



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 31, 2017 – 05:34 AM EDT

PDB ID : 3P4P
Title : Crystal structure of Menaquinol:fumarate oxidoreductase in complex with fumarate
Authors : Tomasiak, T.M.; Archuleta, T.L.; Andr ll, J.; Luna-Ch vez, C.; Davis, T.A.; Sarwar, M.; Ham, A.J.; McDonald, W.H.; Yankowskaya, V.; Stern, H.A.; Johnston, J.N.; Maklashina, E.; Cecchini, G.; Iverson, T.M.
Deposited on : unknown
Resolution : 2.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

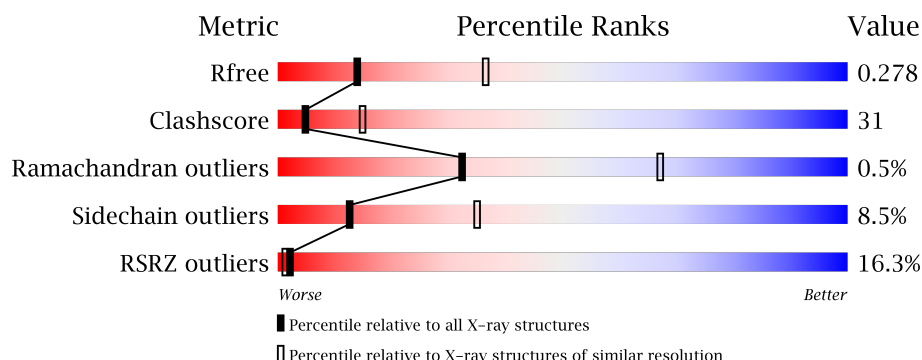
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	577	
1	M	577	
2	B	243	
2	N	243	
3	C	130	

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Mol	Chain	Length	Quality of chain
3	O	130	<div> <div>4%</div> <div>58%</div> <div>38%</div> <div>.</div> </div>
4	D	119	<div> <div>2%</div> <div>53%</div> <div>41%</div> <div>6%</div> </div>
4	P	119	<div> <div>3%</div> <div>49%</div> <div>45%</div> <div>6%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	FAD	M	601	-	-	X	-
6	FUM	A	577	-	-	-	X
7	FES	B	244	-	-	X	-
8	F3S	B	245	-	-	X	-
9	SF4	B	246	-	-	X	-
9	SF4	N	246	-	-	X	-

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 16873 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 Fumarate reductase flavoprotein subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	577	Total	C	N	O	S	0	0	0
			4449	2775	802	841	31			
1	M	577	Total	C	N	O	S	0	0	0
			4449	2775	802	841	31			

- Molecule 2 is a protein called Fumarate reductase iron-sulfur protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	243	Total	C	N	O	S	0	0	0
			1888	1189	323	357	19			
2	N	243	Total	C	N	O	S	0	0	0
			1888	1189	323	357	19			

- Molecule 3 is a protein called Fumarate reductase subunit C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	130	Total	C	N	O	S	0	0	0
			1058	720	166	169	3			
3	O	130	Total	C	N	O	S	0	0	0
			1058	720	166	169	3			

- Molecule 4 is a protein called Fumarate reductase subunit D.

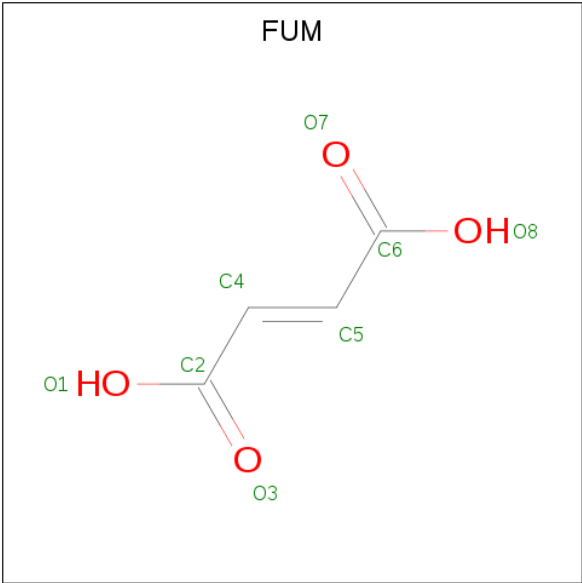
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	119	Total	C	N	O	S	0	0	0
			926	626	151	142	7			
4	P	119	Total	C	N	O	S	0	0	0
			926	626	151	142	7			

- Molecule 5 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula: $C_{27}H_{33}N_9O_{15}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			53	27	9	15	2		
5	M	1	Total	C	N	O	P	0	0
			53	27	9	15	2		

- Molecule 6 is FUMARIC ACID (three-letter code: FUM) (formula: C₄H₄O₄).



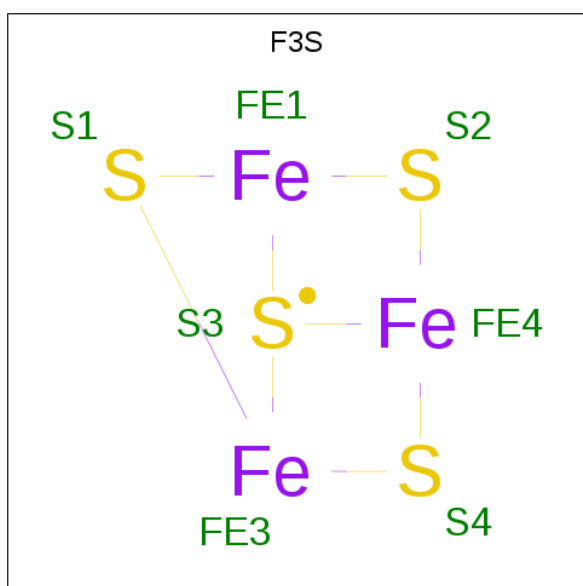
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			8	4	4		

- Molecule 7 is FE2/S2 (INORGANIC) CLUSTER (three-letter code: FES) (formula: Fe₂S₂).



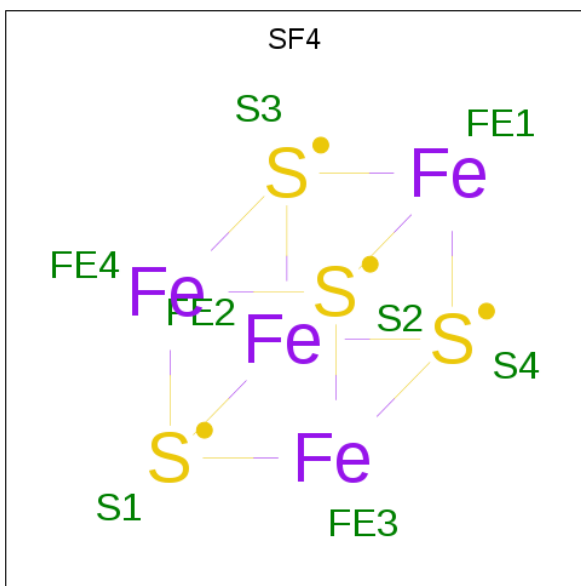
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	Fe	S	0	0
			4	2	2		
7	N	1	Total	Fe	S	0	0
			4	2	2		

- Molecule 8 is FE3-S4 CLUSTER (three-letter code: F3S) (formula: Fe₃S₄).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	Fe	S	0	0
			7	3	4		
8	N	1	Total	Fe	S	0	0
			7	3	4		

- Molecule 9 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	B	1	Total	Fe	S	0	0
			8	4	4		
9	N	1	Total	Fe	S	0	0
			8	4	4		

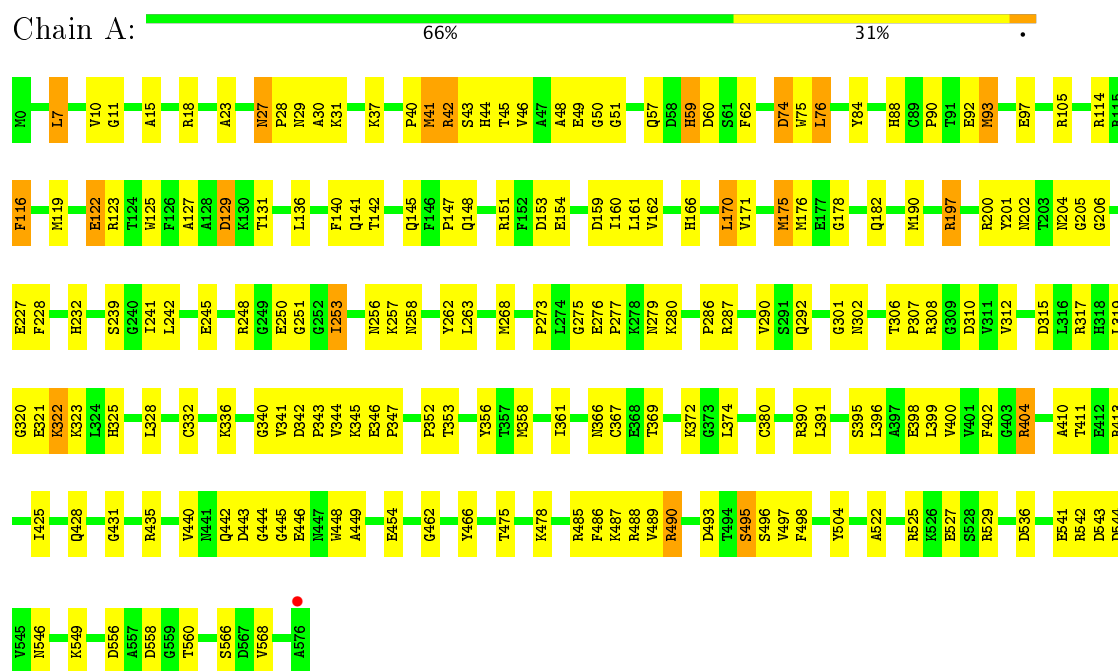
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	60	Total	O	0	0
			60	60		
10	B	10	Total	O	0	0
			10	10		
10	C	2	Total	O	0	0
			2	2		
10	D	4	Total	O	0	0
			4	4		
10	M	1	Total	O	0	0
			1	1		
10	N	2	Total	O	0	0
			2	2		

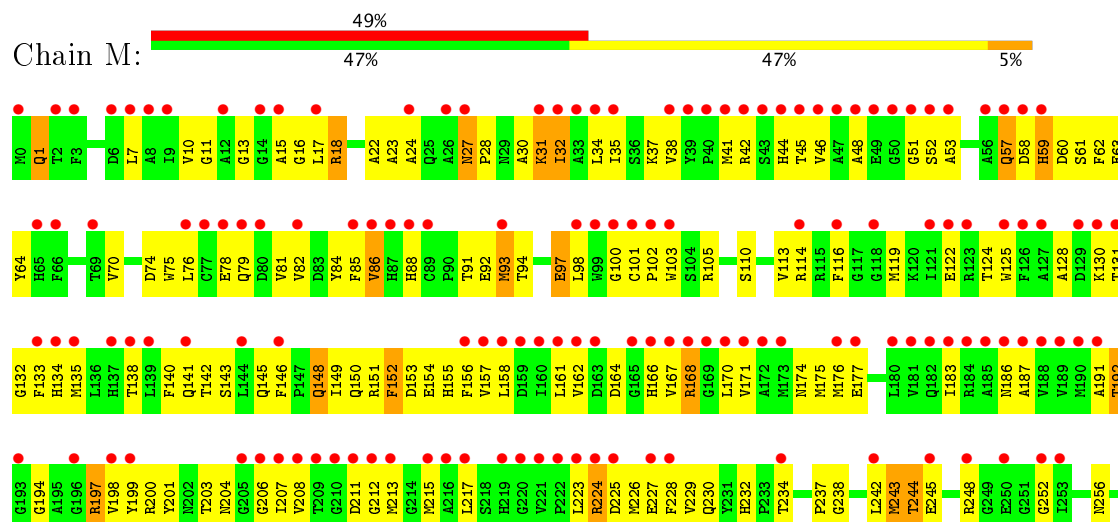
3 Residue-property plots

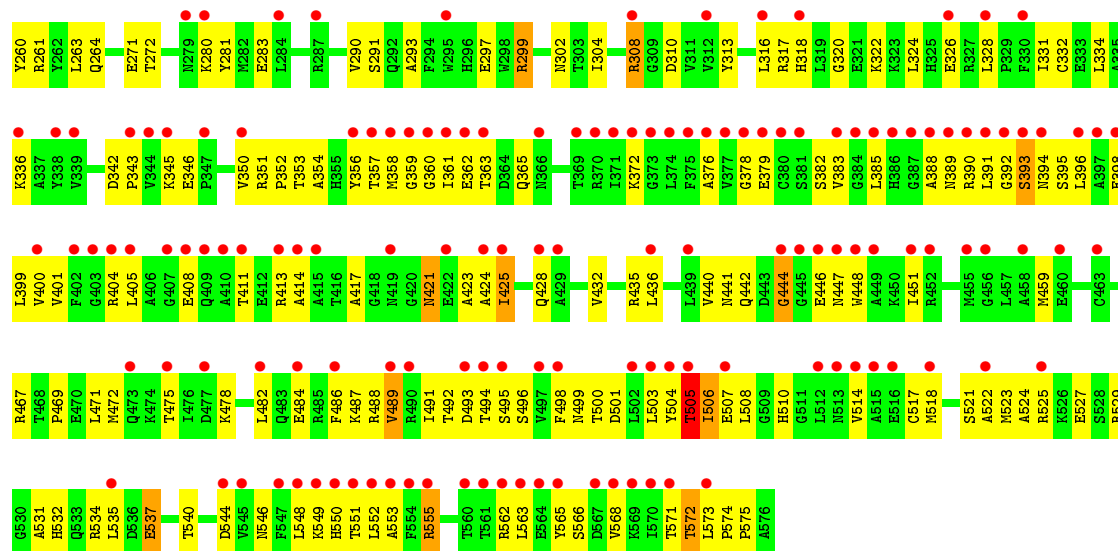
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

• Molecule 1: Fumarate reductase flavoprotein subunit

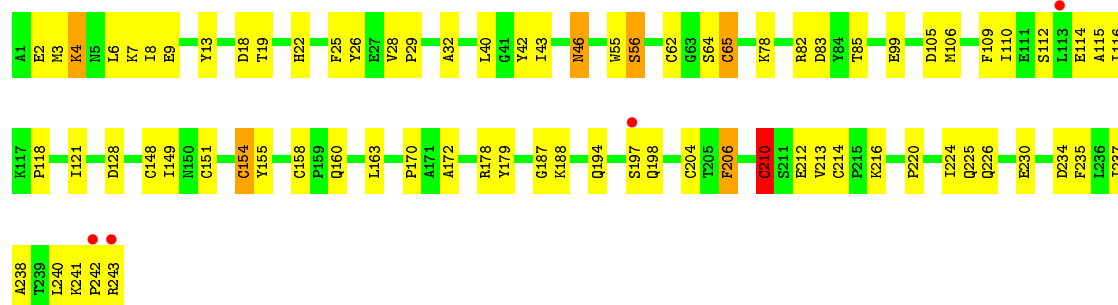


• Molecule 1: Fumarate reductase flavoprotein subunit

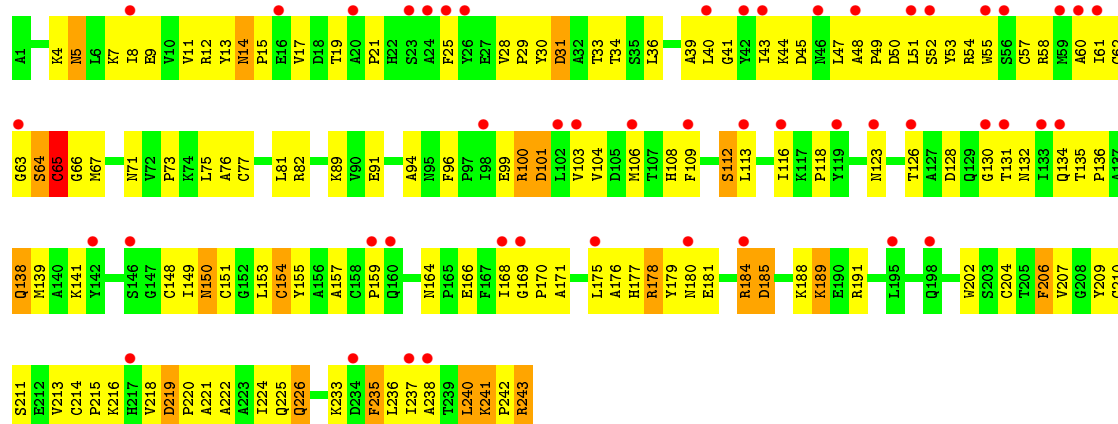
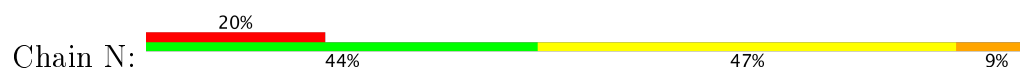




