



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 10:27 AM GMT

PDB ID : 3LSH  
Title : Pyranose 2-oxidase T169A, monoclinic  
Authors : Divne, C.; Tan, T.C.; Spadiut, O.  
Deposited on : 2010-02-12  
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

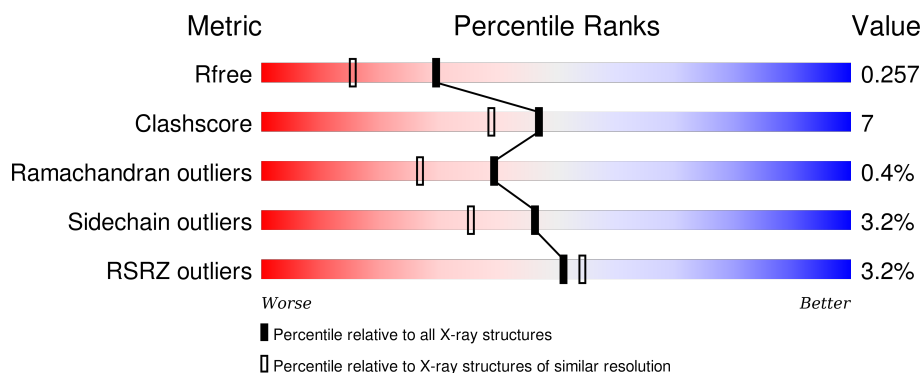
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	623	<div> <div>3%</div> <div>81% 9% • 8%</div> </div>
1	B	623	<div> <div>2%</div> <div>79% 12% • 8%</div> </div>
1	C	623	<div> <div>3%</div> <div>78% 12% • 8%</div> </div>
1	D	623	<div> <div>4%</div> <div>77% 14% • 8%</div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 20177 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 Pyranose 2-oxidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	576	Total	C	N	O	S	0	0	0
			4540	2867	777	871	25			
1	B	576	Total	C	N	O	S	0	0	0
			4540	2867	777	871	25			
1	C	575	Total	C	N	O	S	0	0	0
			4531	2862	776	869	24			
1	D	574	Total	C	N	O	S	0	0	0
			4524	2858	775	867	24			

There are 4 discrepancies between the modelled and reference sequences:

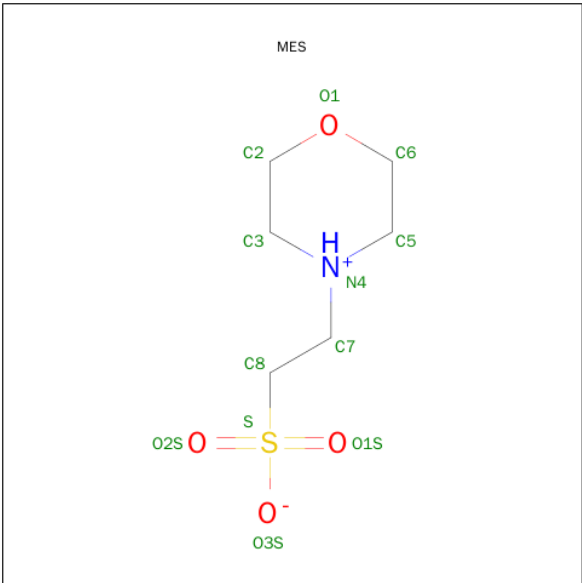
Chain	Residue	Modelled	Actual	Comment	Reference
A	169	ALA	THR	ENGINEERED	UNP Q7ZA32
B	169	ALA	THR	ENGINEERED	UNP Q7ZA32
C	169	ALA	THR	ENGINEERED	UNP Q7ZA32
D	169	ALA	THR	ENGINEERED	UNP Q7ZA32

- Molecule 2 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



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

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C<sub>6</sub>H<sub>13</sub>NO<sub>4</sub>S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	C	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

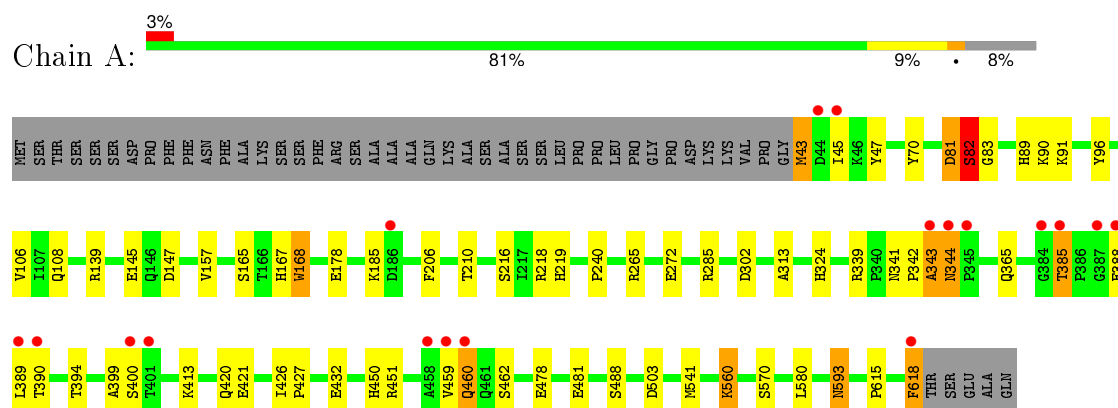
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	450	Total	O	0	0
			450	450		
4	B	554	Total	O	0	0
			554	554		
4	C	472	Total	O	0	0
			472	472		
4	D	342	Total	O	0	0
			342	342		

