.95	119.71
3	C	2301	FAD	C4A-C5A-N7A	2.20	111.41	109.52
3	G	6301	FAD	C4X-C10-N10	-2.20	119.41	120.51
3	E	4301	FAD	C4A-C5A-N7A	2.20	111.41	109.52
3	A	301	FAD	C4X-C10-N10	-2.20	119.41	120.51
2	H	6280	DTC	C5-C20-C14	2.20	122.94	119.71
2	A	2280	DTC	C1-C9-C8	2.19	122.93	119.71
2	B	3280	DTC	C13-C15-C7	2.18	119.75	114.77
3	C	2301	FAD	O5'-P-O1P	-2.17	100.88	109.37
3	H	7301	FAD	C4X-C10-N10	-2.17	119.43	120.51
2	B	3280	DTC	O5-C10-C4	2.17	119.34	116.26
2	E	4280	DTC	C5-C20-C14	2.16	122.89	119.71
2	A	2280	DTC	O5-C10-C4	2.15	119.33	116.26
3	D	3301	FAD	C4X-C10-N1	-2.15	120.58	122.73
2	C	280	DTC	O5-C10-C4	2.14	119.31	116.26
3	D	3301	FAD	C2A-N1A-C6A	2.15	122.64	118.77
2	C	280	DTC	C13-C15-C7	2.14	119.67	114.77
2	D	1280	DTC	C5-C20-C14	2.14	122.85	119.71
2	G	7280	DTC	O5-C10-C4	2.13	119.29	116.26
2	G	7280	DTC	C5-C20-C14	2.13	122.84	119.71
3	G	6301	FAD	C2A-N1A-C6A	2.12	122.61	118.77
3	E	4301	FAD	C4-N3-C2	-2.12	121.03	125.39
3	H	7301	FAD	N3A-C4A-N9A	2.12	129.27	125.43
3	D	3301	FAD	O5'-P-O1P	-2.12	101.07	109.37
3	A	301	FAD	P-O3P-PA	2.11	137.87	131.68
2	E	4280	DTC	C19-C20-C14	-2.11	118.88	120.40
3	B	1301	FAD	C5'-C4'-C3'	-2.10	108.09	112.06
2	E	4280	DTC	O5-C10-C4	2.10	119.25	116.26
2	H	6280	DTC	C1-C9-C8	2.09	122.79	119.71
2	A	2280	DTC	C19-C20-C14	-2.09	118.89	120.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3301	FAD	C4A-C5A-N7A	2.08	111.30	109.52
3	C	2301	FAD	C2B-C1B-N9A	2.07	118.57	113.27
3	D	3301	FAD	O3B-C3B-C2B	2.06	118.54	111.83
3	G	6301	FAD	O3B-C3B-C2B	2.05	118.51	111.83
3	C	2301	FAD	C4-N3-C2	-2.05	121.19	125.39
3	C	2301	FAD	N3A-C4A-N9A	2.04	129.12	125.43
3	A	301	FAD	C5A-C4A-N9A	-2.04	104.22	107.16
3	A	301	FAD	C2A-N1A-C6A	2.03	122.43	118.77
2	E	5280	DTC	C10-C9-C8	-2.02	118.94	120.40
3	F	5301	FAD	O3B-C3B-C2B	2.02	118.41	111.83
2	A	2280	DTC	C10-C9-C8	-2.01	118.95	120.40
2	E	4280	DTC	C1-C9-C8	2.01	122.67	119.71
3	E	4301	FAD	O3B-C3B-C2B	2.01	118.37	111.83
3	F	5301	FAD	C4-N3-C2	-2.01	121.27	125.39
3	A	301	FAD	C4-N3-C2	-2.01	121.27	125.39
3	F	5301	FAD	C2A-N1A-C6A	2.01	122.39	118.77
3	A	301	FAD	O3B-C3B-C2B	2.01	118.37	111.83

All (16) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	1280	DTC	C13
2	D	1280	DTC	C7
2	C	280	DTC	C13
2	C	280	DTC	C7
2	H	6280	DTC	C13
2	H	6280	DTC	C7
2	A	2280	DTC	C13
2	A	2280	DTC	C7
2	G	7280	DTC	C13
2	G	7280	DTC	C7
2	E	5280	DTC	C13
2	E	5280	DTC	C7
2	B	3280	DTC	C13
2	B	3280	DTC	C7
2	E	4280	DTC	C13
2	E	4280	DTC	C7

There are no torsion outliers.