• Molecule 2: Fumarate reductase iron-sulfur protein

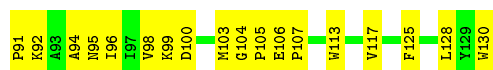


• Molecule 2: Fumarate reductase iron-sulfur protein



• Molecule 3: Fumarate reductase subunit C

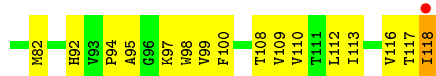
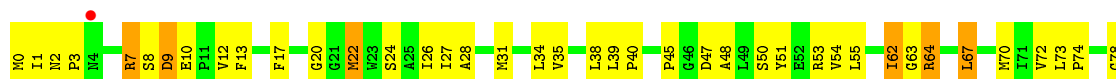




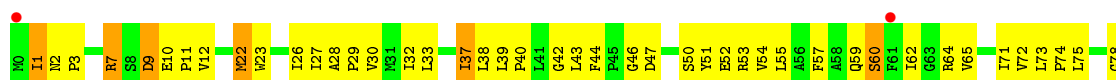
• Molecule 3: Fumarate reductase subunit C



• Molecule 4: Fumarate reductase subunit D



• Molecule 4: Fumarate reductase subunit D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	96.32Å 137.63Å 270.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.92 – 2.80 90.74 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (38.92-2.80) 94.9 (90.74-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.51 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.249 , 0.272 0.256 , 0.278	Depositor DCC
R_{free} test set	1408 reflections (1.69%)	DCC
Wilson B-factor (Å ²)	55.3	Xtriage
Anisotropy	0.176	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 92.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	16873	wwPDB-VP
Average B, all atoms (Å ²)	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4, F3S, FUM, FES, 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	0.77	0/4541	0.83	3/6139 (0.0%)
1	M	0.53	1/4541 (0.0%)	0.64	2/6139 (0.0%)
2	B	0.76	1/1931 (0.1%)	0.84	3/2617 (0.1%)
2	N	0.58	3/1931 (0.2%)	0.73	3/2617 (0.1%)
3	C	0.60	0/1094	0.70	2/1496 (0.1%)
3	O	0.57	0/1094	0.65	0/1496
4	D	0.60	0/956	0.72	0/1303
4	P	0.55	0/956	0.68	0/1303
All	All	0.65	5/17044 (0.0%)	0.74	13/23110 (0.1%)

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

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

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	210	CYS	C-N	10.72	1.58	1.34
2	N	77	CYS	C-N	8.04	1.52	1.34
2	N	65	CYS	CB-SG	7.05	1.94	1.82
1	M	505	THR	C-N	6.89	1.49	1.34
2	N	77	CYS	CB-SG	5.33	1.91	1.82

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	210	CYS	O-C-N	10.16	138.96	122.70
2	B	210	CYS	CA-C-N	-8.65	98.16	117.20
2	N	65	CYS	N-CA-CB	-7.65	96.83	110.60
2	B	210	CYS	C-N-CA	-7.21	103.66	121.70
3	C	28	ARG	NE-CZ-NH1	6.72	123.66	120.30
3	C	28	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	A	404	ARG	NE-CZ-NH1	6.41	123.51	120.30
1	A	170	LEU	CA-CB-CG	6.37	129.95	115.30
2	N	77	CYS	CA-CB-SG	5.63	124.14	114.00
2	N	65	CYS	O-C-N	-5.39	114.04	123.20
1	A	404	ARG	NE-CZ-NH2	-5.28	117.66	120.30
1	M	1	GLN	N-CA-C	-5.14	97.13	111.00
1	M	1	GLN	N-CA-CB	5.00	119.61	110.60

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	N	64	SER	Mainchain

5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4449	0	4335	169	0
1	M	4449	0	4335	401	0
2	B	1888	0	1844	91	0
2	N	1888	0	1839	199	0
3	C	1058	0	1108	63	0
3	O	1058	0	1108	74	0
4	D	926	0	971	79	0
4	P	926	0	970	68	0
5	A	53	0	30	14	0
5	M	53	0	30	25	0
6	A	8	0	2	1	0
7	B	4	0	0	3	0
7	N	4	0	0	1	0
8	B	7	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	N	7	0	0	1	0
9	B	8	0	0	12	0
9	N	8	0	0	6	0
10	A	60	0	0	2	0
10	B	10	0	0	0	0
10	C	2	0	0	0	0
10	D	4	0	0	0	0
10	M	1	0	0	5	0
10	N	2	0	0	0	0
All	All	16873	0	16572	1016	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 31.