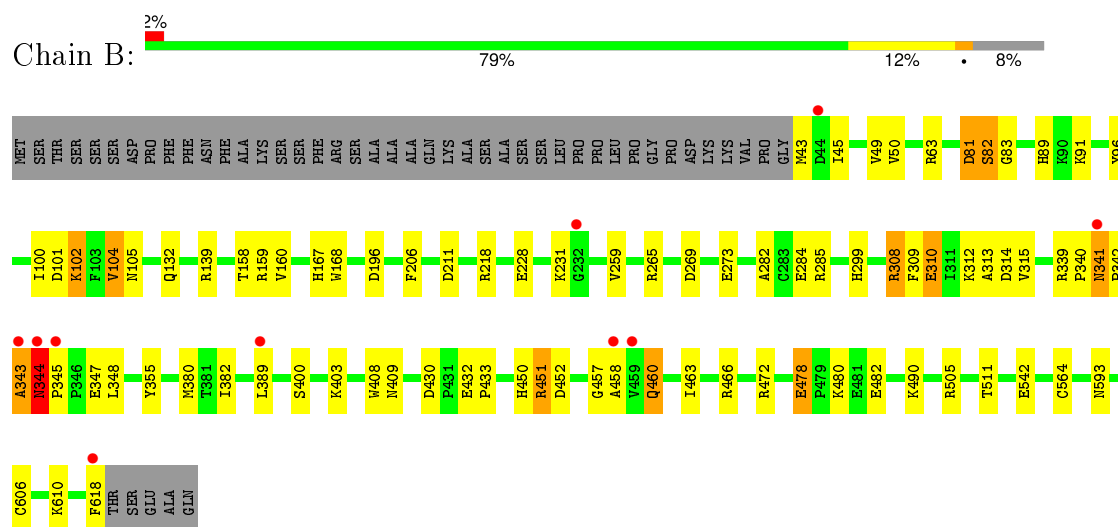
### 3 Residue-property plots [i](#)

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.

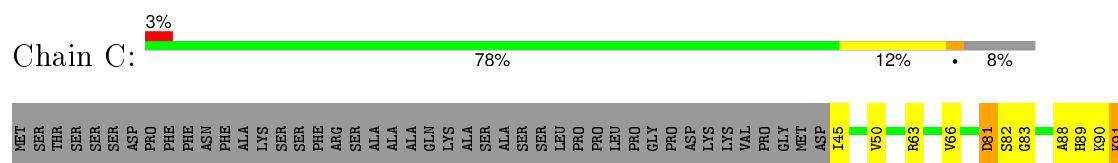
#### • Molecule 1: Pyranose 2-oxidase

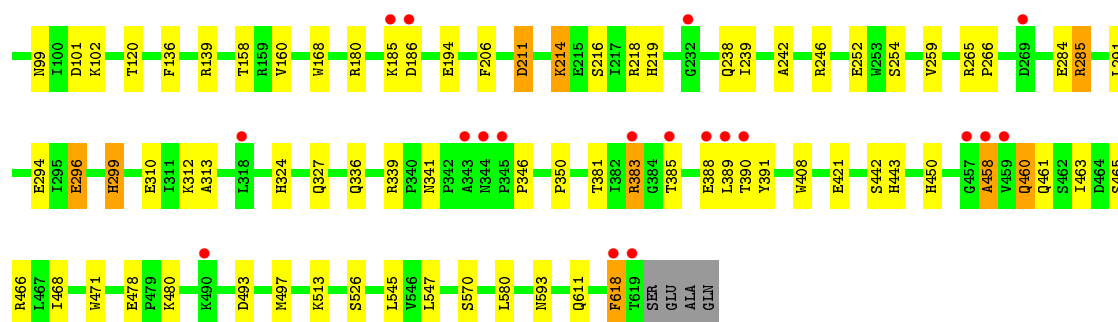


#### • Molecule 1: Pyranose 2-oxidase

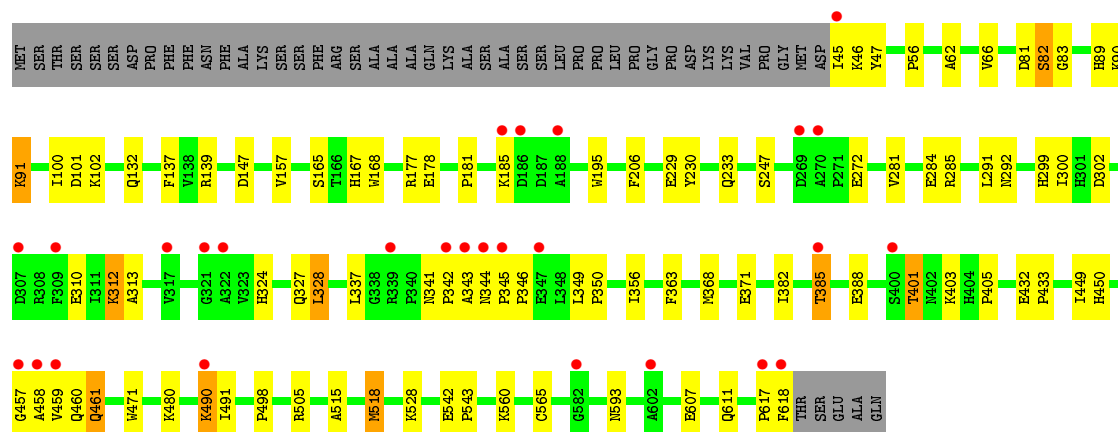
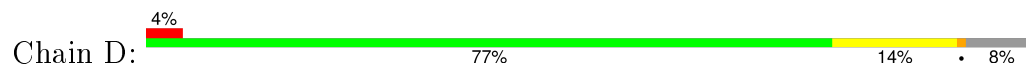


#### • Molecule 1: Pyranose 2-oxidase





• Molecule 1: Pyranose 2-oxidase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	100.40Å 102.73Å 137.82Å 90.00° 91.02° 90.00°	Depositor
Resolution (Å)	28.50 – 1.90 28.46 – 1.90	Depositor EDS
% Data completeness (in resolution range)	98.8 (28.50-1.90) 98.8 (28.46-1.90)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.35 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, $R_{free}$	0.195 , 0.246 0.212 , 0.257	Depositor DCC
$R_{free}$ test set	3217 reflections (1.50%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.2	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 45.2	EDS
Estimated twinning fraction	0.011 for -k,-h,-l 0.008 for k,h,-l 0.015 for h,-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 217369 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	20177	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.36% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup> Intensities estimated from amplitudes.