There are no ring outliers.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	273/273 (100%)	-0.18	3 (1%) 77 79	13, 31, 50, 78	0
1	B	273/273 (100%)	-0.24	4 (1%) 70 73	14, 29, 47, 74	0
1	C	273/273 (100%)	-0.22	4 (1%) 70 73	12, 28, 53, 71	0
1	D	273/273 (100%)	-0.15	3 (1%) 77 79	13, 33, 52, 80	0
1	E	273/273 (100%)	-0.24	1 (0%) 90 92	11, 27, 52, 69	0
1	F	273/273 (100%)	-0.17	2 (0%) 84 87	15, 32, 53, 68	0
1	G	273/273 (100%)	-0.06	10 (3%) 39 42	15, 35, 65, 81	0
1	H	273/273 (100%)	0.12	8 (2%) 49 53	18, 41, 70, 82	0
All	All	2184/2184 (100%)	-0.14	35 (1%) 68 71	11, 32, 58, 82	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	1	VAL	10.0
1	E	1	VAL	9.2
1	A	1	VAL	6.3
1	B	1	VAL	5.5
1	G	1	VAL	5.0
1	D	273	LYS	4.3
1	G	273	LYS	3.9
1	G	233	GLN	3.4
1	H	1	VAL	3.1
1	G	232	PHE	3.1
1	H	2	GLY	3.1
1	C	1	VAL	3.0
1	F	1	VAL	2.7
1	G	59	LEU	2.7
1	H	273	LYS	2.7
1	A	232	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	G	58	LYS	2.5
1	G	234	ALA	2.5
1	H	216	ASP	2.5
1	H	272	ARG	2.4
1	C	233	GLN	2.4
1	H	233	GLN	2.3
1	C	235	GLY	2.3
1	A	2	GLY	2.2
1	D	233	GLN	2.2
1	B	107	GLY	2.2
1	G	240	LYS	2.2
1	F	123	GLU	2.2
1	C	234	ALA	2.2
1	H	196	PRO	2.1
1	G	272	ARG	2.1
1	G	242	VAL	2.1
1	B	233	GLN	2.1
1	H	28	ALA	2.1
1	B	273	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	DTC	D	1280	25/25	0.30	5.65	34,74,75,75	0
2	DTC	A	2280	25/25	0.29	3.75	34,74,75,75	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	DTC	E	4280	25/25	0.28	3.72	34,74,75,75	0
2	DTC	B	3280	25/25	0.27	3.39	34,74,75,75	0
2	DTC	C	280	25/25	0.27	3.02	34,74,75,75	0
2	DTC	H	6280	25/25	0.27	2.90	34,74,75,75	0
2	DTC	E	5280	25/25	0.27	2.14	34,74,75,75	0
2	DTC	G	7280	25/25	0.27	1.12	34,74,75,75	0
3	FAD	A	301	53/53	0.17	0.45	25,34,42,42	0
3	FAD	G	6301	53/53	0.16	0.21	20,28,34,37	0
3	FAD	D	3301	53/53	0.16	0.10	19,28,38,39	0
3	FAD	H	7301	53/53	0.17	-0.07	25,45,53,55	0
3	FAD	F	5301	53/53	0.16	-0.09	21,30,38,41	0
3	FAD	C	2301	53/53	0.15	-0.23	19,27,34,34	0
3	FAD	E	4301	53/53	0.14	-0.28	14,23,34,34	0
3	FAD	B	1301	53/53	0.16	-0.30	17,22,34,34	0

6.5 Other polymers ⓘ

There are no such residues in this entry.