All (1016) 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:A:44:HIS:NE2	5:A:601:FAD:C8M	1.77	1.45
1:A:44:HIS:CE1	5:A:601:FAD:HM82	1.53	1.44
1:M:44:HIS:NE2	5:M:601:FAD:HM82	1.41	1.34
2:N:31:ASP:OD2	2:N:33:THR:N	1.57	1.33
1:M:168:ARG:HD2	10:M:577:HOH:O	1.19	1.27
1:M:527:GLU:OE1	1:M:529:ARG:NH1	1.72	1.21
1:A:44:HIS:NE2	5:A:601:FAD:HM81	1.50	1.13
1:A:44:HIS:NE2	5:A:601:FAD:HM82	1.44	1.12
2:N:116:ILE:HG21	2:N:176:ALA:HB2	1.17	1.09
2:N:189:LYS:HD2	2:N:189:LYS:H	0.99	1.08
3:C:86:TRP:HE1	4:D:22:MET:CE	1.67	1.07
4:P:1:ILE:HD12	4:P:1:ILE:H	1.16	1.06
1:A:346:GLU:HG3	1:A:347:PRO:HD2	1.31	1.06
1:M:44:HIS:NE2	5:M:601:FAD:C8M	2.20	1.04
2:N:71:ASN:HB3	3:O:18:LYS:HE3	1.33	1.04
1:M:100:GLY:C	2:N:184:ARG:NH2	2.12	1.02
1:M:155:HIS:CE1	1:M:174:ASN:HD22	1.76	1.02
1:M:146:PHE:HB2	1:M:149:ILE:HD13	1.39	1.02
2:B:204:CYS:SG	8:B:245:F3S:FE1	1.51	1.02
1:M:168:ARG:CD	10:M:577:HOH:O	1.81	1.01
2:N:178:ARG:HH11	2:N:178:ARG:HG2	1.22	1.01
3:C:86:TRP:NE1	4:D:22:MET:CE	2.24	1.01
3:C:86:TRP:HE1	4:D:22:MET:HE3	1.25	1.01
1:A:151:ARG:NH1	1:A:153:ASP:OD2	1.95	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:192:THR:HG21	1:M:212:GLY:HA3	1.42	1.00
3:C:50:LYS:HE2	3:C:50:LYS:HA	1.44	0.99
1:M:451:ILE:HG23	1:M:482:LEU:HD12	1.38	0.99
2:B:198:GLN:HE22	4:D:10:GLU:HG3	1.27	0.99
2:N:13:TYR:HB2	2:N:21:PRO:HB3	1.45	0.99
2:N:159:PRO:HG2	2:N:207:VAL:HG21	1.45	0.99
1:M:549:LYS:HD2	1:M:565:TYR:HB3	1.45	0.98
2:B:151:CYS:SG	9:B:246:SF4:FE1	1.55	0.98
2:B:214:CYS:HG	9:B:246:SF4:FE4	0.80	0.97
1:A:57:GLN:HE22	1:A:122:GLU:HG2	1.25	0.97
1:M:100:GLY:CA	2:N:184:ARG:HH21	1.76	0.97
1:A:44:HIS:CE1	5:A:601:FAD:C8M	2.37	0.97
1:M:425:ILE:HD11	10:M:577:HOH:O	1.63	0.96
3:C:86:TRP:CD1	4:D:22:MET:HE2	2.01	0.96
1:M:421:ASN:OD1	1:M:424:ALA:N	1.96	0.96
2:B:151:CYS:HG	9:B:246:SF4:FE1	0.78	0.95
2:B:198:GLN:OE1	4:D:8:SER:OG	1.85	0.95
3:O:130:TRP:O	4:P:53:ARG:NH2	2.00	0.95
1:M:81:VAL:HG11	1:M:383:VAL:HG12	1.48	0.94
1:M:537:GLU:CD	1:M:537:GLU:H	1.71	0.93
1:M:328:LEU:O	1:M:332:CYS:SG	2.26	0.93
2:N:189:LYS:HD2	2:N:189:LYS:N	1.84	0.92
2:N:154:CYS:HB2	2:N:170:PRO:HG2	1.50	0.92
2:N:71:ASN:HB3	3:O:18:LYS:CE	1.98	0.92
1:A:328:LEU:O	1:A:332:CYS:SG	2.29	0.91
1:M:197:ARG:HD2	1:M:206:GLY:HA2	1.51	0.91
1:M:155:HIS:CE1	1:M:174:ASN:HA	2.04	0.91
2:N:189:LYS:H	2:N:189:LYS:CD	1.84	0.91
2:N:116:ILE:HG21	2:N:176:ALA:CB	2.00	0.90
1:M:42:ARG:NH2	2:N:150:ASN:O	2.04	0.90
2:N:151:CYS:HG	9:N:246:SF4:FE1	0.76	0.90
1:M:192:THR:HG21	1:M:212:GLY:CA	2.02	0.90
2:B:154:CYS:SG	9:B:246:SF4:FE2	1.64	0.89
1:M:149:ILE:HD12	1:M:149:ILE:H	1.36	0.89
1:M:100:GLY:HA2	2:N:184:ARG:HH21	1.36	0.89
1:M:11:GLY:HA2	5:M:601:FAD:O4B	1.72	0.89
1:M:93:MET:HE2	1:M:93:MET:HA	1.55	0.88
3:C:86:TRP:CD1	4:D:22:MET:CE	2.55	0.88
1:M:525:ARG:O	1:M:534:ARG:NH1	2.07	0.88
3:C:50:LYS:HA	3:C:50:LYS:CE	2.05	0.87
2:B:242:PRO:HB2	4:P:92:HIS:HB3	1.55	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:42:ARG:HD2	2:N:64:SER:HB3	1.56	0.87
4:D:92:HIS:HB3	2:N:243:ARG:HB2	1.56	0.87
1:M:146:PHE:HB2	1:M:149:ILE:CD1	2.05	0.87
1:M:444:GLY:HA3	1:M:488:ARG:C	1.95	0.86
4:D:0:MET:HG3	4:D:1:ILE:H	1.40	0.86
1:A:60:ASP:OD1	1:A:123:ARG:NH2	2.08	0.86
1:A:57:GLN:NE2	1:A:122:GLU:HG2	1.89	0.86
4:P:22:MET:HA	4:P:22:MET:HE3	1.56	0.85
2:N:222:ALA:O	2:N:226:GLN:NE2	2.10	0.85
2:N:149:ILE:HG23	2:N:216:LYS:HG3	1.58	0.85
1:A:60:ASP:CG	1:A:123:ARG:HH21	1.80	0.84
1:M:44:HIS:CE1	5:M:601:FAD:HM82	2.11	0.84
4:D:64:ARG:HG2	4:D:64:ARG:HH11	1.40	0.84
2:N:63:GLY:O	2:N:151:CYS:HA	1.77	0.84
4:P:1:ILE:CD1	4:P:1:ILE:H	1.92	0.83
2:B:4:LYS:H	2:B:4:LYS:CE	1.90	0.83
1:M:24:ALA:HB2	1:M:32:ILE:HD11	1.59	0.83
3:C:86:TRP:NE1	4:D:22:MET:HE2	1.91	0.82
1:M:155:HIS:CE1	1:M:174:ASN:ND2	2.47	0.82
2:N:148:CYS:SG	9:N:246:SF4:FE3	1.70	0.82
1:M:360:GLY:C	1:M:382:SER:OG	2.17	0.82
2:B:214:CYS:SG	9:B:246:SF4:FE4	1.70	0.82
3:O:31:THR:HG21	3:O:82:HIS:HB2	1.61	0.82
2:B:46:ASN:N	2:B:46:ASN:HD22	1.78	0.82
1:M:425:ILE:CD1	10:M:577:HOH:O	2.22	0.82
2:N:116:ILE:CG2	2:N:176:ALA:HB2	2.07	0.82
1:M:157:VAL:HG22	5:M:601:FAD:N1A	1.95	0.81
2:N:71:ASN:CB	3:O:18:LYS:HE3	2.11	0.81
2:N:148:CYS:HG	9:N:246:SF4:FE3	0.92	0.81
3:O:120:THR:HG23	4:P:30:VAL:HB	1.62	0.81
1:M:100:GLY:CA	2:N:184:ARG:NH2	2.42	0.81
1:M:260:TYR:CE1	1:M:264:GLN:NE2	2.47	0.81
1:M:297:GLU:OE1	1:M:297:GLU:HA	1.81	0.81
1:M:97:GLU:OE2	2:N:132:ASN:N	2.14	0.81
1:M:390:ARG:HD2	1:M:391:LEU:O	1.81	0.80
1:A:154:GLU:O	1:A:175:MET:HG3	1.81	0.80
1:M:62:PHE:HB3	1:M:86:VAL:CG1	2.11	0.80
2:B:46:ASN:HD22	2:B:46:ASN:H	1.27	0.80
1:M:155:HIS:NE2	1:M:174:ASN:ND2	2.28	0.80
1:M:7:LEU:HB2	1:M:32:ILE:HG22	1.63	0.80
1:M:155:HIS:ND1	1:M:174:ASN:HA	1.96	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:146:PHE:CB	1:M:149:ILE:HD13	2.11	0.79
1:M:152:PHE:HB3	1:M:155:HIS:CD2	2.17	0.79
1:M:158:LEU:HG	1:M:506:ILE:HD12	1.62	0.79
1:M:92:GLU:HB3	1:M:400:VAL:HB	1.63	0.78
3:C:50:LYS:CA	3:C:50:LYS:HE2	2.14	0.78
4:D:92:HIS:HB3	2:N:243:ARG:CB	2.13	0.78
1:M:79:GLN:NE2	1:M:571:THR:H	1.81	0.78
2:B:32:ALA:O	2:B:82:ARG:NH1	2.17	0.77
1:M:152:PHE:O	1:M:155:HIS:HB2	1.83	0.77
1:A:232:HIS:CE1	1:A:242:LEU:HD11	2.19	0.77
2:N:12:ARG:NH2	2:N:50:ASP:OD1	2.18	0.77
3:O:33:VAL:HB	3:O:34:PRO:HD3	1.67	0.77
1:M:100:GLY:HA2	2:N:184:ARG:NH2	1.98	0.77
1:A:321:GLU:HG2	1:A:344:VAL:HG11	1.67	0.77
2:B:9:GLU:HB2	2:B:25:PHE:CE2	2.20	0.76
2:N:116:ILE:O	2:N:191:ARG:HG2	1.85	0.76
1:A:44:HIS:HE1	5:A:601:FAD:HM82	1.44	0.76
1:M:102:PRO:HG2	1:M:134:HIS:CD2	2.21	0.76
1:M:230:GLN:HB3	1:M:356:TYR:H	1.51	0.76
1:M:156:PHE:CE1	5:M:601:FAD:N6A	2.53	0.76
1:M:237:PRO:HB2	1:M:308:ARG:HB3	1.68	0.76
1:M:146:PHE:CB	1:M:149:ILE:CD1	2.65	0.75
1:M:24:ALA:CA	1:M:32:ILE:HD11	2.16	0.75
1:M:62:PHE:HB3	1:M:86:VAL:HG13	1.67	0.75
1:M:81:VAL:HG11	1:M:383:VAL:CG1	2.17	0.75
4:D:34:LEU:HD23	4:D:38:LEU:HD12	1.68	0.75
4:P:9:ASP:C	4:P:11:PRO:HD2	2.07	0.75
4:D:26:ILE:HG22	4:D:27:ILE:HG13	1.69	0.74
1:M:155:HIS:CE1	1:M:174:ASN:CA	2.70	0.74
1:M:11:GLY:HA2	5:M:601:FAD:C1B	2.16	0.74
1:M:24:ALA:CB	1:M:32:ILE:HD11	2.17	0.74
2:B:46:ASN:N	2:B:46:ASN:ND2	2.35	0.74
1:M:114:ARG:O	1:M:124:THR:HB	1.88	0.74
2:N:31:ASP:OD2	2:N:33:THR:CA	2.35	0.74
2:N:12:ARG:NH1	2:N:50:ASP:OD1	2.21	0.74
2:N:177:HIS:O	2:N:181:GLU:HB2	1.87	0.74
2:N:96:PHE:O	3:O:9:ARG:NH1	2.20	0.74
3:C:54:GLU:HA	3:C:54:GLU:OE1	1.87	0.74
1:M:328:LEU:HD22	1:M:331:ILE:CD1	2.16	0.73
2:B:65:CYS:SG	7:B:244:FES:FE1	1.79	0.73
1:M:444:GLY:HA3	1:M:488:ARG:O	1.89	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:45:THR:OG1	5:A:601:FAD:O2A	2.06	0.73
1:M:527:GLU:CD	1:M:529:ARG:NH1	2.41	0.73
1:M:360:GLY:O	1:M:382:SER:OG	2.07	0.72
2:B:99:GLU:OE2	3:C:4:ARG:NH1	2.23	0.72
3:O:19:LEU:HD21	3:O:22:TYR:CE2	2.25	0.72
2:B:154:CYS:HG	9:B:246:SF4:FE2	0.90	0.72
1:M:192:THR:HG21	1:M:212:GLY:N	2.03	0.72
1:A:49:GLU:HG2	1:A:129:ASP:O	1.89	0.72
1:M:546:ASN:O	1:M:549:LYS:NZ	2.23	0.72
1:M:224:ARG:HB2	1:M:552:LEU:HD23	1.72	0.72
1:M:13:GLY:H	5:M:601:FAD:H4B	1.54	0.72
1:M:212:GLY:HA2	1:M:215:MET:HE3	1.71	0.72
1:M:549:LYS:HD2	1:M:565:TYR:CB	2.19	0.72
1:A:275:GLY:O	1:A:277:PRO:HD3	1.89	0.72
1:M:166:HIS:CD2	1:M:372:LYS:HB3	2.24	0.72
1:A:200:ARG:HD3	1:A:201:TYR:CZ	2.24	0.71
1:M:176:MET:HE2	2:N:99:GLU:HG3	1.72	0.71
1:M:93:MET:CE	1:M:93:MET:HA	2.20	0.71
1:A:151:ARG:NH2	2:B:114:GLU:OE1	2.23	0.71
1:A:346:GLU:HG3	1:A:347:PRO:CD	2.14	0.71
1:M:100:GLY:C	2:N:184:ARG:HH22	1.94	0.71
1:A:18:ARG:NH1	1:A:92:GLU:OE2	2.23	0.71
2:B:241:LYS:O	2:B:241:LYS:CG	2.39	0.71
1:M:141:GLN:HB3	2:N:118:PRO:O	1.90	0.70
3:O:54:GLU:H	3:O:54:GLU:CD	1.94	0.70
1:A:366:ASN:O	1:A:367:CYS:HB2	1.90	0.70
1:M:242:LEU:HG	1:M:244:THR:H	1.56	0.70
1:A:497:VAL:HG12	1:A:497:VAL:O	1.90	0.70
1:M:212:GLY:HA2	1:M:215:MET:CE	2.22	0.70
1:M:192:THR:HG21	1:M:212:GLY:H	1.56	0.70
1:A:197:ARG:HD2	1:A:206:GLY:HA2	1.72	0.70
2:B:148:CYS:HG	9:B:246:SF4:FE3	1.07	0.70
2:B:148:CYS:SG	9:B:246:SF4:FE3	1.84	0.70
3:C:19:LEU:HD13	3:C:20:PRO:HD2	1.73	0.70
1:M:217:LEU:HG	1:M:555:ARG:HB2	1.72	0.70
2:N:15:PRO:HB3	3:O:5:LYS:H	1.54	0.70
1:A:119:MET:CE	1:A:391:LEU:HD23	2.21	0.70
1:M:243:MET:HA	1:M:243:MET:HE2	1.72	0.70
1:M:467:ARG:NH1	1:M:532:HIS:ND1	2.39	0.70
1:M:37:LYS:HE2	5:M:601:FAD:C8A	2.22	0.70
1:M:149:ILE:HD12	1:M:149:ILE:N	2.06	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:105:ARG:HD3	2:N:134:GLN:O	1.92	0.69
1:A:200:ARG:HD3	1:A:201:TYR:CE1	2.27	0.69
4:D:92:HIS:CB	2:N:243:ARG:HB2	2.22	0.69
3:O:75:THR:HG22	4:P:32:ILE:HD13	1.74	0.69
4:D:0:MET:HG3	4:D:1:ILE:N	2.08	0.69
1:M:213:MET:HB3	1:M:223:LEU:HD21	1.74	0.69
3:O:49:LEU:HD21	4:P:55:LEU:HA	1.73	0.69
4:P:33:LEU:HD12	4:P:37:ILE:HD12	1.73	0.69
1:A:342:ASP:OD2	1:A:344:VAL:HG23	1.93	0.68
1:M:243:MET:HA	1:M:243:MET:CE	2.22	0.68
1:M:357:THR:HG22	1:M:359:GLY:O	1.93	0.68
2:N:240:LEU:O	2:N:243:ARG:CZ	2.41	0.68
1:A:125:TRP:CD1	1:A:125:TRP:N	2.54	0.68
1:M:553:ALA:HA	1:M:562:ARG:O	1.93	0.68
4:P:79:LEU:HD12	4:P:104:ALA:HB2	1.75	0.68
4:D:9:ASP:OD2	4:D:97:LYS:NZ	2.24	0.68
1:M:421:ASN:OD1	1:M:421:ASN:C	2.30	0.68
2:N:109:PHE:CE2	2:N:113:LEU:HD11	2.28	0.68
3:C:59:PHE:HE2	3:C:63:LEU:HD11	1.59	0.68
1:M:84:TYR:CE2	1:M:405:LEU:HD22	2.29	0.68
1:M:342:ASP:HB3	1:M:345:LYS:CB	2.24	0.68
2:B:4:LYS:H	2:B:4:LYS:HE3	1.58	0.68
4:D:64:ARG:HH12	4:D:117:THR:HG23	1.58	0.68
1:M:102:PRO:C	2:N:139:MET:HE1	2.15	0.68
1:M:227:GLU:HB2	1:M:522:ALA:HB2	1.76	0.68
1:M:260:TYR:OH	1:M:264:GLN:NE2	2.27	0.67
4:P:105:ALA:O	4:P:109:VAL:HG23	1.94	0.67
1:A:10:VAL:HB	1:A:190:MET:CE	2.24	0.67
1:M:244:THR:HG23	1:M:245:GLU:N	2.08	0.67
4:P:55:LEU:O	4:P:59:GLN:HG3	1.93	0.67
1:A:341:VAL:HG13	1:A:346:GLU:HB3	1.75	0.67
2:N:214:CYS:SG	2:N:218:VAL:HG23	2.35	0.67
2:N:41:GLY:HA2	2:N:53:TYR:OH	1.94	0.67
3:C:50:LYS:HD3	4:D:118:ILE:H	1.60	0.67
1:A:346:GLU:CG	1:A:347:PRO:HD2	2.17	0.67
4:D:95:ALA:HB1	4:D:98:TRP:HB2	1.76	0.66
2:N:31:ASP:OD1	2:N:33:THR:OG1	2.12	0.66
3:O:18:LYS:HE2	3:O:19:LEU:HD22	1.75	0.66
1:M:158:LEU:O	1:M:158:LEU:HD23	1.95	0.66
3:O:54:GLU:N	3:O:54:GLU:CD	2.48	0.66
3:C:50:LYS:HB3	4:D:118:ILE:HG22	1.77	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:125:TRP:HD1	1:A:125:TRP:N	1.93	0.66
1:A:306:THR:HB	1:A:307:PRO:HD2	1.78	0.66
1:A:166:HIS:CD2	1:A:372:LYS:HB3	2.30	0.66
1:A:549:LYS:HB2	1:A:566:SER:O	1.96	0.66
2:N:210:CYS:SG	2:N:221:ALA:HB2	2.36	0.66
1:M:151:ARG:NH1	1:M:153:ASP:OD2	2.22	0.66
1:M:146:PHE:HB3	1:M:148:GLN:HE22	1.61	0.65
1:M:358:MET:SD	1:M:389:ASN:HA	2.37	0.65
1:M:53:ALA:HB2	1:M:393:SER:OG	1.95	0.65
1:A:37:LYS:HE2	5:A:601:FAD:N7A	2.11	0.65
1:M:299:ARG:HE	1:M:299:ARG:CA	2.06	0.65
1:M:332:CYS:HA	1:M:343:PRO:HG2	1.77	0.65
1:A:321:GLU:HG2	1:A:344:VAL:CG1	2.27	0.65
1:M:37:LYS:HD3	1:M:156:PHE:CE1	2.31	0.65
1:A:322:LYS:HA	1:A:322:LYS:HE3	1.78	0.65
1:M:436:LEU:O	1:M:440:VAL:HG23	1.97	0.65
1:A:27:ASN:OD1	1:A:27:ASN:C	2.35	0.65
1:A:341:VAL:O	1:A:343:PRO:HD3	1.96	0.65
2:B:65:CYS:SG	7:B:244:FES:S1	2.94	0.65
1:M:51:GLY:O	1:M:396:LEU:HD12	1.97	0.65
1:M:328:LEU:HB3	1:M:331:ILE:HD12	1.78	0.65
1:M:44:HIS:CD2	1:M:44:HIS:O	2.50	0.64
1:M:573:LEU:HD12	1:M:574:PRO:HD2	1.78	0.64
2:B:4:LYS:HE2	2:B:4:LYS:H	1.60	0.64
4:D:92:HIS:HA	2:N:243:ARG:O	1.97	0.64
2:N:108:HIS:O	2:N:112:SER:OG	2.13	0.64