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



## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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

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	1.07	5/4656 (0.1%)	0.98	12/6330 (0.2%)
1	B	1.15	12/4656 (0.3%)	1.02	15/6330 (0.2%)
1	C	1.03	5/4647 (0.1%)	0.94	9/6319 (0.1%)
1	D	0.92	1/4640 (0.0%)	0.90	6/6309 (0.1%)
All	All	1.05	23/18599 (0.1%)	0.96	42/25288 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	C	0	1
1	D	0	1
All	All	0	3

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	296	GLU	CG-CD	9.41	1.66	1.51
1	B	310	GLU	CG-CD	7.83	1.63	1.51
1	B	564	CYS	CB-SG	-6.71	1.70	1.82
1	B	478	GLU	CD-OE1	6.53	1.32	1.25
1	A	421	GLU	CB-CG	5.85	1.63	1.52
1	B	104	VAL	CB-CG1	-5.83	1.40	1.52
1	C	478	GLU	CD-OE2	5.71	1.31	1.25
1	A	106	VAL	CB-CG1	-5.60	1.41	1.52
1	D	371	GLU	CB-CG	-5.56	1.41	1.52
1	B	309	PHE	CE2-CZ	5.51	1.47	1.37
1	B	96	TYR	CG-CD1	-5.49	1.32	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	282	ALA	CA-CB	-5.46	1.41	1.52
1	B	482	GLU	CG-CD	5.43	1.60	1.51
1	B	82	SER	N-CA	5.39	1.57	1.46
1	A	96	TYR	CD1-CE1	-5.38	1.31	1.39
1	B	284	GLU	CD-OE1	-5.36	1.19	1.25
1	C	66	VAL	CB-CG2	-5.25	1.41	1.52
1	C	88	ALA	CA-CB	5.22	1.63	1.52
1	B	273	GLU	CD-OE1	5.16	1.31	1.25
1	A	478	GLU	CG-CD	5.13	1.59	1.51
1	A	478	GLU	CD-OE2	5.13	1.31	1.25
1	B	542	GLU	CD-OE1	5.11	1.31	1.25
1	C	296	GLU	CB-CG	5.01	1.61	1.52

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	139	ARG	NE-CZ-NH2	-9.30	115.65	120.30
1	B	81	ASP	CB-CG-OD1	-9.24	109.99	118.30
1	C	139	ARG	NE-CZ-NH2	-8.73	115.93	120.30
1	B	211	ASP	CB-CG-OD1	8.18	125.67	118.30
1	C	139	ARG	NE-CZ-NH1	8.12	124.36	120.30
1	B	265	ARG	NE-CZ-NH1	7.43	124.01	120.30
1	D	368	MET	CG-SD-CE	7.30	111.89	100.20
1	A	147	ASP	CB-CG-OD1	7.02	124.62	118.30
1	B	211	ASP	CB-CG-OD2	-6.91	112.08	118.30
1	B	308	ARG	NE-CZ-NH1	-6.90	116.85	120.30
1	D	518	MET	CG-SD-CE	6.84	111.15	100.20
1	C	493	ASP	CB-CG-OD1	6.80	124.42	118.30
1	A	82	SER	CB-CA-C	-6.74	97.29	110.10
1	B	81	ASP	CB-CA-C	6.70	123.80	110.40
1	D	147	ASP	CB-CG-OD1	6.40	124.06	118.30
1	A	451	ARG	NE-CZ-NH2	-6.35	117.12	120.30
1	B	505	ARG	NE-CZ-NH1	6.35	123.47	120.30
1	B	472	ARG	NE-CZ-NH2	-6.32	117.14	120.30
1	A	503	ASP	CB-CG-OD1	6.17	123.85	118.30
1	B	451	ARG	NE-CZ-NH1	6.05	123.32	120.30
1	C	180	ARG	NE-CZ-NH1	-6.03	117.28	120.30
1	B	466	ARG	NE-CZ-NH1	5.91	123.26	120.30
1	B	196	ASP	CB-CG-OD1	5.85	123.56	118.30
1	A	302	ASP	CB-CG-OD1	5.79	123.51	118.30
1	C	211	ASP	CB-CG-OD1	5.74	123.47	118.30
1	A	82	SER	N-CA-C	5.67	126.31	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	472	ARG	NE-CZ-NH1	5.61	123.11	120.30
1	D	147	ASP	CB-CG-OD2	-5.59	113.27	118.30
1	D	82	SER	CB-CA-C	-5.56	99.53	110.10
1	B	82	SER	N-CA-C	5.55	125.98	111.00
1	A	139	ARG	NE-CZ-NH2	-5.49	117.56	120.30
1	A	339	ARG	NE-CZ-NH2	5.48	123.04	120.30
1	A	265	ARG	NE-CZ-NH2	-5.41	117.60	120.30
1	C	466	ARG	NE-CZ-NH1	5.38	122.99	120.30
1	C	81	ASP	CB-CG-OD1	-5.33	113.50	118.30
1	A	81	ASP	CB-CG-OD1	-5.32	113.51	118.30
1	C	296	GLU	OE1-CD-OE2	-5.30	116.94	123.30
1	D	505	ARG	NE-CZ-NH1	-5.29	117.65	120.30
1	B	43	MET	CG-SD-CE	5.27	108.63	100.20
1	C	339	ARG	NE-CZ-NH1	-5.25	117.67	120.30
1	A	82	SER	CA-C-N	5.19	126.57	116.20
1	A	81	ASP	CB-CA-C	5.15	120.69	110.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	460	GLN	Peptide
1	C	458	ALA	Peptide
1	D	458	ALA	Peptide

## 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	4540	0	4386	66	0
1	B	4540	0	4386	57	0
1	C	4531	0	4380	68	0
1	D	4524	0	4373	79	0
2	A	53	0	30	2	0
2	B	53	0	29	2	0
2	C	53	0	29	2	0
2	D	53	0	28	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	12	0	12	1	0
4	A	450	0	0	15	0
4	B	554	0	0	12	0
4	C	472	0	0	18	0
4	D	342	0	0	14	0
All	All	20177	0	17653	269	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 7.

All (269) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:383:ARG:HB3	1:C:383:ARG:NH1	1.29	1.41
1:C:383:ARG:CB	1:C:383:ARG:HH11	1.45	1.28
1:C:285:ARG:HD3	4:C:2746:HOH:O	1.30	1.23
1:B:458:ALA:HB2	4:B:2756:HOH:O	1.33	1.22
1:C:383:ARG:CB	1:C:383:ARG:NH1	2.03	1.16
1:C:299:HIS:CE1	1:C:310:GLU:HG2	1.84	1.13
1:B:460:GLN:HB3	4:B:2630:HOH:O	1.54	1.07
1:D:299:HIS:NE2	1:D:310:GLU:CG	2.21	1.03
1:D:285:ARG:HA	1:D:328:LEU:CD1	1.88	1.03
1:B:343:ALA:O	1:B:344:ASN:ND2	1.91	1.02
1:B:101:ASP:O	1:B:104:VAL:HG12	1.60	0.97
1:D:299:HIS:CD2	1:D:310:GLU:CG	2.52	0.93
1:D:299:HIS:CD2	1:D:310:GLU:HG2	2.04	0.93
1:D:299:HIS:NE2	1:D:310:GLU:HG3	1.88	0.89
1:A:560:LYS:NZ	1:A:560:LYS:HB3	1.89	0.87
1:B:308:ARG:HH11	1:B:308:ARG:HG3	1.38	0.87
1:D:457:GLY:HA2	4:D:2302:HOH:O	1.78	0.84
1:C:285:ARG:HH12	1:C:299:HIS:HD2	1.21	0.84
1:D:285:ARG:HA	1:D:328:LEU:HD11	1.59	0.82
1:A:459:VAL:HG12	1:A:460:GLN:N	1.94	0.82
1:B:132:GLN:HG2	4:B:2633:HOH:O	1.78	0.82
1:C:211:ASP:O	1:C:214:LYS:HD3	1.80	0.82
1:D:299:HIS:CD2	1:D:310:GLU:HG3	2.15	0.81
1:D:299:HIS:HE2	1:D:310:GLU:CD	1.85	0.80
1:D:299:HIS:HE2	1:D:310:GLU:CG	1.92	0.79
1:A:459:VAL:O	1:A:460:GLN:HG2	1.82	0.79
1:C:385:THR:HG23	1:C:388:GLU:OE2	1.82	0.78
1:B:308:ARG:HG3	1:B:308:ARG:NH1	2.00	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:459:VAL:CG1	1:A:460:GLN:N	2.48	0.76
1:C:285:ARG:HH12	1:C:299:HIS:CD2	2.03	0.76
1:D:461:GLN:HG3	4:D:2627:HOH:O	1.87	0.74
1:C:299:HIS:HE1	1:C:310:GLU:HG2	1.53	0.73
1:C:443:HIS:HB3	4:C:2237:HOH:O	1.89	0.73
1:A:344:ASN:C	1:A:344:ASN:HD22	1.92	0.72
1:C:299:HIS:CE1	1:C:310:GLU:CG	2.70	0.71
1:A:560:LYS:NZ	1:A:560:LYS:CB	2.52	0.71
1:D:490:LYS:HE3	1:D:491:ILE:CD1	2.21	0.71
1:A:365:GLN:HE22	1:A:459:VAL:CG2	2.03	0.70
1:B:342:PRO:O	1:B:344:ASN:N	2.21	0.70
1:D:457:GLY:CA	4:D:2302:HOH:O	2.35	0.70
1:D:490:LYS:HE3	1:D:491:ILE:HD13	1.75	0.69
1:A:459:VAL:CG1	1:A:460:GLN:H	2.05	0.69
1:A:481:GLU:HG2	4:A:2559:HOH:O	1.92	0.68
1:C:460:GLN:O	1:C:460:GLN:HG3	1.93	0.68
1:A:560:LYS:HZ2	1:A:560:LYS:HB3	1.57	0.68
1:C:285:ARG:NH1	1:C:299:HIS:HD2	1.91	0.67
1:D:285:ARG:NE	4:D:2772:HOH:O	2.25	0.67
1:D:81:ASP:OD2	1:D:90:LYS:NZ	2.24	0.67
1:B:132:GLN:CG	4:B:2633:HOH:O	2.40	0.67
1:C:185:LYS:NZ	4:C:2610:HOH:O	2.27	0.67
1:A:45:ILE:HD12	1:A:45:ILE:N	2.10	0.66
1:B:310:GLU:OE1	1:B:312:LYS:NZ	2.28	0.66
1:A:157:VAL:HG21	1:A:324:HIS:HE1	1.61	0.66
1:C:299:HIS:CG	4:C:2768:HOH:O	2.47	0.65
1:B:341:ASN:HD22	1:B:341:ASN:C	2.00	0.65
1:B:452:ASP:HA	4:B:2765:HOH:O	1.97	0.65
1:A:618:PHE:HD1	1:A:618:PHE:C	2.00	0.65
1:A:167:HIS:CD2	2:A:801:FAD:HM82	2.31	0.65
1:A:560:LYS:HB3	1:A:560:LYS:HZ3	1.61	0.65
1:A:343:ALA:C	4:A:2620:HOH:O	2.36	0.64
1:D:349:LEU:HD22	1:D:565:CYS:HA	1.80	0.64
1:A:541:MET:HE1	4:A:2585:HOH:O	1.98	0.64
1:A:481:GLU:CG	4:A:2559:HOH:O	2.44	0.63
1:C:383:ARG:CB	1:C:383:ARG:CZ	2.73	0.63
1:C:383:ARG:HB2	1:C:383:ARG:NH1	2.07	0.63
1:A:344:ASN:C	1:A:344:ASN:ND2	2.53	0.62
1:B:460:GLN:OE1	1:B:463:ILE:N	2.23	0.62
1:A:185:LYS:HD2	4:A:2187:HOH:O	1.99	0.62