2:N:164:ASN:C	2:N:164:ASN:OD1	2.36	0.64
1:M:478:LYS:O	1:M:482:LEU:HD23	1.97	0.64
4:P:95:ALA:HB1	4:P:98:TRP:HB2	1.79	0.64
1:A:361:ILE:HG13	1:A:380:CYS:O	1.97	0.64
1:M:320:GLY:O	1:M:324:LEU:HB2	1.98	0.64
2:B:198:GLN:HE22	4:D:10:GLU:CG	2.06	0.64
4:D:64:ARG:CG	4:D:64:ARG:HH11	2.10	0.64
1:M:226:MET:O	1:M:518:MET:HG2	1.98	0.64
3:O:53:PRO:HG3	4:P:51:TYR:CE2	2.33	0.64
3:C:125:PHE:CE2	3:C:130:TRP:HH2	2.16	0.64
2:N:54:ARG:HE	2:N:103:VAL:HG13	1.62	0.63
4:D:20:GLY:HA2	4:D:73:LEU:HB3	1.79	0.63
1:M:97:GLU:OE2	2:N:132:ASN:O	2.15	0.63
1:A:59:HIS:H	1:A:59:HIS:CD2	2.15	0.63
1:M:192:THR:CG2	1:M:212:GLY:HA3	2.22	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:155:HIS:CE1	1:M:174:ASN:CB	2.82	0.63
1:M:11:GLY:CA	5:M:601:FAD:O4B	2.46	0.63
1:A:425:ILE:O	1:A:428:GLN:HB2	1.98	0.63
1:A:37:LYS:HE2	5:A:601:FAD:C8A	2.29	0.63
1:M:342:ASP:HB3	1:M:345:LYS:HB3	1.81	0.63
1:A:443:ASP:OD1	1:A:444:GLY:N	2.32	0.63
1:M:70:VAL:HG11	1:M:573:LEU:HD23	1.81	0.63
2:N:141:LYS:HB3	2:N:181:GLU:OE1	1.99	0.63
2:B:28:VAL:CG2	2:B:43:ILE:HD11	2.29	0.63
1:M:156:PHE:HE1	5:M:601:FAD:N6A	1.96	0.63
2:N:151:CYS:SG	9:N:246:SF4:FE1	1.85	0.62
1:M:234:THR:HA	1:M:350:VAL:HG13	1.80	0.62
1:A:10:VAL:HB	1:A:190:MET:HE3	1.80	0.62
3:C:33:VAL:HA	4:D:82:MET:HE2	1.80	0.62
1:M:360:GLY:C	1:M:382:SER:HG	2.00	0.62
3:C:50:LYS:HD3	4:D:118:ILE:HG22	1.81	0.62
1:M:61:SER:N	1:M:64:TYR:HD1	1.97	0.62
2:N:73:PRO:HG2	2:N:213:VAL:HG11	1.79	0.62
4:P:1:ILE:N	4:P:1:ILE:HD12	2.00	0.62
1:A:529:ARG:CZ	1:A:542:ARG:HD2	2.29	0.62
2:N:12:ARG:CZ	2:N:50:ASP:OD1	2.47	0.62
1:A:542:ARG:NH1	1:A:544:ASP:OD2	2.32	0.61
1:A:556:ASP:HB2	1:A:558:ASP:OD2	2.00	0.61
3:C:90:ALA:N	3:C:91:PRO:HD2	2.15	0.61
1:M:149:ILE:CD1	1:M:149:ILE:H	2.11	0.61
1:M:102:PRO:CG	1:M:134:HIS:HD2	2.12	0.61
1:M:361:ILE:O	1:M:363:THR:HG23	2.00	0.61
3:C:12:THR:HG23	3:C:14:THR:H	1.66	0.61
1:M:38:VAL:HG11	1:M:207:ILE:HG21	1.82	0.61
1:M:299:ARG:NE	1:M:299:ARG:HA	2.14	0.61
1:A:41:MET:HE3	1:A:140:PHE:CE2	2.36	0.61
1:A:202:ASN:HA	1:A:353:THR:HG22	1.80	0.61
4:D:48:ALA:O	4:D:53:ARG:HD3	2.01	0.61
1:M:113:VAL:HG12	1:M:125:TRP:HA	1.82	0.61
4:P:10:GLU:OE2	4:P:84:HIS:NE2	2.32	0.61
1:A:176:MET:HG3	3:C:4:ARG:HD3	1.83	0.61
4:D:13:PHE:HE2	4:D:97:LYS:HZ1	1.49	0.61
1:M:15:ALA:HB2	1:M:399:LEU:HD22	1.82	0.61
1:M:304:ILE:HD12	1:M:304:ILE:H	1.65	0.61
1:M:51:GLY:O	5:M:601:FAD:N3	2.33	0.61
3:C:15:TRP:O	3:C:18:LYS:HG2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:34:THR:HG22	2:N:81:LEU:HD13	1.83	0.60
4:P:28:ALA:N	4:P:29:PRO:HD2	2.16	0.60
1:M:15:ALA:HB2	1:M:399:LEU:CD2	2.31	0.60
1:A:11:GLY:HA2	5:A:601:FAD:H1B	1.82	0.60
1:M:176:MET:CE	2:N:99:GLU:HG3	2.30	0.60
1:M:76:LEU:HG	1:M:529:ARG:HD3	1.83	0.60
3:O:75:THR:HG22	4:P:32:ILE:CD1	2.31	0.60
4:P:10:GLU:N	4:P:11:PRO:CD	2.64	0.60
4:P:22:MET:CE	4:P:22:MET:HA	2.31	0.60
2:B:240:LEU:O	2:B:242:PRO:HD3	2.00	0.60
1:M:134:HIS:O	1:M:138:THR:OG1	2.15	0.60
2:B:212:GLU:HG3	3:C:21:PHE:CE2	2.37	0.60
2:B:28:VAL:HG22	2:B:43:ILE:HD11	1.84	0.60
1:M:151:ARG:HH12	1:M:153:ASP:CG	2.03	0.60
2:N:12:ARG:NH2	2:N:101:ASP:OD1	2.31	0.60
2:B:9:GLU:HB2	2:B:25:PHE:CD2	2.37	0.60
3:O:86:TRP:CD1	4:P:22:MET:HE3	2.37	0.60
1:A:148:GLN:N	1:A:148:GLN:OE1	2.33	0.60
4:D:0:MET:CG	4:D:1:ILE:H	2.14	0.60
2:N:65:CYS:HB3	2:N:75:LEU:HD22	1.82	0.60
1:M:152:PHE:HB3	1:M:155:HIS:HD2	1.61	0.60
1:M:500:THR:HA	1:M:503:LEU:HB2	1.84	0.60
1:M:232:HIS:O	1:M:352:PRO:HA	2.01	0.59
1:M:491:ILE:HD13	1:M:491:ILE:N	2.15	0.59
2:N:9:GLU:HG3	2:N:25:PHE:CZ	2.37	0.59
3:O:33:VAL:O	3:O:36:VAL:HG22	2.01	0.59
1:M:102:PRO:CG	1:M:134:HIS:CD2	2.84	0.59
1:A:250:GLU:O	1:A:319:LEU:HD11	2.01	0.59
1:A:546:ASN:O	1:A:549:LYS:HE2	2.02	0.59
1:M:208:VAL:HG12	1:M:208:VAL:O	2.01	0.59
3:O:103:MET:HG2	3:O:104:GLY:N	2.17	0.59
2:B:3:MET:CE	2:B:29:PRO:HB2	2.31	0.59
4:D:92:HIS:HA	2:N:243:ARG:C	2.23	0.59
3:C:50:LYS:HB3	4:D:118:ILE:CG2	2.31	0.59
2:N:5:ASN:HD22	2:N:5:ASN:N	2.00	0.59
1:M:234:THR:HG22	1:M:350:VAL:HG11	1.85	0.59
2:B:170:PRO:HA	2:B:224:ILE:HD11	1.85	0.59
1:A:27:ASN:OD1	1:A:29:ASN:N	2.36	0.58
1:M:11:GLY:O	1:M:16:GLY:HA3	2.03	0.58
1:M:217:LEU:HD13	1:M:223:LEU:HG	1.84	0.58
2:N:157:ALA:HB1	2:N:209:TYR:CD2	2.38	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:74:ASP:O	1:M:75:TRP:HB2	2.02	0.58
3:O:118:VAL:O	3:O:122:VAL:HG23	2.03	0.58
1:A:493:ASP:OD1	1:A:495:SER:OG	2.20	0.58
1:A:527:GLU:CD	1:A:529:ARG:HH11	2.07	0.58
1:M:224:ARG:NH1	1:M:382:SER:O	2.36	0.58
2:N:238:ALA:O	2:N:242:PRO:HD3	2.02	0.58
1:M:34:LEU:O	1:M:151:ARG:HA	2.03	0.58
1:M:260:TYR:HE1	1:M:264:GLN:NE2	2.00	0.58
2:N:36:LEU:HD23	2:N:76:ALA:HA	1.85	0.58
1:A:119:MET:HE2	1:A:391:LEU:HD23	1.86	0.58
2:B:206:PHE:CE1	2:B:225:GLN:HG3	2.38	0.58
1:M:360:GLY:CA	1:M:382:SER:OG	2.51	0.58
1:M:392:GLY:O	1:M:393:SER:HB3	2.03	0.58
1:M:155:HIS:HE1	1:M:174:ASN:HB2	1.69	0.58
3:C:59:PHE:CE2	3:C:63:LEU:HD11	2.39	0.57
1:M:245:GLU:HG2	1:M:245:GLU:O	2.04	0.57
1:A:28:PRO:HA	1:A:148:GLN:HE21	1.70	0.57
1:A:306:THR:HB	1:A:307:PRO:CD	2.34	0.57
1:M:198:VAL:CG1	1:M:459:MET:HG3	2.33	0.57
2:N:206:PHE:CE1	2:N:225:GLN:HG3	2.39	0.57
4:P:60:SER:O	4:P:64:ARG:HG3	2.04	0.57
1:A:336:LYS:O	1:A:340:GLY:HA2	2.04	0.57
1:A:228:PHE:O	1:A:358:MET:HB2	2.05	0.57
1:A:390:ARG:HD2	1:A:395:SER:HB2	1.87	0.57
1:M:280:LYS:C	1:M:281:TYR:HD2	2.08	0.57
2:N:178:ARG:NH1	2:N:178:ARG:HG2	2.00	0.57
1:A:116:PHE:HE2	6:A:577:FUM:H4	1.68	0.57
1:A:142:THR:O	1:A:145:GLN:HG2	2.04	0.57
3:C:50:LYS:CG	4:D:118:ILE:HG22	2.35	0.57
2:N:235:PHE:C	2:N:235:PHE:CD2	2.78	0.57
1:A:286:PRO:O	1:A:290:VAL:HG23	2.04	0.57
3:C:33:VAL:HA	4:D:82:MET:CE	2.35	0.57
1:M:444:GLY:CA	1:M:488:ARG:O	2.53	0.57
1:M:552:LEU:HD11	1:M:566:SER:HB2	1.86	0.57
3:O:68:ILE:HD12	3:O:68:ILE:N	2.18	0.57
4:P:78:GLY:O	4:P:82:MET:HG3	2.05	0.57
1:A:10:VAL:CB	1:A:190:MET:CE	2.82	0.56
3:O:15:TRP:CD2	3:O:16:TRP:N	2.73	0.56
1:A:178:GLY:HA3	1:A:496:SER:O	2.05	0.56
3:C:94:ALA:HB1	3:C:96:ILE:HD11	1.86	0.56
4:D:112:LEU:O	4:D:116:VAL:HG22	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:342:ASP:HB3	1:M:345:LYS:HB2	1.86	0.56
4:D:92:HIS:HB3	2:N:243:ARG:CG	2.34	0.56
2:B:241:LYS:O	2:B:241:LYS:HG2	2.05	0.56
1:M:146:PHE:HB3	1:M:148:GLN:NE2	2.19	0.56
1:M:151:ARG:NH1	1:M:153:ASP:OD1	2.37	0.56
1:M:24:ALA:HA	1:M:32:ILE:HD11	1.86	0.56
3:C:54:GLU:CA	3:C:54:GLU:OE1	2.54	0.56
1:M:85:PHE:HE1	1:M:398:GLU:HA	1.71	0.56
4:P:113:ILE:O	4:P:117:THR:OG1	2.24	0.56
2:N:14:ASN:HD22	2:N:15:PRO:HD2	1.69	0.56
1:A:44:HIS:NE2	5:A:601:FAD:C8	2.65	0.56
2:N:180:ASN:ND2	2:N:188:LYS:HG3	2.20	0.56
2:N:202:TRP:CZ2	4:P:11:PRO:HG3	2.41	0.56
3:O:86:TRP:CD1	4:P:22:MET:CE	2.89	0.56
2:B:210:CYS:O	2:B:213:VAL:HG22	2.04	0.56
1:M:13:GLY:N	5:M:601:FAD:H4B	2.19	0.56
1:M:61:SER:H	1:M:64:TYR:HD1	1.51	0.56
2:N:31:ASP:OD2	2:N:31:ASP:C	2.42	0.56
3:O:15:TRP:CE3	3:O:16:TRP:HA	2.41	0.56
1:A:141:GLN:HB3	2:B:118:PRO:O	2.05	0.56
1:M:27:ASN:C	1:M:27:ASN:HD22	2.09	0.56
2:N:21:PRO:HD3	3:O:7:TYR:CE2	2.41	0.56
4:P:112:LEU:O	4:P:116:VAL:HG22	2.07	0.55
1:M:225:ASP:HB3	1:M:228:PHE:CD2	2.41	0.55
1:A:119:MET:HE1	1:A:391:LEU:HD23	1.88	0.55
1:A:529:ARG:HG3	1:A:542:ARG:HD3	1.87	0.55
4:P:51:TYR:CZ	4:P:55:LEU:HD22	2.41	0.55
2:B:194:GLN:O	2:B:197:SER:HB3	2.05	0.55
1:M:243:MET:HE2	1:M:331:ILE:HG23	1.88	0.55
1:M:469:PRO:HG3	1:M:534:ARG:HH21	1.70	0.55
1:M:243:MET:O	1:M:244:THR:HG22	2.06	0.55
1:M:24:ALA:N	1:M:32:ILE:CD1	2.69	0.55
4:P:62:ILE:O	4:P:65:VAL:HG22	2.06	0.55
3:C:130:TRP:HB2	4:D:53:ARG:NH2	2.22	0.55
3:O:33:VAL:CB	3:O:34:PRO:HD3	2.36	0.55
4:D:51:TYR:C	4:D:51:TYR:CD2	2.80	0.55
1:M:27:ASN:ND2	1:M:27:ASN:C	2.60	0.55
2:N:71:ASN:HD22	3:O:18:LYS:NZ	2.04	0.55
3:O:39:SER:OG	4:P:71:ILE:O	2.25	0.55
1:A:127:ALA:HB3	1:A:131:THR:HA	1.89	0.55
1:M:10:VAL:HG13	5:M:601:FAD:C2A	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:389:ASN:OD1	1:M:531:ALA:HB2	2.07	0.55
1:M:18:ARG:NH1	1:M:92:GLU:OE2	2.40	0.55
1:M:62:PHE:HB3	1:M:86:VAL:HG11	1.89	0.55
2:N:13:TYR:HB2	2:N:21:PRO:CB	2.29	0.55
2:B:154:CYS:HB2	2:B:170:PRO:HG2	1.88	0.54
1:M:322:LYS:O	1:M:326:GLU:HB3	2.06	0.54
1:M:93:MET:CE	1:M:400:VAL:HG21	2.37	0.54
2:N:71:ASN:HD22	3:O:18:LYS:HZ2	1.55	0.54
1:M:225:ASP:HB3	1:M:228:PHE:HD2	1.72	0.54
1:M:24:ALA:HB2	1:M:32:ILE:CD1	2.35	0.54
1:M:299:ARG:HA	1:M:299:ARG:HE	1.69	0.54
1:M:52:SER:O	1:M:125:TRP:N	2.39	0.54
2:N:241:LYS:O	2:N:243:ARG:HG2	2.06	0.54
1:A:42:ARG:HG2	2:B:64:SER:HB3	1.88	0.54
2:B:154:CYS:SG	9:B:246:SF4:S4	3.04	0.54
1:M:30:ALA:O	1:M:148:GLN:HB3	2.08	0.54
1:A:440:VAL:HG13	10:A:606:HOH:O	2.08	0.54
1:M:299:ARG:NE	1:M:299:ARG:CA	2.71	0.54
1:M:7:LEU:HD11	1:M:411:THR:CG2	2.37	0.54
1:M:97:GLU:C	1:M:97:GLU:OE1	2.46	0.54
2:N:135:THR:HB	2:N:138:GLN:HB2	1.90	0.54
2:N:8:ILE:HD11	2:N:81:LEU:HD21	1.89	0.54
1:A:273:PRO:HG2	1:A:276:GLU:HB2	1.89	0.54
1:M:151:ARG:NH1	1:M:153:ASP:CG	2.61	0.54
1:M:308:ARG:NH2	2:N:33:THR:HB	2.22	0.54
1:M:472:MET:SD	1:M:523:MET:HA	2.48	0.54
1:A:59:HIS:HD2	1:A:59:HIS:H	1.56	0.54
3:O:50:LYS:HD2	4:P:117:THR:HB	1.89	0.54
1:M:448:TRP:CH2	1:M:504:TYR:HB3	2.43	0.54
1:M:88:HIS:CB	1:M:401:VAL:HG13	2.38	0.53
1:M:94:THR:HA	2:N:131:THR:CG2	2.38	0.53
1:A:15:ALA:HB2	1:A:399:LEU:HD22	1.90	0.53
2:N:31:ASP:CG	2:N:33:THR:OG1	2.46	0.53
2:N:73:PRO:HB2	2:N:153:LEU:HD22	1.90	0.53
3:O:68:ILE:N	3:O:68:ILE:CD1	2.70	0.53
4:D:92:HIS:HD2	2:N:243:ARG:OXT	1.91	0.53
1:M:152:PHE:N	1:M:152:PHE:CD2	2.77	0.53
1:M:194:GLY:O	1:M:208:VAL:HG13	2.09	0.53
2:N:51:LEU:HD23	2:N:52:SER:N	2.23	0.53
1:A:493:ASP:C	1:A:493:ASP:OD1	2.47	0.53
2:N:236:LEU:HD23	2:N:236:LEU:C	2.28	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:19:LEU:CD2	3:O:22:TYR:CD2	2.91	0.53
1:M:94:THR:O	1:M:98:LEU:HG	2.08	0.53
2:N:153:LEU:HD12	2:N:215:PRO:HD3	1.89	0.53
3:O:33:VAL:HB	3:O:34:PRO:CD	2.37	0.53
3:C:86:TRP:CD1	4:D:22:MET:HE1	2.42	0.53
2:N:54:ARG:NH2	2:N:104:VAL:O	2.42	0.53
1:A:542:ARG:HG3	1:A:543:ASP:N	2.24	0.53
1:M:207:ILE:HG13	1:M:208:VAL:HG23	1.91	0.53
1:M:81:VAL:CG1	1:M:383:VAL:CG1	2.87	0.53
2:B:151:CYS:SG	9:B:246:SF4:S3	3.07	0.53
1:M:11:GLY:HA2	5:M:601:FAD:H1B	1.91	0.53
1:M:198:VAL:HG12	1:M:459:MET:HG3	1.89	0.53
3:O:38:PHE:HB2	3:O:75:THR:HG21	1.90	0.53
3:C:50:LYS:CB	4:D:118:ILE:HG22	2.39	0.53
1:M:396:LEU:HG	5:M:601:FAD:C2	2.38	0.53
2:N:60:ALA:HA	7:N:244:FES:S1	2.49	0.53
1:A:442:GLN:NE2	1:A:487:LYS:C	2.63	0.53
1:M:421:ASN:OD1	1:M:423:ALA:N	2.42	0.53
1:M:451:ILE:HG22	1:M:508:LEU:HD11	1.91	0.53
2:N:116:ILE:CG2	2:N:176:ALA:CB	2.78	0.53
1:A:527:GLU:OE1	1:A:529:ARG:HD2	2.10	0.52
2:N:135:THR:CG2	2:N:136:PRO:HD2	2.39	0.52
1:M:119:MET:CE	1:M:391:LEU:HD23	2.40	0.52
2:N:240:LEU:O	2:N:243:ARG:NH2	2.42	0.52
1:A:200:ARG:NH1	1:A:201:TYR:OH	2.42	0.52
1:M:42:ARG:HH22	2:N:150:ASN:C	2.10	0.52
1:M:37:LYS:HE2	5:M:601:FAD:N7A	2.24	0.52
1:M:97:GLU:OE1	1:M:98:LEU:HD23	2.10	0.52
4:P:22:MET:HE2	4:P:26:ILE:CD1	2.38	0.52
1:A:51:GLY:HA2	1:A:131:THR:HG21	1.91	0.52
1:A:442:GLN:HE21	1:A:489:VAL:H	1.57	0.52
1:M:211:ASP:OD2	1:M:507:GLU:HG2	2.09	0.52
1:M:486:PHE:O	1:M:489:VAL:HB	2.10	0.52
1:M:524:ALA:HB2	1:M:563:LEU:CD1	2.39	0.52
1:A:154:GLU:C	1:A:175:MET:HG3	2.30	0.52
2:N:175:LEU:O	2:N:178:ARG:HB3	2.10	0.52
4:P:50:SER:O	4:P:53:ARG:N	2.43	0.52
1:M:146:PHE:HB3	1:M:149:ILE:CD1	2.38	0.52