1:B:308:ARG:NH1	4:B:2448:HOH:O	2.33	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:81:ASP:O	1:D:83:GLY:N	2.32	0.61
1:C:383:ARG:O	1:C:391:TYR:HA	2.01	0.61
1:B:389:LEU:HG	4:B:2647:HOH:O	2.00	0.61
1:A:618:PHE:CD1	1:A:618:PHE:C	2.73	0.60
1:B:457:GLY:HA2	4:B:2433:HOH:O	2.01	0.60
1:D:299:HIS:NE2	1:D:310:GLU:HG2	2.07	0.60
1:D:449:ILE:HG12	1:D:471:TRP:CZ3	2.37	0.60
1:C:285:ARG:NH1	1:C:299:HIS:CD2	2.67	0.59
1:D:432:GLU:CB	1:D:433:PRO:HD2	2.33	0.59
1:A:394:THR:HA	1:A:413:LYS:HD2	1.85	0.58
1:B:478:GLU:HG3	1:B:511:THR:OG1	2.03	0.58
1:D:382:ILE:CD1	4:D:2488:HOH:O	2.51	0.58
1:C:461:GLN:HE21	1:C:461:GLN:HA	1.68	0.58
1:A:342:PRO:C	1:A:344:ASN:H	2.07	0.58
1:B:101:ASP:O	1:B:104:VAL:CG1	2.44	0.57
1:D:432:GLU:HB2	1:D:433:PRO:HD2	1.86	0.57
1:D:291:LEU:O	1:D:292:ASN:HB2	2.04	0.57
1:A:432:GLU:H	1:A:432:GLU:CD	2.06	0.57
1:B:81:ASP:N	1:B:81:ASP:OD1	2.34	0.57
1:B:308:ARG:NH1	1:B:308:ARG:CG	2.65	0.56
1:C:299:HIS:ND1	1:C:310:GLU:HG2	2.18	0.56
1:D:132:GLN:CG	4:D:2213:HOH:O	2.53	0.56
1:D:363:PHE:HA	1:D:471:TRP:O	2.06	0.56
1:A:70:TYR:CZ	1:A:615:PRO:HD3	2.41	0.56
1:A:89:HIS:CE1	1:A:91:LYS:HB2	2.40	0.55
1:A:218:ARG:HD2	4:A:1614:HOH:O	2.05	0.55
1:A:45:ILE:O	1:A:45:ILE:HG22	2.05	0.55
1:A:459:VAL:C	1:A:460:GLN:CG	2.75	0.55
1:C:442:SER:C	4:C:2237:HOH:O	2.45	0.55
1:B:308:ARG:HH11	1:B:308:ARG:CG	2.06	0.54
1:C:246:ARG:NH2	1:C:252:GLU:OE1	2.31	0.54
1:C:547:LEU:CD1	2:C:801:FAD:HM83	2.37	0.54
1:D:284:GLU:O	1:D:285:ARG:HB3	2.08	0.54
1:A:216:SER:HB3	1:A:219:HIS:HB3	1.88	0.54
1:A:341:ASN:HD21	1:A:343:ALA:HB3	1.73	0.54
1:A:178:GLU:O	1:A:178:GLU:HG3	2.07	0.54
1:B:89:HIS:CE1	1:B:91:LYS:HE3	2.43	0.54
1:C:296:GLU:OE1	1:C:312:LYS:NZ	2.41	0.54
1:C:383:ARG:HB3	1:C:383:ARG:HH11	0.53	0.53
1:A:481:GLU:CD	4:A:2559:HOH:O	2.47	0.53
1:C:421:GLU:OE1	1:C:421:GLU:N	2.37	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:294:GLU:HB2	4:C:2800:HOH:O	2.08	0.53
1:C:216:SER:HB3	1:C:219:HIS:HB3	1.90	0.53
1:A:185:LYS:CE	4:A:2160:HOH:O	2.55	0.53
1:D:480:LYS:HD2	4:D:2568:HOH:O	2.07	0.53
1:D:346:PRO:HG2	1:D:350:PRO:HA	1.89	0.53
1:B:91:LYS:HD3	1:B:100:ILE:HD11	1.91	0.53
1:A:81:ASP:OD2	1:A:90:LYS:NZ	2.42	0.52
1:A:45:ILE:H	1:A:45:ILE:HD12	1.74	0.52
1:C:460:GLN:OE1	1:C:463:ILE:N	2.28	0.52
1:A:185:LYS:CD	4:A:2187:HOH:O	2.56	0.52
1:D:285:ARG:HA	1:D:328:LEU:HD12	1.85	0.51
1:D:56:PRO:HG3	1:D:165:SER:HB3	1.92	0.51
1:A:459:VAL:O	1:A:460:GLN:CG	2.57	0.51
1:D:607:GLU:O	1:D:611:GLN:HG3	2.10	0.51
1:D:47:TYR:O	1:D:313:ALA:HA	2.11	0.51
1:B:342:PRO:C	1:B:344:ASN:H	2.11	0.51
1:D:167:HIS:CD2	2:D:801:FAD:HM82	2.44	0.51
1:D:449:ILE:HG12	1:D:471:TRP:CE3	2.46	0.51
1:D:167:HIS:HD2	2:D:801:FAD:HM82	1.74	0.51
1:D:490:LYS:HE3	1:D:491:ILE:HD11	1.92	0.51
1:A:82:SER:HB2	4:A:2548:HOH:O	2.11	0.51
1:D:137:PHE:CE2	1:D:139:ARG:HG3	2.46	0.51
1:D:89:HIS:CE1	1:D:91:LYS:HB2	2.47	0.51
1:A:342:PRO:C	1:A:344:ASN:N	2.65	0.50
1:D:302:ASP:C	1:D:302:ASP:OD1	2.49	0.50
1:C:458:ALA:HB3	4:C:2203:HOH:O	2.11	0.50
1:C:265:ARG:HB3	1:C:266:PRO:HA	1.93	0.50