2:N:155:TYR:CE2	2:N:169:GLY:HA3	2.45	0.52
2:N:123:ASN:ND2	2:N:184:ARG:O	2.43	0.52
1:M:101:CYS:N	2:N:184:ARG:NH2	2.57	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:103:TRP:O	1:M:105:ARG:HG3	2.10	0.52
1:M:243:MET:CE	1:M:331:ILE:HG23	2.39	0.52
1:M:93:MET:CE	1:M:93:MET:CA	2.87	0.52
1:A:462:GLY:HA3	1:A:475:THR:OG1	2.10	0.52
2:B:188:LYS:HZ3	2:B:230:GLU:HG3	1.75	0.52
2:N:178:ARG:CG	2:N:178:ARG:HH11	2.07	0.52
1:A:43:SER:O	1:A:46:VAL:HG12	2.10	0.51
1:A:317:ARG:HD3	1:A:345:LYS:O	2.10	0.51
3:C:59:PHE:O	3:C:62:PHE:HB3	2.11	0.51
1:M:23:ALA:CB	1:M:32:ILE:HG21	2.40	0.51
1:M:225:ASP:OD2	1:M:550:HIS:HD2	1.93	0.51
4:P:33:LEU:HA	4:P:37:ILE:HG13	1.91	0.51
3:C:63:LEU:HB3	4:D:40:PRO:HG3	1.93	0.51
4:D:62:ILE:CG2	4:D:63:GLY:N	2.74	0.51
1:M:199:TYR:CE1	1:M:229:VAL:HG11	2.46	0.51
1:M:525:ARG:NH2	1:M:549:LYS:O	2.36	0.51
1:M:24:ALA:CA	1:M:32:ILE:CD1	2.87	0.51
1:M:527:GLU:CD	1:M:529:ARG:HH12	2.09	0.51
4:D:92:HIS:CD2	2:N:243:ARG:OXT	2.64	0.51
3:O:9:ARG:HB3	3:O:10:PRO:HD2	1.91	0.51
1:A:448:TRP:CG	1:A:449:ALA:N	2.78	0.51
1:A:356:TYR:HE1	5:A:601:FAD:O3'	1.93	0.51
1:M:510:HIS:O	1:M:514:VAL:HG23	2.11	0.51
1:M:100:GLY:C	2:N:184:ARG:HH21	1.92	0.51
1:A:257:LYS:NZ	1:A:301:GLY:O	2.39	0.51
1:A:50:GLY:HA3	1:A:116:PHE:CZ	2.46	0.51
2:N:151:CYS:SG	9:N:246:SF4:S3	3.09	0.51
2:N:57:CYS:O	2:N:58:ARG:HB2	2.11	0.51
2:B:188:LYS:NZ	2:B:230:GLU:HG3	2.25	0.51
1:M:34:LEU:N	1:M:150:GLN:O	2.36	0.51
1:M:414:ALA:HA	1:M:417:ALA:HB2	1.93	0.51
1:M:447:ASN:ND2	2:N:45:ASP:O	2.44	0.51
1:M:211:ASP:OD1	1:M:507:GLU:HA	2.11	0.51
1:M:51:GLY:N	5:M:601:FAD:O4	2.44	0.51
2:N:155:TYR:CE1	2:N:170:PRO:HD2	2.46	0.51
2:N:206:PHE:HA	8:N:245:F3S:S1	2.51	0.51
1:A:525:ARG:NH2	1:A:549:LYS:O	2.39	0.51
1:M:524:ALA:CB	1:M:563:LEU:CD1	2.89	0.51
1:A:18:ARG:HG2	1:A:400:VAL:HA	1.93	0.50
3:C:130:TRP:HB2	4:D:53:ARG:HH21	1.75	0.50
2:N:112:SER:O	2:N:116:ILE:HG12	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:42:ARG:NH1	2:N:62:CYS:O	2.44	0.50
3:O:59:PHE:O	3:O:62:PHE:HB3	2.11	0.50
4:P:64:ARG:HH21	4:P:116:VAL:HA	1.77	0.50
1:A:493:ASP:OD2	1:A:495:SER:OG	2.29	0.50
1:M:263:LEU:CD1	1:M:283:GLU:HA	2.41	0.50
1:M:535:LEU:O	1:M:540:THR:HG22	2.11	0.50
1:M:61:SER:HB3	1:M:64:TYR:CD1	2.47	0.50
1:A:527:GLU:OE1	1:A:529:ARG:NH1	2.41	0.50
2:N:64:SER:O	2:N:66:GLY:N	2.45	0.50
1:A:279:ASN:O	1:A:280:LYS:HB2	2.12	0.50
1:A:442:GLN:HG2	1:A:489:VAL:O	2.11	0.50
2:B:204:CYS:SG	8:B:245:F3S:S2	2.90	0.50
4:D:92:HIS:HB3	2:N:243:ARG:HG3	1.94	0.50
1:M:155:HIS:HE1	1:M:174:ASN:CB	2.20	0.50
1:M:232:HIS:HE1	1:M:244:THR:O	1.93	0.50
1:M:342:ASP:O	1:M:346:GLU:N	2.44	0.50
1:M:48:ALA:HA	5:M:601:FAD:C6	2.42	0.50
1:M:388:ALA:HB2	1:M:529:ARG:HD3	1.93	0.50
4:D:92:HIS:C	2:N:243:ARG:HB2	2.32	0.50
3:O:28:ARG:O	3:O:31:THR:HB	2.11	0.50
1:A:84:TYR:CE1	1:A:88:HIS:CE1	2.99	0.50
2:B:13:TYR:OH	3:C:5:LYS:O	2.25	0.50
2:B:115:ALA:HB2	4:D:1:ILE:HD12	1.94	0.50
2:B:234:ASP:OD1	4:D:7:ARG:NH2	2.45	0.50
1:M:168:ARG:HD3	10:M:577:HOH:O	1.78	0.50
1:M:158:LEU:HD13	1:M:436:LEU:HD23	1.94	0.50
4:P:50:SER:O	4:P:51:TYR:C	2.50	0.50
1:A:97:GLU:OE1	1:A:105:ARG:NH2	2.45	0.50
2:B:3:MET:HE1	2:B:29:PRO:HB2	1.94	0.50
1:M:224:ARG:CB	1:M:552:LEU:HD23	2.41	0.50
2:N:28:VAL:CG1	2:N:29:PRO:HD2	2.42	0.50
1:M:521:SER:HA	1:M:551:THR:HG21	1.94	0.50
1:M:7:LEU:HD22	1:M:187:ALA:HB3	1.93	0.50
1:M:256:ASN:HB2	1:M:302:ASN:O	2.12	0.50
4:D:22:MET:HE2	4:D:22:MET:HA	1.94	0.49
1:M:113:VAL:HB	1:M:124:THR:O	2.11	0.49
1:M:70:VAL:CG1	1:M:573:LEU:HD23	2.41	0.49
2:B:149:ILE:HG23	2:B:216:LYS:HG3	1.93	0.49
2:B:241:LYS:O	2:B:241:LYS:HG3	2.12	0.49
3:C:2:THR:HG1	3:C:4:ARG:H	1.60	0.49
1:M:105:ARG:NH1	2:N:134:GLN:H	2.10	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:44:LYS:HA	2:N:48:ALA:O	2.12	0.49
2:N:51:LEU:HA	2:N:101:ASP:OD1	2.13	0.49
4:P:27:ILE:C	4:P:29:PRO:HD2	2.33	0.49
1:A:262:TYR:OH	1:A:312:VAL:HG11	2.13	0.49
1:A:493:ASP:CG	1:A:495:SER:OG	2.51	0.49
1:A:556:ASP:CB	1:A:558:ASP:OD2	2.59	0.49
2:B:154:CYS:SG	9:B:246:SF4:S3	2.95	0.49
1:M:114:ARG:NE	1:M:116:PHE:HE1	2.11	0.49
1:M:177:GLU:OE1	1:M:177:GLU:HA	2.11	0.49
1:M:331:ILE:HA	1:M:334:LEU:HD12	1.95	0.49
1:M:48:ALA:O	1:M:132:GLY:N	2.43	0.49
2:N:135:THR:HG22	2:N:136:PRO:HD2	1.95	0.49
2:N:155:TYR:HE1	2:N:171:ALA:CB	2.25	0.49
3:O:56:TRP:CD1	4:P:51:TYR:HB2	2.47	0.49
3:C:98:VAL:HG23	3:C:98:VAL:O	2.12	0.49
1:M:85:PHE:CD2	1:M:385:LEU:HD11	2.48	0.49
4:P:10:GLU:N	4:P:11:PRO:HD2	2.28	0.49
1:A:10:VAL:CB	1:A:190:MET:HE3	2.41	0.49
1:A:27:ASN:OD1	1:A:30:ALA:N	2.42	0.49
4:D:73:LEU:HB2	4:D:74:PRO:HD3	1.94	0.49
1:M:17:LEU:HD22	1:M:140:PHE:HA	1.94	0.49
1:M:245:GLU:HG3	1:M:248:ARG:NH2	2.28	0.49
1:M:395:SER:OG	5:M:601:FAD:H2'	2.12	0.49
4:P:2:ASN:HB2	4:P:3:PRO:CD	2.42	0.49
1:M:158:LEU:CD1	1:M:436:LEU:HD23	2.42	0.49
2:N:5:ASN:N	2:N:5:ASN:ND2	2.60	0.49
1:M:378:GLY:HA2	1:M:399:LEU:HD23	1.94	0.49
2:N:28:VAL:HG13	2:N:29:PRO:HD2	1.94	0.49
3:O:28:ARG:HG3	3:O:85:THR:HG21	1.95	0.49
1:A:536:ASP:OD1	1:A:536:ASP:N	2.40	0.49
4:D:39:LEU:HB3	4:D:40:PRO:HD3	1.95	0.49
1:M:7:LEU:HD21	1:M:411:THR:HA	1.94	0.49
3:O:19:LEU:HD23	3:O:22:TYR:CD2	2.48	0.49
4:P:22:MET:HE2	4:P:26:ILE:HD12	1.95	0.49
1:M:161:LEU:HD21	1:M:171:VAL:HG23	1.95	0.49
1:M:186:ASN:HB3	1:M:417:ALA:HB1	1.95	0.49
1:M:365:GLN:H	1:M:365:GLN:CD	2.16	0.49
1:M:472:MET:HE1	1:M:532:HIS:CE1	2.48	0.49
1:M:78:GLU:OE1	1:M:550:HIS:HE1	1.96	0.49
1:A:256:ASN:HB2	1:A:302:ASN:O	2.12	0.48
1:M:499:ASN:O	1:M:503:LEU:HG	2.12	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:P:86:MET:CE	4:P:91:ILE:HG21	2.42	0.48
2:B:188:LYS:NZ	2:B:230:GLU:CG	2.77	0.48
2:N:185:ASP:OD2	2:N:185:ASP:C	2.52	0.48
1:A:44:HIS:CE1	1:A:204:ASN:HA	2.48	0.48
1:M:225:ASP:OD1	1:M:550:HIS:HB3	2.13	0.48
1:M:28:PRO:O	1:M:148:GLN:HG2	2.12	0.48
1:M:442:GLN:NE2	1:M:487:LYS:HA	2.29	0.48
4:P:30:VAL:O	4:P:33:LEU:HB3	2.13	0.48
4:P:42:GLY:C	4:P:44:PHE:H	2.16	0.48
3:C:50:LYS:CD	4:D:118:ILE:HG22	2.43	0.48
1:M:85:PHE:CE1	1:M:398:GLU:HA	2.49	0.48
2:N:109:PHE:CZ	2:N:113:LEU:HD11	2.48	0.48
1:M:31:LYS:O	1:M:31:LYS:HD3	2.14	0.48
1:M:232:HIS:CE1	1:M:242:LEU:CD1	2.97	0.48
1:M:75:TRP:O	1:M:568:VAL:HG11	2.14	0.48
2:N:134:GLN:NE2	2:N:184:ARG:HH11	2.11	0.48
1:A:292:GLN:HG2	1:A:466:TYR:CZ	2.48	0.48
3:C:50:LYS:CD	4:D:118:ILE:H	2.26	0.48
1:M:363:THR:HG21	1:M:376:ALA:HB3	1.94	0.48
2:N:54:ARG:HH21	2:N:103:VAL:HG12	1.78	0.48
3:O:114:ALA:O	3:O:118:VAL:HG23	2.14	0.48
3:O:63:LEU:O	3:O:69:VAL:HG22	2.13	0.48
1:A:40:PRO:HG2	1:A:140:PHE:CE1	2.48	0.48
1:M:82:VAL:HG22	1:M:385:LEU:HD12	1.96	0.48
2:B:28:VAL:HG22	2:B:43:ILE:CD1	2.42	0.48
2:B:3:MET:HE2	2:B:29:PRO:HB2	1.96	0.48
1:A:62:PHE:CZ	1:A:90:PRO:HG2	2.49	0.47
3:O:18:LYS:HG2	3:O:19:LEU:HD22	1.94	0.47
3:O:65:ASN:O	3:O:69:VAL:HG23	2.14	0.47
4:P:9:ASP:C	4:P:11:PRO:CD	2.79	0.47
1:M:102:PRO:CD	1:M:134:HIS:HD2	2.27	0.47
1:M:223:LEU:HD13	1:M:226:MET:HE2	1.96	0.47
2:N:5:ASN:HA	2:N:28:VAL:O	2.14	0.47
2:N:57:CYS:HB3	2:N:62:CYS:HB3	1.96	0.47
2:N:7:LYS:HE2	2:N:25:PHE:CD1	2.49	0.47
3:O:68:ILE:H	3:O:68:ILE:CD1	2.26	0.47
2:B:42:TYR:CD2	2:B:42:TYR:C	2.87	0.47
1:M:194:GLY:HA2	1:M:379:GLU:HG2	1.95	0.47
1:M:88:HIS:HB3	1:M:401:VAL:HG13	1.95	0.47
3:O:43:ILE:HG13	4:P:71:ILE:HD13	1.96	0.47
1:A:529:ARG:NH2	1:A:542:ARG:HD2	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:45:GLY:N	3:C:59:PHE:CE1	2.82	0.47
1:M:37:LYS:HD3	1:M:156:PHE:CD1	2.49	0.47
1:M:290:VAL:O	1:M:293:ALA:HB3	2.14	0.47
2:N:14:ASN:HD22	2:N:15:PRO:CD	2.27	0.47
3:C:56:TRP:O	3:C:59:PHE:HB3	2.15	0.47
1:M:252:GLY:HA3	1:M:316:LEU:CD2	2.44	0.47
1:M:332:CYS:O	1:M:336:LYS:HG3	2.15	0.47
1:M:76:LEU:HD12	1:M:228:PHE:CZ	2.50	0.47
1:M:101:CYS:C	2:N:184:ARG:HH22	2.18	0.47
2:N:30:TYR:HA	2:N:34:THR:OG1	2.14	0.47
1:A:396:LEU:HG	5:A:601:FAD:C2	2.45	0.47
3:C:113:TRP:O	3:C:117:VAL:HG23	2.15	0.47
1:M:146:PHE:CB	1:M:149:ILE:HD11	2.44	0.47
1:M:194:GLY:CA	1:M:379:GLU:HG2	2.44	0.47
1:M:432:VAL:HA	1:M:435:ARG:HH11	1.79	0.47
4:P:38:LEU:HD22	4:P:43:LEU:HB2	1.96	0.47
2:B:116:ILE:HD12	2:B:172:ALA:O	2.15	0.47
3:C:125:PHE:CE2	3:C:130:TRP:CH2	3.01	0.47
4:D:109:VAL:O	4:D:112:LEU:HB3	2.15	0.47
2:N:226:GLN:HE21	2:N:226:GLN:HB2	1.57	0.47
1:M:38:VAL:HG11	1:M:207:ILE:CG2	2.44	0.47
1:M:261:ARG:HD3	1:M:271:GLU:OE1	2.15	0.47
2:N:11:VAL:HG21	2:N:91:GLU:HG2	1.95	0.47
3:O:15:TRP:HZ3	3:O:22:TYR:CG	2.33	0.47
1:M:114:ARG:NE	1:M:116:PHE:CE1	2.83	0.47
3:O:53:PRO:HG3	4:P:51:TYR:CD2	2.49	0.47
1:A:398:GLU:HG3	1:A:402:PHE:CD1	2.50	0.46
1:M:101:CYS:N	2:N:184:ARG:HH22	2.14	0.46
2:N:36:LEU:HD21	2:N:67:MET:SD	2.55	0.46
1:M:224:ARG:HG2	1:M:362:GLU:HA	1.97	0.46
1:M:7:LEU:HD12	1:M:23:ALA:HB1	1.96	0.46
1:A:159:ASP:OD1	1:A:160:ILE:N	2.48	0.46
1:M:57:GLN:HB2	1:M:59:HIS:CD2	2.51	0.46
1:A:232:HIS:O	1:A:352:PRO:HA	2.15	0.46
3:C:49:LEU:HG	4:D:55:LEU:HD12	1.96	0.46
1:M:177:GLU:OE1	3:O:2:THR:HB	2.16	0.46
1:M:94:THR:HA	2:N:131:THR:HG22	1.97	0.46
4:D:92:HIS:CA	2:N:243:ARG:HB2	2.44	0.46
4:D:64:ARG:HH22	4:D:117:THR:CG2	2.28	0.46
2:N:96:PHE:HB3	2:N:104:VAL:HB	1.97	0.46
1:A:454:GLU:CD	1:A:485:ARG:HH22	2.19	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:62:CYS:HG	7:B:244:FES:FE2	1.31	0.46
3:C:36:VAL:HG23	4:D:78:GLY:HA3	1.96	0.46
2:N:15:PRO:HG3	2:N:99:GLU:O	2.15	0.46
1:M:203:THR:CG2	1:M:353:THR:HG23	2.46	0.46
4:P:72:VAL:O	4:P:75:LEU:HB2	2.16	0.46
1:A:10:VAL:CG2	1:A:190:MET:HE3	2.46	0.46
1:M:130:LYS:NZ	2:N:216:LYS:HD2	2.31	0.46
1:M:154:GLU:O	1:M:175:MET:HB2	2.16	0.46
1:M:203:THR:HG22	1:M:353:THR:HG23	1.98	0.46
2:B:204:CYS:SG	8:B:245:F3S:S3	3.14	0.46
1:M:122:GLU:HG2	1:M:122:GLU:O	2.15	0.46
1:M:158:LEU:HG	1:M:506:ILE:CD1	2.40	0.46
1:M:444:GLY:CA	1:M:488:ARG:C	2.78	0.46
2:B:6:LEU:HD23	2:B:8:ILE:HG12	1.99	0.45
2:B:99:GLU:CD	3:C:4:ARG:HH11	2.20	0.45
1:M:320:GLY:O	1:M:324:LEU:CB	2.63	0.45
1:M:358:MET:SD	1:M:390:ARG:N	2.89	0.45
1:M:227:GLU:HB3	1:M:521:SER:HB2	1.98	0.45
2:N:36:LEU:HB3	2:N:76:ALA:O	2.17	0.45
1:A:395:SER:O	1:A:399:LEU:HG	2.15	0.45
1:A:398:GLU:HG3	1:A:402:PHE:HD1	1.80	0.45
1:M:51:GLY:HA2	1:M:131:THR:HG21	1.97	0.45
1:M:98:LEU:CD2	2:N:132:ASN:ND2	2.79	0.45
4:D:31:MET:HG3	4:D:70:MET:SD	2.57	0.45
1:M:113:VAL:HG23	1:M:122:GLU:O	2.16	0.45
2:B:26:TYR:HB3	2:B:43:ILE:HD12	1.97	0.45
4:D:35:VAL:O	4:D:40:PRO:HD3	2.16	0.45
1:A:7:LEU:HD21	1:A:410:ALA:HB1	1.99	0.45
2:B:112:SER:HA	4:D:1:ILE:CD1	2.46	0.45
2:N:219:ASP:N	2:N:220:PRO:CD	2.79	0.45
4:P:2:ASN:HB2	4:P:3:PRO:HD2	1.99	0.45
1:A:549:LYS:HA	1:A:568:VAL:HG23	1.98	0.45
2:B:226:GLN:OE1	3:C:95:ASN:ND2	2.49	0.45
2:N:155:TYR:HE1	2:N:171:ALA:HB3	1.81	0.45
1:A:93:MET:HB3	1:A:125:TRP:CZ3	2.52	0.45
2:N:17:VAL:O	2:N:17:VAL:HG12	2.16	0.45
2:N:204:CYS:CB	2:N:224:ILE:HG21	2.47	0.45
1:A:74:ASP:O	1:A:75:TRP:HB2	2.16	0.45
2:B:2:GLU:CD	2:B:2:GLU:N	2.70	0.45
4:D:63:GLY:O	4:D:67:LEU:HD22	2.17	0.45
1:M:243:MET:O	1:M:244:THR:C	2.54	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:27:ASN:O	1:M:30:ALA:HB3	2.17	0.45
2:N:149:ILE:HD11	2:N:151:CYS:HB3	1.99	0.45
4:D:94:PRO:HG3	2:N:243:ARG:HE	1.82	0.45
2:N:65:CYS:HB3	2:N:75:LEU:CD2	2.46	0.45
3:O:15:TRP:CE3	3:O:16:TRP:CA	3.00	0.45
4:P:42:GLY:O	4:P:44:PHE:N	2.38	0.45
1:A:227:GLU:HB2	1:A:522:ALA:HB2	1.98	0.45
4:D:110:VAL:O	4:D:113:ILE:HB	2.17	0.45