1:A:81:ASP:O	1:A:83:GLY:N	2.43	0.50
1:A:385:THR:HG23	1:A:388:GLU:HB3	1.92	0.50
1:B:347:GLU:HB3	1:B:348:LEU:HG	1.93	0.50
1:D:401:THR:O	1:D:401:THR:HG23	2.10	0.49
1:A:365:GLN:HE22	1:A:459:VAL:HG22	1.75	0.49
1:D:81:ASP:N	1:D:81:ASP:OD1	2.43	0.49
1:B:343:ALA:C	1:B:344:ASN:HD22	2.16	0.49
1:C:385:THR:CG2	1:C:388:GLU:OE2	2.55	0.49
1:B:339:ARG:O	1:B:340:PRO:C	2.50	0.49
1:D:230:TYR:CZ	1:D:528:LYS:HE3	2.48	0.48
1:C:513:LYS:NZ	4:C:2361:HOH:O	2.45	0.48
1:B:432:GLU:HB2	1:B:433:PRO:HD2	1.96	0.48
1:B:89:HIS:CE1	1:B:91:LYS:HB3	2.48	0.48
1:A:459:VAL:HG13	1:A:460:GLN:H	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:291:LEU:HA	4:C:2749:HOH:O	2.14	0.48
1:D:132:GLN:HG2	4:D:2213:HOH:O	2.14	0.48
1:C:443:HIS:CB	4:C:2237:HOH:O	2.56	0.47
1:C:50:VAL:HG13	1:C:313:ALA:HB2	1.96	0.47
1:C:284:GLU:C	1:C:285:ARG:HG2	2.33	0.47
1:B:380:MET:HE1	1:B:409:ASN:HB3	1.96	0.47
1:B:460:GLN:CB	4:B:2630:HOH:O	2.34	0.47
1:A:89:HIS:ND1	1:A:91:LYS:HB2	2.30	0.47
1:B:355:TYR:HA	1:B:480:LYS:O	2.15	0.47
1:D:157:VAL:HG21	1:D:324:HIS:HE1	1.80	0.47
1:B:50:VAL:HG13	1:B:313:ALA:HB2	1.97	0.47
1:B:606:CYS:O	1:B:610:LYS:HG3	2.15	0.47
1:D:324:HIS:HD2	1:D:327:GLN:OE1	1.98	0.46
1:D:233:GLN:CD	4:D:2754:HOH:O	2.53	0.46
1:C:471:TRP:CH2	1:C:526:SER:HA	2.50	0.46
1:A:570:SER:HB3	1:A:580:LEU:O	2.15	0.46
1:B:63:ARG:HD2	1:B:259:VAL:O	2.16	0.46
1:D:337:LEU:HD21	4:D:2566:HOH:O	2.15	0.46
1:B:158:THR:HG22	1:B:160:VAL:HG22	1.97	0.46
1:C:390:THR:HB	4:C:2802:HOH:O	2.15	0.46
1:C:89:HIS:CE1	1:C:91:LYS:HE2	2.51	0.46
3:C:903:MES:H82	3:C:903:MES:H51	1.63	0.46
1:D:299:HIS:NE2	1:D:310:GLU:CD	2.55	0.45
1:D:341:ASN:HD22	1:D:342:PRO:HD2	1.80	0.45
1:B:343:ALA:O	1:B:344:ASN:CG	2.49	0.45
1:D:432:GLU:CB	1:D:433:PRO:CD	2.94	0.45
1:D:177:ARG:HG3	4:D:2751:HOH:O	2.15	0.45
1:B:89:HIS:ND1	1:B:91:LYS:HB3	2.32	0.45
1:D:617:PRO:O	1:D:618:PHE:C	2.55	0.45
1:B:104:VAL:HG13	1:B:105:ASN:N	2.31	0.45
1:C:120:THR:HA	1:C:136:PHE:CD1	2.51	0.45
1:B:167:HIS:CD2	2:B:801:FAD:HM82	2.51	0.45
1:A:108:GLN:HG2	4:A:2267:HOH:O	2.16	0.45
1:C:465:SER:HA	1:C:468:ILE:HD12	1.98	0.45
1:D:405:PRO:HG3	4:D:2742:HOH:O	2.16	0.45
1:A:388:GLU:O	1:A:390:THR:N	2.50	0.45
1:B:432:GLU:HB2	1:B:451:ARG:HB2	1.99	0.45
1:D:328:LEU:O	1:D:328:LEU:HD12	2.17	0.45
1:A:593:ASN:HB3	2:A:801:FAD:C2	2.48	0.44
1:B:478:GLU:HG3	1:B:511:THR:HG1	1.81	0.44
1:A:47:TYR:O	1:A:313:ALA:HA	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:324:HIS:HD2	1:C:327:GLN:OE1	2.00	0.44
1:C:346:PRO:HG2	1:C:350:PRO:HA	1.99	0.44
1:D:285:ARG:CA	1:D:328:LEU:HD11	2.39	0.44
1:A:459:VAL:C	1:A:460:GLN:HG2	2.38	0.44
1:B:218:ARG:HG3	1:B:430:ASP:OD2	2.17	0.44
1:A:83:GLY:N	1:B:81:ASP:O	2.51	0.43
1:D:515:ALA:O	1:D:518:MET:HB3	2.17	0.43
1:C:99:ASN:HB3	1:C:102:LYS:HG2	2.00	0.43
1:C:81:ASP:O	1:D:81:ASP:O	2.37	0.43
1:A:185:LYS:HE2	4:A:2160:HOH:O	2.15	0.43
1:D:344:ASN:O	1:D:345:PRO:C	2.54	0.43
1:C:381:THR:HG23	4:C:2341:HOH:O	2.18	0.43
1:D:542:GLU:HA	1:D:543:PRO:HD3	1.89	0.43
1:C:158:THR:HG22	1:C:160:VAL:HG22	2.00	0.43
1:A:432:GLU:CD	1:A:432:GLU:N	2.72	0.43
1:B:285:ARG:NH1	1:B:299:HIS:ND1	2.67	0.43
1:C:618:PHE:C	1:C:618:PHE:CD1	2.92	0.43
1:C:81:ASP:OD2	1:C:90:LYS:NZ	2.51	0.43
1:B:102:LYS:HD2	1:B:102:LYS:HA	1.78	0.43
1:C:497:MET:HG3	4:C:2391:HOH:O	2.17	0.43
1:C:461:GLN:NE2	1:C:461:GLN:HA	2.34	0.43
1:B:81:ASP:O	1:B:83:GLY:N	2.49	0.43
1:C:480:LYS:HA	1:C:480:LYS:HD3	1.74	0.43
1:D:299:HIS:HD2	1:D:310:GLU:HG2	1.76	0.42
1:C:238:GLN:HG2	1:C:239:ILE:N	2.34	0.42
1:D:101:ASP:HB3	1:D:459:VAL:HG12	2.01	0.42
1:A:145:GLU:HG3	1:A:488:SER:HB2	2.00	0.42
1:D:498:PRO:HA	4:D:2161:HOH:O	2.18	0.42
1:B:159:ARG:HA	2:B:801:FAD:O2B	2.19	0.42
1:C:81:ASP:OD1	1:C:81:ASP:N	2.52	0.42
1:D:385:THR:OG1	1:D:388:GLU:CD	2.58	0.42
1:D:229:GLU:OE2	4:D:2649:HOH:O	2.20	0.42
1:D:56:PRO:HD2	2:D:801:FAD:O1P	2.19	0.42
1:D:100:ILE:HA	1:D:100:ILE:HD12	1.92	0.42
1:D:272:GLU:OE2	1:D:272:GLU:HA	2.20	0.42
1:D:46:LYS:HD2	1:D:312:LYS:HD2	2.01	0.42
1:D:281:VAL:HG11	1:D:300:ILE:HD12	2.02	0.42
1:A:344:ASN:ND2	1:A:344:ASN:O	2.53	0.42
1:B:341:ASN:ND2	1:B:341:ASN:C	2.70	0.42
1:B:380:MET:HE1	1:B:409:ASN:CB	2.49	0.42
1:D:356:ILE:HD13	1:D:356:ILE:HG21	1.73	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:62:ALA:O	1:D:66:VAL:HB	2.20	0.42
1:C:194:GLU:OE1	4:C:2154:HOH:O	2.21	0.42
1:A:91:LYS:NZ	4:A:1656:HOH:O	2.53	0.41
1:C:547:LEU:HD12	2:C:801:FAD:HM83	2.02	0.41
1:B:460:GLN:CG	4:B:2630:HOH:O	2.66	0.41
1:A:45:ILE:CD1	1:A:45:ILE:N	2.80	0.41
2:D:801:FAD:H9	2:D:801:FAD:H1'1	1.82	0.41
1:D:102:LYS:HA	1:D:102:LYS:HD2	1.82	0.41
1:B:314:ASP:OD1	4:B:2780:HOH:O	2.21	0.41
1:A:43:MET:HA	4:A:2377:HOH:O	2.19	0.41
1:B:344:ASN:N	1:B:345:PRO:CD	2.83	0.41
1:A:210:THR:HG22	1:A:240:PRO:HA	2.02	0.41
1:D:285:ARG:CA	1:D:328:LEU:CD1	2.79	0.41
1:A:81:ASP:N	1:A:81:ASP:OD1	2.53	0.41
1:A:342:PRO:O	1:A:344:ASN:N	2.53	0.41
1:D:89:HIS:CE1	1:D:91:LYS:HD3	2.55	0.41
1:B:91:LYS:NZ	1:B:452:ASP:OD1	2.52	0.41
1:A:420:GLN:HG3	4:A:2157:HOH:O	2.20	0.41
1:A:426:ILE:HA	1:A:427:PRO:HD3	1.93	0.41
1:C:83:GLY:N	1:D:81:ASP:O	2.53	0.41
1:D:341:ASN:ND2	1:D:341:ASN:C	2.73	0.41
1:C:218:ARG:HD2	4:C:1448:HOH:O	2.21	0.41
1:C:242:ALA:HB1	1:C:254:SER:HB2	2.02	0.41
1:B:382:ILE:HD13	4:B:1452:HOH:O	2.21	0.41
1:B:228:GLU:HA	1:B:228:GLU:OE1	2.21	0.41
1:A:399:ALA:O	1:A:400:SER:C	2.58	0.41
1:C:381:THR:HA	4:C:2341:HOH:O	2.21	0.40
1:A:165:SER:HA	1:A:168:TRP:CD1	2.56	0.40
1:C:299:HIS:CB	4:C:2768:HOH:O	2.69	0.40
1:C:618:PHE:C	1:C:618:PHE:HD1	2.25	0.40
1:C:570:SER:HB3	1:C:580:LEU:O	2.20	0.40
1:B:49:VAL:HG22	1:B:315:VAL:HB	2.03	0.40
1:D:432:GLU:HB2	1:D:433:PRO:CD	2.51	0.40
1:D:181:PRO:HG2	1:D:195:TRP:HZ2	1.86	0.40
1:C:63:ARG:HD2	1:C:259:VAL:O	2.21	0.40
1:C:299:HIS:CD2	4:C:2768:HOH:O	2.70	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	574/623 (92%)	549 (96%)	22 (4%)	3 (0%)	34	21
1	B	574/623 (92%)	555 (97%)	16 (3%)	3 (0%)	34	21
1	C	573/623 (92%)	554 (97%)	17 (3%)	2 (0%)	46	35
1	D	572/623 (92%)	548 (96%)	22 (4%)	2 (0%)	46	35
All	All	2293/2492 (92%)	2206 (96%)	77 (3%)	10 (0%)	39	27