1:M:242:LEU:CG	1:M:244:THR:H	2.25	0.45
3:O:53:PRO:HA	3:O:56:TRP:HB3	1.98	0.45
1:A:251:GLY:HA2	10:A:617:HOH:O	2.17	0.45
1:A:317:ARG:HD3	1:A:345:LYS:C	2.37	0.45
2:B:18:ASP:OD1	2:B:22:HIS:NE2	2.50	0.45
1:M:176:MET:CE	2:N:99:GLU:CG	2.94	0.45
1:M:245:GLU:HG3	1:M:248:ARG:CZ	2.47	0.45
1:M:38:VAL:HB	1:M:42:ARG:HB2	1.98	0.45
2:N:164:ASN:OD1	2:N:166:GLU:N	2.50	0.45
1:M:206:GLY:HA3	2:N:55:TRP:CZ3	2.52	0.45
1:A:253:ILE:HG13	1:A:315:ASP:HB3	1.99	0.44
3:O:127:ALA:C	3:O:128:LEU:HD23	2.37	0.44
2:B:238:ALA:HA	2:B:241:LYS:HD3	1.99	0.44
1:M:446:GLU:O	1:M:489:VAL:HG22	2.18	0.44
3:O:90:ALA:N	3:O:91:PRO:CD	2.79	0.44
2:N:226:GLN:OE1	3:O:95:ASN:HB2	2.17	0.44
2:B:109:PHE:HE1	2:B:155:TYR:CE1	2.35	0.44
2:B:82:ARG:HG3	2:B:83:ASP:N	2.32	0.44
3:C:103:MET:HG2	3:C:104:GLY:O	2.17	0.44
1:M:223:LEU:HB3	1:M:226:MET:CG	2.47	0.44
1:M:44:HIS:HD2	1:M:44:HIS:O	1.98	0.44
1:M:472:MET:CE	1:M:532:HIS:HE1	2.30	0.44
2:N:5:ASN:C	2:N:30:TYR:HE2	2.21	0.44
1:M:212:GLY:HA2	1:M:215:MET:HE2	1.99	0.44
1:M:304:ILE:HG12	1:M:313:TYR:CE1	2.53	0.44
1:M:44:HIS:CE1	1:M:204:ASN:HA	2.53	0.44
1:M:98:LEU:HD21	2:N:130:GLY:O	2.17	0.44
1:A:162:VAL:HA	1:A:166:HIS:O	2.17	0.44
3:C:99:LYS:O	3:C:100:ASP:HB2	2.17	0.44
1:M:237:PRO:HB2	1:M:308:ARG:CB	2.44	0.44
2:N:154:CYS:HB2	2:N:170:PRO:CG	2.36	0.44
3:O:112:LEU:HD23	3:O:112:LEU:HA	1.85	0.44
2:B:204:CYS:SG	8:B:245:F3S:S1	3.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:35:ILE:CD1	1:M:170:LEU:HD21	2.47	0.44
1:M:161:LEU:HA	1:M:428:GLN:OE1	2.17	0.44
2:N:155:TYR:CE1	2:N:171:ALA:HB3	2.52	0.44
4:D:95:ALA:HB2	2:N:240:LEU:HD23	2.00	0.44
1:M:135:MET:CE	1:M:396:LEU:HD22	2.48	0.44
1:M:18:ARG:HH21	1:M:22:ALA:HB2	1.81	0.44
1:M:322:LYS:O	1:M:326:GLU:N	2.40	0.44
1:M:478:LYS:HA	1:M:478:LYS:HD2	1.80	0.44
1:A:46:VAL:HB	1:A:136:LEU:CD2	2.48	0.43
1:M:135:MET:HE1	1:M:396:LEU:HB3	1.99	0.43
2:N:178:ARG:CG	2:N:178:ARG:NH1	2.71	0.43
3:C:45:GLY:O	3:C:49:LEU:HB2	2.17	0.43
1:M:150:GLN:HG3	1:M:152:PHE:CE2	2.54	0.43
2:N:89:LYS:NZ	2:N:91:GLU:OE2	2.38	0.43
3:O:15:TRP:CE3	3:O:16:TRP:N	2.86	0.43
4:P:9:ASP:O	4:P:12:VAL:HG23	2.17	0.43
1:A:256:ASN:OD1	1:A:258:ASN:N	2.48	0.43
1:A:525:ARG:NH1	1:A:527:GLU:OE1	2.51	0.43
1:A:527:GLU:OE2	1:A:529:ARG:NH1	2.51	0.43
1:M:113:VAL:HG11	1:M:125:TRP:CD1	2.54	0.43
1:M:162:VAL:HG22	1:M:167:VAL:HA	2.00	0.43
1:M:27:ASN:O	1:M:30:ALA:CB	2.66	0.43
1:M:322:LYS:O	1:M:326:GLU:CB	2.66	0.43
1:M:11:GLY:HA3	1:M:191:ALA:O	2.18	0.43
2:N:51:LEU:HD22	2:N:53:TYR:HD2	1.82	0.43
1:A:442:GLN:HE22	1:A:487:LYS:HA	1.82	0.43
2:B:163:LEU:HG	3:C:11:MET:CE	2.47	0.43
1:M:88:HIS:HB2	1:M:401:VAL:HG13	1.99	0.43
2:N:214:CYS:SG	2:N:218:VAL:CG2	3.06	0.43
4:D:2:ASN:HA	4:D:3:PRO:HD2	1.74	0.43
1:M:10:VAL:HG22	1:M:157:VAL:HG11	1.99	0.43
1:M:203:THR:HG22	1:M:353:THR:CG2	2.48	0.43
1:M:203:THR:HG23	1:M:354:ALA:O	2.18	0.43
1:M:441:ASN:O	1:M:442:GLN:C	2.57	0.43
4:P:50:SER:C	4:P:52:GLU:N	2.72	0.43
2:B:121:ILE:HB	2:B:187:GLY:HA3	2.01	0.43
2:B:18:ASP:OD1	2:B:22:HIS:CD2	2.71	0.43
4:D:72:VAL:HG22	4:D:108:THR:HA	2.01	0.43
1:M:10:VAL:CG2	1:M:157:VAL:HG11	2.49	0.43
1:M:76:LEU:CD1	1:M:228:PHE:CZ	3.02	0.43
1:A:206:GLY:HA3	2:B:55:TRP:CH2	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:LYS:HE3	2:B:4:LYS:N	2.28	0.43
4:P:28:ALA:N	4:P:29:PRO:CD	2.81	0.43
1:A:369:THR:HG23	1:A:374:LEU:O	2.19	0.43
1:M:7:LEU:CD2	1:M:187:ALA:HB3	2.49	0.43
2:N:211:SER:OG	2:N:219:ASP:HA	2.19	0.43
3:O:86:TRP:HD1	4:P:22:MET:HE1	1.83	0.43
2:B:158:CYS:SG	2:B:160:GLN:HB2	2.59	0.43
1:M:7:LEU:HD11	1:M:411:THR:HG23	2.01	0.43
2:N:39:ALA:O	2:N:43:ILE:HG12	2.19	0.43
2:N:12:ARG:NH2	2:N:51:LEU:HA	2.34	0.43
1:A:308:ARG:HE	1:A:308:ARG:HB2	1.68	0.42
1:A:7:LEU:HD12	1:A:23:ALA:HB1	2.01	0.42
4:D:50:SER:O	4:D:51:TYR:C	2.56	0.42
1:M:93:MET:HE3	1:M:400:VAL:HG21	1.99	0.42
1:M:471:LEU:HD23	1:M:471:LEU:HA	1.93	0.42
1:M:399:LEU:CD2	5:M:601:FAD:O2P	2.67	0.42
2:N:241:LYS:HG3	2:N:242:PRO:N	2.34	0.42
2:N:64:SER:C	2:N:66:GLY:H	2.22	0.42
1:A:245:GLU:O	1:A:248:ARG:N	2.40	0.42
1:A:76:LEU:HD22	1:A:568:VAL:HG21	2.01	0.42
2:B:7:LYS:HE3	2:B:25:PHE:HB3	2.00	0.42
4:D:13:PHE:HE2	4:D:97:LYS:NZ	2.15	0.42
1:M:200:ARG:NH1	1:M:201:TYR:OH	2.52	0.42
1:M:501:ASP:O	1:M:505:THR:OG1	2.23	0.42
1:M:58:ASP:C	1:M:60:ASP:H	2.22	0.42
2:N:153:LEU:HB2	9:N:246:SF4:S3	2.59	0.42
3:O:36:VAL:HG23	3:O:37:TRP:N	2.34	0.42
4:P:54:VAL:O	4:P:57:PHE:HB3	2.19	0.42
2:B:106:MET:O	2:B:109:PHE:HB3	2.19	0.42
3:C:31:THR:O	3:C:34:PRO:HD2	2.19	0.42
1:M:176:MET:HB3	1:M:176:MET:HE3	1.68	0.42
1:M:498:PHE:CD2	2:N:103:VAL:HG21	2.54	0.42
4:D:113:ILE:HG12	4:P:113:ILE:HG12	2.01	0.42
2:B:220:PRO:HG3	9:B:246:SF4:S1	2.58	0.42
2:B:235:PHE:C	2:B:235:PHE:CD2	2.93	0.42
1:M:495:SER:O	1:M:499:ASN:HB2	2.20	0.42
1:M:537:GLU:CD	1:M:537:GLU:N	2.51	0.42
3:C:91:PRO:HB2	3:C:105:PRO:HB3	2.01	0.42
3:C:105:PRO:HD2	3:C:106:GLU:CD	2.39	0.42
1:M:98:LEU:HD22	2:N:132:ASN:ND2	2.35	0.42
2:N:43:ILE:HD13	2:N:47:LEU:HD13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:239:SER:OG	1:A:241:ILE:HG13	2.19	0.42
1:M:232:HIS:CE1	1:M:242:LEU:HD11	2.55	0.42
1:M:421:ASN:O	1:M:425:ILE:HG12	2.19	0.42
2:N:150:ASN:OD1	2:N:150:ASN:N	2.53	0.42
1:M:493:ASP:OD1	2:N:50:ASP:CB	2.68	0.42
1:M:200:ARG:HD3	1:M:201:TYR:CE1	2.54	0.42
1:M:52:SER:O	1:M:125:TRP:HB2	2.20	0.42
1:M:544:ASP:O	1:M:548:LEU:HB2	2.20	0.42
1:M:572:THR:O	1:M:574:PRO:HD3	2.19	0.42
1:M:45:THR:OG1	5:M:601:FAD:O2A	2.33	0.42
2:N:40:LEU:HB3	2:N:53:TYR:CE2	2.55	0.42
1:A:48:ALA:HA	5:A:601:FAD:C6	2.50	0.42
1:M:223:LEU:HB3	1:M:226:MET:HG3	2.01	0.42
1:M:78:GLU:OE1	1:M:568:VAL:HA	2.19	0.42
2:N:185:ASP:OD1	2:N:191:ARG:NH2	2.45	0.42
3:O:86:TRP:NE1	4:P:22:MET:HE3	2.34	0.42
1:A:332:CYS:HA	1:A:343:PRO:HG2	2.01	0.42
1:A:446:GLU:HB2	1:A:488:ARG:O	2.20	0.42
1:A:442:GLN:NE2	1:A:486:PHE:O	2.53	0.42
1:M:203:THR:OG1	5:M:601:FAD:HM83	2.20	0.42
1:M:23:ALA:HB3	1:M:32:ILE:HG21	2.02	0.42
2:N:65:CYS:O	2:N:66:GLY:C	2.57	0.42
4:P:23:TRP:CD2	4:P:27:ILE:HD13	2.55	0.42
1:A:161:LEU:HD21	1:A:171:VAL:HG23	2.02	0.42
1:A:446:GLU:HB2	1:A:489:VAL:HA	2.02	0.42
4:D:24:SER:O	4:D:28:ALA:HB3	2.20	0.42
2:N:204:CYS:HB2	2:N:224:ILE:HG21	2.01	0.42
2:N:235:PHE:HA	4:P:7:ARG:NH2	2.34	0.42
2:N:48:ALA:HA	2:N:49:PRO:HD3	1.80	0.42
4:P:26:ILE:HG22	4:P:27:ILE:HG13	2.01	0.42
3:C:63:LEU:CD1	4:D:39:LEU:HD23	2.50	0.41
1:M:260:TYR:CZ	1:M:264:GLN:NE2	2.62	0.41
1:M:38:VAL:HG22	5:M:601:FAD:O2B	2.20	0.41
1:A:448:TRP:CH2	1:A:504:TYR:HB3	2.55	0.41
1:A:205:GLY:HA2	2:B:56:SER:O	2.20	0.41
1:M:46:VAL:HG23	1:M:133:PHE:HA	2.02	0.41
1:M:23:ALA:HB1	1:M:32:ILE:HG21	2.02	0.41
2:N:151:CYS:SG	2:N:153:LEU:HB2	2.60	0.41
2:N:99:GLU:HA	2:N:99:GLU:OE1	2.21	0.41
3:O:106:GLU:N	3:O:107:PRO:CD	2.83	0.41
4:P:39:LEU:N	4:P:40:PRO:HD2	2.34	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:238:GLY:HA3	1:M:308:ARG:HD2	2.02	0.41
2:N:61:ILE:O	2:N:61:ILE:HG13	2.19	0.41
4:P:42:GLY:HA2	4:P:44:PHE:CE2	2.54	0.41
1:A:306:THR:CB	1:A:307:PRO:CD	2.95	0.41
1:M:213:MET:CB	1:M:223:LEU:HD21	2.48	0.41
2:N:242:PRO:O	2:N:243:ARG:OXT	2.38	0.41
4:P:73:LEU:HB2	4:P:74:PRO:HD3	2.02	0.41
1:A:10:VAL:HG11	1:A:190:MET:HE1	2.03	0.41
2:B:110:ILE:O	2:B:114:GLU:HG3	2.21	0.41
3:C:65:ASN:O	3:C:69:VAL:HG23	2.20	0.41
1:M:404:ARG:HG2	1:M:408:GLU:OE1	2.21	0.41
2:N:216:LYS:HA	2:N:216:LYS:HD3	1.78	0.41
2:N:94:ALA:HA	3:O:9:ARG:NH2	2.36	0.41
3:O:15:TRP:CZ3	3:O:16:TRP:HA	2.55	0.41
3:O:33:VAL:CB	3:O:34:PRO:CD	2.97	0.41
3:O:49:LEU:HD21	4:P:55:LEU:CA	2.48	0.41
1:A:232:HIS:ND1	1:A:242:LEU:HD11	2.34	0.41
1:M:170:LEU:HG	1:M:183:ILE:HB	2.02	0.41
1:M:232:HIS:CE1	1:M:244:THR:O	2.73	0.41
1:M:392:GLY:O	1:M:393:SER:CB	2.67	0.41
3:O:98:VAL:HG23	3:O:103:MET:HB2	2.02	0.41
3:C:72:ASN:HA	3:C:72:ASN:HD22	1.62	0.41
1:M:174:ASN:HB3	1:M:177:GLU:HB2	2.01	0.41
1:M:18:ARG:NH2	1:M:404:ARG:HG3	2.36	0.41
1:M:261:ARG:NH1	1:M:272:THR:O	2.35	0.41
1:M:79:GLN:NE2	1:M:571:THR:N	2.60	0.41
1:M:91:THR:HG22	1:M:92:GLU:OE1	2.21	0.41
2:N:149:ILE:CG2	2:N:216:LYS:HG3	2.39	0.41
2:N:4:LYS:HB3	2:N:30:TYR:CE2	2.56	0.41
1:A:442:GLN:NE2	1:A:487:LYS:HA	2.36	0.41
4:D:50:SER:O	4:D:54:VAL:HG23	2.20	0.41
1:M:142:THR:O	1:M:145:GLN:HB3	2.20	0.41
1:M:328:LEU:CB	1:M:331:ILE:HD12	2.49	0.41
1:M:206:GLY:HA3	2:N:55:TRP:CH2	2.56	0.41
3:O:18:LYS:CE	3:O:19:LEU:HD22	2.47	0.41
1:A:147:PRO:HD2	1:A:148:GLN:OE1	2.21	0.41
1:A:542:ARG:HH11	1:A:544:ASP:CG	2.23	0.41
3:C:47:PHE:HA	3:C:50:LYS:HB2	2.03	0.41
1:M:57:GLN:NE2	1:M:122:GLU:O	2.47	0.41
1:M:243:MET:O	1:M:244:THR:CG2	2.68	0.41
1:M:408:GLU:O	1:M:411:THR:OG1	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:322:LYS:HE3	1:A:322:LYS:CA	2.48	0.41
2:B:216:LYS:HA	2:B:216:LYS:HD3	1.91	0.41
3:C:106:GLU:HB2	3:C:107:PRO:HD3	2.02	0.41
3:C:56:TRP:O	3:C:60:VAL:HG23	2.20	0.41
1:M:324:LEU:O	1:M:328:LEU:N	2.50	0.41
2:N:106:MET:HE3	2:N:109:PHE:CD2	2.56	0.41
2:N:116:ILE:HD11	2:N:168:ILE:HD12	2.03	0.41
2:N:159:PRO:CG	2:N:207:VAL:HG21	2.31	0.41
1:M:492:THR:HG21	2:N:49:PRO:HG2	2.03	0.41
3:O:7:TYR:CD1	3:O:7:TYR:C	2.94	0.41
1:A:445:GLY:H	1:A:490:ARG:HB2	1.86	0.41
1:A:141:GLN:NE2	2:B:179:TYR:OH	2.54	0.41
2:B:40:LEU:HD23	2:B:40:LEU:HA	1.82	0.41
1:M:44:HIS:H	1:M:207:ILE:HD11	1.86	0.41
2:N:100:ARG:O	2:N:101:ASP:C	2.59	0.41
3:O:50:LYS:CG	4:P:118:ILE:HA	2.51	0.41
2:B:6:LEU:HD23	2:B:8:ILE:CG1	2.51	0.40
1:M:574:PRO:HA	1:M:575:PRO:HD2	1.99	0.40
2:N:236:LEU:HD22	2:N:237:ILE:HD12	2.01	0.40
3:O:16:TRP:HA	3:O:22:TYR:HB3	2.03	0.40
3:O:25:TYR:HD1	3:O:28:ARG:NH2	2.19	0.40
1:A:15:ALA:HB2	1:A:399:LEU:CD2	2.50	0.40
1:A:319:LEU:O	1:A:323:LYS:HB2	2.21	0.40
1:A:92:GLU:OE1	1:A:404:ARG:HD2	2.22	0.40
1:A:431:GLY:O	1:A:435:ARG:HB2	2.21	0.40
2:B:105:ASP:C	2:B:105:ASP:OD1	2.60	0.40
4:D:99:VAL:HG12	4:D:100:PHE:N	2.36	0.40
2:B:198:GLN:NE2	4:D:10:GLU:HG3	2.11	0.40
3:C:56:TRP:CD1	4:D:51:TYR:HB2	2.57	0.40
1:M:224:ARG:HG3	1:M:382:SER:CB	2.51	0.40
3:O:50:LYS:HG2	4:P:118:ILE:HA	2.03	0.40
1:A:10:VAL:HG21	1:A:190:MET:CE	2.52	0.40
1:A:263:LEU:HB3	1:A:268:MET:HE3	2.03	0.40
1:M:503:LEU:O	1:M:507:GLU:HG3	2.21	0.40
2:N:44:LYS:NZ	2:N:49:PRO:O	2.47	0.40
3:O:19:LEU:HA	3:O:20:PRO:HD3	1.90	0.40
2:B:112:SER:HA	4:D:1:ILE:HD11	2.03	0.40
1:M:119:MET:HE2	1:M:391:LEU:HD23	2.03	0.40
1:M:522:ALA:HB1	1:M:532:HIS:CE1	2.56	0.40
2:N:113:LEU:HD22	2:N:175:LEU:HD22	2.03	0.40
2:N:179:TYR:C	2:N:181:GLU:N	2.74	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:O:45:GLY:HA3	3:O:59:PHE:CZ	2.57	0.40
2:B:116:ILE:CD1	2:B:172:ALA:O	2.69	0.40
2:B:242:PRO:HD2	2:B:243:ARG:HG2	2.03	0.40
3:C:128:LEU:HD22	4:D:45:PRO:HD2	2.02	0.40
1:M:328:LEU:HD22	1:M:331:ILE:HD11	1.99	0.40
1:M:192:THR:OG1	5:M:601:FAD:N7A	2.55	0.40
1:M:88:HIS:HB2	1:M:401:VAL:CG1	2.51	0.40
2:N:180:ASN:OD1	2:N:191:ARG:NH1	2.42	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	575/577 (100%)	551 (96%)	23 (4%)	1 (0%)	51	83
1	M	575/577 (100%)	546 (95%)	24 (4%)	5 (1%)	20	52
2	B	241/243 (99%)	225 (93%)	15 (6%)	1 (0%)	38	72
2	N	241/243 (99%)	227 (94%)	12 (5%)	2 (1%)	22	55
3	C	128/130 (98%)	124 (97%)	3 (2%)	1 (1%)	22	55
3	O	128/130 (98%)	118 (92%)	10 (8%)	0	100	100
4	D	117/119 (98%)	113 (97%)	4 (3%)	0	100	100
4	P	117/119 (98%)	104 (89%)	12 (10%)	1 (1%)	20	52
All	All	2122/2138 (99%)	2008 (95%)	103 (5%)	11 (0%)	32	67

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	N	65	CYS
1	M	1	GLN

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Mol	Chain	Res	Type
1	M	244	THR
4	P	46	GLY
1	M	128	ALA
3	C	18	LYS
1	M	59	HIS
2	N	101	ASP
2	B	56	SER
1	M	444	GLY
1	A	320	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	460/460 (100%)	430 (94%)	30 (6%)	20	49
1	M	460/460 (100%)	417 (91%)	43 (9%)	10	30
2	B	205/205 (100%)	193 (94%)	12 (6%)	23	54
2	N	205/205 (100%)	180 (88%)	25 (12%)	6	17
3	C	111/111 (100%)	99 (89%)	12 (11%)	7	22
3	O	111/111 (100%)	104 (94%)	7 (6%)	21	51
4	D	97/97 (100%)	87 (90%)	10 (10%)	8	24
4	P	97/97 (100%)	88 (91%)	9 (9%)	10	30
All	All	1746/1746 (100%)	1598 (92%)	148 (8%)	12	35

All (148) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	27	ASN
1	A	31	LYS
1	A	41	MET
1	A	42	ARG
1	A	59	HIS

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Mol	Chain	Res	Type
1	A	74	ASP
1	A	76	LEU
1	A	93	MET
1	A	114	ARG
1	A	116	PHE
1	A	122	GLU
1	A	129	ASP
1	A	170	LEU
1	A	175	MET
1	A	182	GLN
1	A	197	ARG
1	A	253	ILE
1	A	287	ARG
1	A	310	ASP
1	A	322	LYS
1	A	325	HIS
1	A	411	THR
1	A	413	ARG
1	A	478	LYS
1	A	490	ARG
1	A	495	SER
1	A	498	PHE
1	A	541	GLU
1	A	560	THR
2	B	4	LYS
2	B	19	THR
2	B	46	ASN
2	B	65	CYS
2	B	78	LYS
2	B	85	THR
2	B	128	ASP
2	B	154	CYS
2	B	178	ARG
2	B	206	PHE
2	B	210	CYS
2	B	237	ILE
3	C	2	THR
3	C	5	LYS
3	C	19	LEU
3	C	27	LEU
3	C	37	TRP
3	C	39	SER

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Mol	Chain	Res	Type
3	C	50	LYS
3	C	54	GLU
3	C	76	LEU
3	C	84	LYS
3	C	85	THR
3	C	92	LYS
4	D	7	ARG
4	D	9	ASP
4	D	12	VAL
4	D	17	PHE
4	D	22	MET
4	D	47	ASP
4	D	62	ILE
4	D	64	ARG
4	D	67	LEU
4	D	118	ILE
1	M	18	ARG
1	M	27	ASN
1	M	31	LYS
1	M	32	ILE
1	M	41	MET
1	M	57	GLN
1	M	63	GLU
1	M	86	VAL
1	M	93	MET
1	M	97	GLU
1	M	110	SER
1	M	143	SER
1	M	148	GLN
1	M	152	PHE
1	M	164	ASP
1	M	168	ARG
1	M	192	THR
1	M	197	ARG
1	M	224	ARG
1	M	243	MET
1	M	291	SER
1	M	299	ARG
1	M	308	ARG
1	M	310	ASP
1	M	317	ARG
1	M	318	HIS

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Mol	Chain	Res	Type
1	M	351	ARG
1	M	393	SER
1	M	394	ASN
1	M	413	ARG
1	M	421	ASN
1	M	425	ILE
1	M	475	THR
1	M	484	GLU
1	M	489	VAL
1	M	494	THR
1	M	496	SER
1	M	505	THR
1	M	506	ILE
1	M	517	CYS
1	M	537	GLU
1	M	555	ARG
1	M	572	THR
2	N	5	ASN
2	N	14	ASN
2	N	19	THR
2	N	31	ASP
2	N	65	CYS
2	N	82	ARG
2	N	100	ARG
2	N	112	SER
2	N	126	THR
2	N	128	ASP
2	N	138	GLN
2	N	150	ASN
2	N	154	CYS
2	N	178	ARG
2	N	184	ARG
2	N	185	ASP
2	N	189	LYS
2	N	206	PHE
2	N	219	ASP
2	N	226	GLN
2	N	233	LYS
2	N	235	PHE
2	N	240	LEU
2	N	241	LYS
2	N	243	ARG

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Mol	Chain	Res	Type
3	O	2	THR
3	O	12	THR
3	O	31	THR
3	O	39	SER
3	O	40	ILE
3	O	50	LYS
3	O	98	VAL
4	P	1	ILE
4	P	7	ARG
4	P	9	ASP
4	P	22	MET
4	P	37	ILE
4	P	47	ASP
4	P	60	SER
4	P	115	VAL
4	P	117	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (37) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	141	GLN
1	A	166	HIS
1	A	204	ASN
1	A	230	GLN
1	A	292	GLN
1	A	409	GLN
1	A	442	GLN
2	B	5	ASN
2	B	46	ASN
2	B	134	GLN
2	B	143	HIS
2	B	150	ASN
2	B	194	GLN
3	C	51	ASN
3	C	72	ASN
4	D	59	GLN
4	D	92	HIS
1	M	27	ASN
1	M	59	HIS
1	M	79	GLN
1	M	134	HIS
1	M	145	GLN

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Mol	Chain	Res	Type
1	M	148	GLN
1	M	166	HIS
1	M	264	GLN
1	M	442	GLN
1	M	546	ASN
1	M	550	HIS
2	N	5	ASN
2	N	14	ASN
2	N	22	HIS
2	N	71	ASN
2	N	95	ASN
2	N	123	ASN
2	N	132	ASN
2	N	160	GLN
3	O	95	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

9 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	FUM	A	577	-	1,7,7	4.04	1 (100%)	0,8,8	0.00	-
5	FAD	A	601	-	51,58,58	2.17	8 (15%)	54,89,89	2.24	17 (31%)
7	FES	B	244	2	0,4,4	0.00	-	0,4,4	0.00	-
8	F3S	B	245	2	0,9,9	0.00	-	0,15,15	0.00	-
9	SF4	B	246	-	0,12,12	0.00	-	0,24,24	0.00	-
5	FAD	M	601	-	51,58,58	2.06	9 (17%)	54,89,89	2.18	12 (22%)
7	FES	N	244	2	0,4,4	0.00	-	0,4,4	0.00	-
8	F3S	N	245	2	0,9,9	0.00	-	0,15,15	0.00	-
9	SF4	N	246	2	0,12,12	0.00	-	0,24,24	0.00	-

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
6	FUM	A	577	-	-	0/0/5/5	0/0/0/0
5	FAD	A	601	-	-	0/28/50/50	0/6/6/6
7	FES	B	244	2	-	0/0/4/4	0/1/1/1
8	F3S	B	245	2	-	0/0/24/24	0/0/3/3
9	SF4	B	246	-	-	0/0/48/48	0/6/5/5
5	FAD	M	601	-	-	0/28/50/50	0/6/6/6
7	FES	N	244	2	-	0/0/4/4	0/1/1/1
8	F3S	N	245	2	-	0/0/24/24	0/0/3/3
9	SF4	N	246	2	-	0/0/48/48	0/6/5/5

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	601	FAD	O2B-C2B	-10.28	1.19	1.43
5	M	601	FAD	O2B-C2B	-9.49	1.21	1.43
5	M	601	FAD	O4B-C1B	2.22	1.44	1.41
5	A	601	FAD	C4-N3	2.33	1.37	1.33
5	A	601	FAD	O3B-C3B	2.44	1.48	1.43
5	A	601	FAD	C2B-C3B	2.54	1.60	1.53
5	M	601	FAD	C10-N1	2.55	1.36	1.33
5	M	601	FAD	C4-N3	2.60	1.37	1.33
5	M	601	FAD	C5X-N5	3.25	1.40	1.35
5	M	601	FAD	C2B-C3B	3.44	1.62	1.53
5	A	601	FAD	C10-N1	3.60	1.38	1.33
5	A	601	FAD	C4X-N5	3.61	1.38	1.33
5	M	601	FAD	C4X-N5	3.79	1.38	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	577	FUM	C5-C4	4.04	1.52	1.31
5	M	601	FAD	C9A-N10	4.58	1.44	1.38
5	A	601	FAD	C9A-N10	4.74	1.45	1.38
5	M	601	FAD	C2B-C1B	5.17	1.61	1.53
5	A	601	FAD	C2B-C1B	6.23	1.63	1.53

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	601	FAD	N3A-C2A-N1A	-9.34	120.72	128.86
5	A	601	FAD	N3A-C2A-N1A	-7.65	122.20	128.86
5	A	601	FAD	O3'-C3'-C2'	-3.85	99.28	108.82
5	M	601	FAD	C4-C4X-C10	-3.43	117.18	119.96
5	M	601	FAD	C1B-N9A-C4A	-3.20	121.10	126.64
5	M	601	FAD	O2B-C2B-C1B	-3.14	101.79	111.61
5	A	601	FAD	O4'-C4'-C5'	-3.13	103.03	110.00
5	A	601	FAD	C4B-O4B-C1B	-3.11	106.46	109.77
5	A	601	FAD	C4X-C10-N10	-3.01	118.43	120.52
5	A	601	FAD	C1B-N9A-C4A	-2.95	121.55	126.64
5	A	601	FAD	O2'-C2'-C3'	-2.64	102.54	109.09
5	M	601	FAD	C9A-C5X-N5	-2.11	119.10	122.24
5	A	601	FAD	C9A-C5X-N5	-2.10	119.11	122.24
5	A	601	FAD	C4A-C5A-N7A	-2.01	107.47	109.41
5	A	601	FAD	O3B-C3B-C4B	2.07	117.12	111.09
5	M	601	FAD	C5X-C9A-N10	2.15	119.26	117.66
5	M	601	FAD	C1'-N10-C10	2.21	120.77	118.50
5	A	601	FAD	O4B-C4B-C3B	2.24	109.62	105.17
5	M	601	FAD	C6-C5X-N5	2.32	121.69	118.97
5	A	601	FAD	C1'-C2'-C3'	2.34	116.52	109.82
5	A	601	FAD	C6-C5X-C9A	2.49	122.23	119.00
5	M	601	FAD	O2B-C2B-C3B	2.60	120.17	111.83
5	A	601	FAD	C4-C4X-N5	2.79	121.73	118.68
5	A	601	FAD	C1'-N10-C9A	3.17	121.25	118.35
5	M	601	FAD	C4-C4X-N5	3.57	122.60	118.68
5	A	601	FAD	C4-N3-C2	5.22	119.72	115.16
5	M	601	FAD	C4X-N5-C5X	5.52	122.58	116.76
5	M	601	FAD	C4-N3-C2	5.60	120.06	115.16
5	A	601	FAD	C4X-N5-C5X	6.71	123.85	116.76

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 67 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	577	FUM	1	0
5	A	601	FAD	14	0
7	B	244	FES	3	0
8	B	245	F3S	4	0
9	B	246	SF4	12	0
5	M	601	FAD	25	0
7	N	244	FES	1	0
8	N	245	F3S	1	0
9	N	246	SF4	6	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	577/577 (100%)	0.47	1 (0%) 94 94	38, 56, 93, 138	0
1	M	577/577 (100%)	2.35	285 (49%) 0 0	68, 160, 235, 266	0
2	B	243/243 (100%)	0.71	4 (1%) 72 65	39, 71, 104, 151	0
2	N	243/243 (100%)	1.35	49 (20%) 1 1	64, 131, 202, 235	0
3	C	130/130 (100%)	0.22	0 100 100	51, 74, 110, 136	0
3	O	130/130 (100%)	0.44	5 (3%) 41 30	60, 93, 154, 215	0
4	D	119/119 (100%)	0.34	2 (1%) 70 63	55, 76, 107, 144	0
4	P	119/119 (100%)	0.46	3 (2%) 58 47	64, 86, 144, 224	0
All	All	2138/2138 (100%)	1.08	349 (16%) 2 1	38, 88, 208, 266	0

All (349) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	M	407	GLY	15.4
1	M	219	HIS	10.5
1	M	167	VAL	10.4
1	M	411	THR	10.3
1	M	386	HIS	10.1
1	M	188	VAL	9.4
1	M	17	LEU	9.4
1	M	170	LEU	9.1
1	M	125	TRP	8.8
1	M	361	ILE	8.4
1	M	396	LEU	8.3
1	M	376	ALA	7.8
1	M	165	GLY	7.6
1	M	489	VAL	7.6
4	P	0	MET	7.1
1	M	573	LEU	7.1

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Mol	Chain	Res	Type	RSRZ
1	M	385	LEU	7.0
1	M	43	SER	6.8
1	M	217	LEU	6.7
1	M	375	PHE	6.7
1	M	220	GLY	6.6
1	M	129	ASP	6.5
1	M	169	GLY	6.5
1	M	89	CYS	6.4
1	M	172	ALA	6.4
2	B	243	ARG	6.4
1	M	77	CYS	6.3
1	M	215	MET	6.2
1	M	121	ILE	5.8
1	M	101	CYS	5.8
1	M	187	ALA	5.7
1	M	356	TYR	5.7
1	M	362	GLU	5.7
1	M	8	ALA	5.6
1	M	0	MET	5.6
1	M	502	LEU	5.5
1	M	191	ALA	5.5
1	M	486	PHE	5.5
1	M	7	LEU	5.4
1	M	377	VAL	5.3
1	M	130	LYS	5.3
1	M	494	THR	5.2
1	M	189	VAL	5.2
1	M	212	GLY	5.1
1	M	429	ALA	5.1
1	M	224	ARG	5.1
4	D	118	ILE	5.0
1	M	378	GLY	4.9
2	N	198	GLN	4.9
1	M	99	TRP	4.9
1	M	160	ILE	4.9
1	M	482	LEU	4.9
1	M	373	GLY	4.9
2	N	184	ARG	4.8
1	M	223	LEU	4.8
1	M	228	PHE	4.8
1	M	48	ALA	4.8
1	M	14	GLY	4.8

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Mol	Chain	Res	Type	RSRZ
2	N	130	GLY	4.7
1	M	46	VAL	4.7
1	M	222	PRO	4.7
1	M	383	VAL	4.7
1	M	161	LEU	4.7
1	M	392	GLY	4.7
1	M	6	ASP	4.6
1	M	449	ALA	4.6
1	M	78	GLU	4.6
1	M	400	VAL	4.6
1	M	137	HIS	4.6
1	M	190	MET	4.5
1	M	545	VAL	4.5
1	M	102	PRO	4.5
2	N	63	GLY	4.5
1	M	374	LEU	4.5
1	M	182	GLN	4.5
1	M	181	VAL	4.5
1	M	425	ILE	4.4
1	M	330	PHE	4.4
1	M	571	THR	4.4
2	N	52	SER	4.4
1	M	44	HIS	4.4
2	N	142	TYR	4.4
1	M	475	THR	4.3
1	M	34	LEU	4.3
1	M	32	ILE	4.3
1	M	544	ASP	4.2
1	M	384	GLY	4.2
1	M	369	THR	4.2
1	M	495	SER	4.2
1	M	551	THR	4.2
1	M	424	ALA	4.2
1	M	553	ALA	4.1
1	M	498	PHE	4.1
1	M	210	GLY	4.1
1	M	452	ARG	4.1
1	M	422	GLU	4.1
1	M	490	ARG	4.1
1	M	380	CYS	4.1
1	M	308	ARG	4.0
1	M	394	ASN	4.0

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Mol	Chain	Res	Type	RSRZ
2	N	55	TRP	4.0
1	M	444	GLY	4.0
1	M	88	HIS	4.0
1	M	162	VAL	4.0
1	M	135	MET	4.0
1	M	456	GLY	4.0
1	M	513	ASN	4.0
1	M	198	VAL	4.0
1	M	565	TYR	4.0
1	M	24	ALA	4.0
1	M	387	GLY	3.9
1	M	345	LYS	3.9
1	M	552	LEU	3.9
2	N	146	SER	3.9
2	N	26	TYR	3.9
2	N	98	ILE	3.9
1	M	177	GLU	3.9
1	M	41	MET	3.9
1	M	402	PHE	3.8
1	M	370	ARG	3.8
1	M	463	CYS	3.8
1	M	316	LEU	3.8
1	M	183	ILE	3.8
1	M	358	MET	3.8
1	M	144	LEU	3.8
1	M	448	TRP	3.8
1	M	134	HIS	3.7
1	M	404	ARG	3.7
1	M	40	PRO	3.7
1	M	27	ASN	3.7
1	M	166	HIS	3.7
1	M	569	LYS	3.6
1	M	381	SER	3.6
1	M	122	GLU	3.6
2	N	48	ALA	3.6
1	M	141	GLN	3.6
1	M	390	ARG	3.6
2	N	25	PHE	3.6
1	M	199	TYR	3.5
1	M	549	LYS	3.5
1	M	66	PHE	3.5
1	M	473	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
1	M	139	LEU	3.5
2	N	113	LEU	3.5
1	M	15	ALA	3.4
1	M	252	GLY	3.4
1	M	405	LEU	3.4
2	N	23	SER	3.4
1	M	455	MET	3.4
1	M	3	PHE	3.4
1	M	253	ILE	3.4
1	M	250	GLU	3.4
1	M	560	THR	3.4
1	M	458	ALA	3.4
1	M	391	LEU	3.4
1	M	398	GLU	3.3
1	M	410	ALA	3.3
1	M	39	TYR	3.3
1	M	497	VAL	3.3
1	M	248	ARG	3.3
1	M	379	GLU	3.3
1	M	159	ASP	3.3
1	M	413	ARG	3.3
1	M	393	SER	3.3
1	M	207	ILE	3.3
1	M	216	ALA	3.3
1	M	49	GLU	3.2
1	M	518	MET	3.2
1	M	79	GLN	3.2
2	N	40	LEU	3.2
1	M	163	ASP	3.2
1	M	103	TRP	3.2
2	N	126	THR	3.2
1	M	80	ASP	3.2
1	M	33	ALA	3.1
1	M	359	GLY	3.1
1	M	554	PHE	3.1
1	M	328	LEU	3.1
1	M	360	GLY	3.1
1	M	168	ARG	3.1
2	N	20	ALA	3.1
2	N	102	LEU	3.1
1	M	389	ASN	3.1
1	M	504	TYR	3.1

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Mol	Chain	Res	Type	RSRZ
1	M	205	GLY	3.1
1	M	138	THR	3.0
2	N	180	ASN	3.0
1	M	206	GLY	3.0
1	M	38	VAL	3.0
2	N	43	ILE	3.0
2	N	217	HIS	3.0
1	M	460	GLU	3.0
1	M	50	GLY	3.0
1	M	51	GLY	3.0
1	M	221	VAL	3.0
1	M	31	LYS	3.0
1	M	12	ALA	3.0
1	M	85	PHE	3.0
2	N	175	LEU	3.0
1	M	9	ILE	3.0
1	M	516	GLU	3.0
1	M	209	THR	3.0
1	M	493	ASP	2.9
1	M	568	VAL	2.9
1	M	445	GLY	2.9
1	M	114	ARG	2.9
2	N	109	PHE	2.9
1	M	451	ILE	2.9
2	N	238	ALA	2.9
1	M	59	HIS	2.9
1	M	567	ASP	2.9
2	N	195	LEU	2.9
4	D	4	ASN	2.8
1	M	371	ILE	2.8
1	M	56	ALA	2.8
2	N	16	GLU	2.8
1	M	133	PHE	2.8
1	M	514	VAL	2.8
2	N	237	ILE	2.8
1	M	42	ARG	2.8
1	M	180	LEU	2.8
1	M	347	PRO	2.8
4	P	88	ASP	2.8
1	M	45	THR	2.8
1	M	2	THR	2.7
1	M	100	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	M	171	VAL	2.7
1	M	186	ASN	2.7
1	M	116	PHE	2.7
1	M	156	PHE	2.7
1	M	211	ASP	2.7
1	M	338	TYR	2.7
2	N	131	THR	2.7
1	M	287	ARG	2.7
2	N	24	ALA	2.7
1	M	213	MET	2.7
1	M	312	VAL	2.7
1	M	173	MET	2.7
1	M	208	VAL	2.7
1	M	535	LEU	2.6
2	N	123	ASN	2.6
1	M	446	GLU	2.6
3	O	96	ILE	2.6
1	M	184	ARG	2.6
1	M	409	GLN	2.6
1	M	58	ASP	2.6
1	M	570	ILE	2.6
1	A	576	ALA	2.6
1	M	98	LEU	2.6
1	M	53	ALA	2.6
1	M	447	ASN	2.6
4	P	61	PHE	2.6
1	M	87	HIS	2.6
1	M	336	LYS	2.6
2	N	46	ASN	2.6
2	N	133	ILE	2.6
1	M	350	VAL	2.6
1	M	227	GLU	2.5
2	B	113	LEU	2.5
1	M	318	HIS	2.5
1	M	118	GLY	2.5
2	N	8	ILE	2.5
1	M	555	ARG	2.5
1	M	126	PHE	2.5
2	N	119	TYR	2.5
1	M	403	GLY	2.5
1	M	339	VAL	2.5
1	M	366	ASN	2.5

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Mol	Chain	Res	Type	RSRZ
1	M	414	ALA	2.5
1	M	515	ALA	2.5
1	M	343	PRO	2.5
2	N	159	PRO	2.5
1	M	57	GLN	2.5
1	M	127	ALA	2.5
1	M	522	ALA	2.5
2	N	169	GLY	2.5
2	B	242	PRO	2.5
1	M	82	VAL	2.4
3	O	1	THR	2.4
1	M	176	MET	2.4
1	M	525	ARG	2.4
1	M	564	GLU	2.4
1	M	484	GLU	2.4
1	M	245	GLU	2.4
1	M	561	THR	2.4
1	M	26	ALA	2.3
2	N	59	MET	2.3
1	M	47	ALA	2.3
1	M	52	SER	2.3
2	N	61	ILE	2.3
1	M	372	LYS	2.3
1	M	242	LEU	2.3
1	M	505	THR	2.3
1	M	363	THR	2.3
1	M	419	ASN	2.3
1	M	295	TRP	2.3
1	M	225	ASP	2.3
1	M	280	LYS	2.3
1	M	234	THR	2.3
3	O	16	TRP	2.3
1	M	507	GLU	2.3
2	B	197	SER	2.3
2	N	56	SER	2.3
1	M	65	HIS	2.3
1	M	76	LEU	2.3
2	N	160	GLN	2.3
1	M	439	LEU	2.3
2	N	134	GLN	2.3
2	N	234	ASP	2.2
1	M	146	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	M	185	ALA	2.2
2	N	106	MET	2.2
1	M	69	THR	2.2
1	M	503	LEU	2.2
1	M	357	THR	2.2
2	N	116	ILE	2.2
1	M	158	LEU	2.2
1	M	279	ASN	2.2
2	N	51	LEU	2.2
1	M	562	ARG	2.2
2	N	103	VAL	2.2
3	O	8	VAL	2.2
1	M	550	HIS	2.1
1	M	344	VAL	2.1
1	M	157	VAL	2.1
2	N	42	TYR	2.1
1	M	284	LEU	2.1
1	M	512	LEU	2.1
1	M	548	LEU	2.1
1	M	415	ALA	2.1
1	M	131	THR	2.1
1	M	123	ARG	2.1
1	M	196	GLY	2.1
1	M	388	ALA	2.1
3	O	4	ARG	2.1
1	M	326	GLU	2.1
1	M	477	ASP	2.1
1	M	563	LEU	2.1
1	M	397	ALA	2.1
1	M	547	PHE	2.1
2	N	60	ALA	2.1
1	M	86	VAL	2.1
1	M	436	LEU	2.0
1	M	408	GLU	2.0
1	M	93	MET	2.0
1	M	193	GLY	2.0
1	M	35	ILE	2.0
2	N	168	ILE	2.0
1	M	428	GLN	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
6	FUM	A	577	8/8	0.89	0.38	2.91	66,67,70,103	0
7	FES	B	244	4/4	0.94	0.31	1.94	98,107,110,114	0
9	SF4	B	246	8/8	0.92	0.27	0.40	86,104,134,134	0
5	FAD	A	601	53/53	0.98	0.25	0.22	34,41,78,78	0
8	F3S	B	245	7/7	0.98	0.20	-0.84	60,64,70,93	0
5	FAD	M	601	53/53	0.87	0.29	-1.00	49,74,85,86	0
8	F3S	N	245	7/7	0.96	0.20	-1.15	86,90,101,134	0
9	SF4	N	246	8/8	0.97	0.19	-1.18	103,112,131,134	0
7	FES	N	244	4/4	0.96	0.22	-1.27	76,90,94,104	0

6.5 Other polymers [i](#)

There are no such residues in this entry.