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	SER
1	A	389	LEU
1	B	82	SER
1	C	186	ASP
1	D	82	SER
1	B	343	ALA
1	A	343	ALA
1	C	82	SER
1	B	344	ASN
1	D	343	ALA

### 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	503/541 (93%)	491 (98%)	12 (2%)	57	49

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	503/541 (93%)	487 (97%)	16 (3%)	46	35
1	C	502/541 (93%)	483 (96%)	19 (4%)	40	28
1	D	501/541 (93%)	483 (96%)	18 (4%)	42	30
All	All	2009/2164 (93%)	1944 (97%)	65 (3%)	46	35

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	MET
1	A	168	TRP
1	A	206	PHE
1	A	272	GLU
1	A	285	ARG
1	A	344	ASN
1	A	385	THR
1	A	450	HIS
1	A	462	SER
1	A	560	LYS
1	A	593	ASN
1	A	618	PHE
1	B	45	ILE
1	B	102	LYS
1	B	168	TRP
1	B	206	PHE
1	B	231	LYS
1	B	269	ASP
1	B	341	ASN
1	B	344	ASN
1	B	400	SER
1	B	403	LYS
1	B	408	TRP
1	B	450	HIS
1	B	460	GLN
1	B	490	LYS
1	B	593	ASN
1	B	618	PHE
1	C	45	ILE
1	C	91	LYS
1	C	101	ASP
1	C	168	TRP
1	C	206	PHE

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Mol	Chain	Res	Type
1	C	214	LYS
1	C	285	ARG
1	C	299	HIS
1	C	336	GLN
1	C	341	ASN
1	C	383	ARG
1	C	389	LEU
1	C	408	TRP
1	C	450	HIS
1	C	460	GLN
1	C	545	LEU
1	C	593	ASN
1	C	611	GLN
1	C	618	PHE
1	D	45	ILE
1	D	91	LYS
1	D	168	TRP
1	D	178	GLU
1	D	185	LYS
1	D	206	PHE
1	D	247	SER
1	D	312	LYS
1	D	328	LEU
1	D	385	THR
1	D	401	THR
1	D	403	LYS
1	D	450	HIS
1	D	460	GLN
1	D	461	GLN
1	D	490	LYS
1	D	560	LYS
1	D	593	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	132	GLN
1	A	167	HIS
1	A	263	GLN
1	A	324	HIS
1	A	341	ASN
1	A	344	ASN

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Mol	Chain	Res	Type
1	A	365	GLN
1	B	167	HIS
1	B	263	GLN
1	B	324	HIS
1	B	341	ASN
1	B	344	ASN
1	B	611	GLN
1	C	132	GLN
1	C	299	HIS
1	C	324	HIS
1	C	341	ASN
1	C	461	GLN
1	D	167	HIS
1	D	341	ASN
1	D	461	GLN
1	D	539	GLN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

5 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	FAD	A	801	-	48,58,58	1.63	8 (16%)	54,89,89	3.51	12 (22%)
2	FAD	B	801	-	48,58,58	1.33	6 (12%)	54,89,89	2.60	14 (25%)
2	FAD	C	801	-	48,58,58	1.28	4 (8%)	54,89,89	3.85	16 (29%)
3	MES	C	903	-	11,12,12	0.66	0	14,16,16	8.74	9 (64%)
2	FAD	D	801	-	48,58,58	1.37	5 (10%)	54,89,89	3.45	18 (33%)

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	FAD	A	801	-	-	0/30/50/50	0/6/6/6
2	FAD	B	801	-	-	0/30/50/50	0/6/6/6
2	FAD	C	801	-	-	0/30/50/50	0/6/6/6
3	MES	C	903	-	-	0/6/14/14	0/1/1/1
2	FAD	D	801	-	-	0/30/50/50	0/6/6/6

All (23) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	FAD	O4B-C4B	-3.76	1.36	1.45
2	B	801	FAD	O3B-C3B	-3.05	1.35	1.43
2	B	801	FAD	C9A-N10	-2.83	1.34	1.38
2	C	801	FAD	C10-N10	-2.75	1.36	1.39
2	A	801	FAD	O3B-C3B	-2.73	1.36	1.43
2	D	801	FAD	O2B-C2B	-2.65	1.36	1.43
2	C	801	FAD	C3B-C4B	-2.03	1.47	1.53
2	A	801	FAD	C8A-N7A	2.23	1.38	1.34
2	D	801	FAD	C5'-C4'	2.35	1.55	1.51
2	B	801	FAD	C4-N3	2.50	1.37	1.33
2	B	801	FAD	C2A-N3A	2.60	1.36	1.32
2	D	801	FAD	C2A-N3A	2.62	1.36	1.32
2	B	801	FAD	C5'-C4'	2.67	1.55	1.51
2	A	801	FAD	C5'-C4'	2.67	1.55	1.51
2	A	801	FAD	C2A-N3A	2.69	1.37	1.32
2	A	801	FAD	O4B-C1B	2.97	1.45	1.41
2	C	801	FAD	C2A-N3A	3.20	1.37	1.32
2	A	801	FAD	C4-C4X	3.20	1.47	1.41
2	B	801	FAD	C4-C4X	3.24	1.47	1.41
2	D	801	FAD	C4-N3	3.48	1.39	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	801	FAD	C4-C4X	4.25	1.49	1.41
2	C	801	FAD	C4-C4X	4.28	1.49	1.41
2	A	801	FAD	C1'-N10	5.83	1.54	1.48

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	903	MES	O2S-S-C8	-24.83	85.72	106.91
3	C	903	MES	O1S-S-C8	-18.97	90.72	106.91
2	D	801	FAD	N3A-C2A-N1A	-12.75	119.13	128.89
2	C	801	FAD	C4X-C4-N3	-11.83	107.42	123.59
2	A	801	FAD	C4-C4X-C10	-11.22	112.76	119.94
2	C	801	FAD	N3A-C2A-N1A	-10.88	120.57	128.89
2	A	801	FAD	N3A-C2A-N1A	-10.32	120.99	128.89
2	B	801	FAD	N3A-C2A-N1A	-8.52	122.37	128.89
2	D	801	FAD	C4X-C4-N3	-7.46	113.39	123.59
2	A	801	FAD	C4X-C4-N3	-5.96	115.44	123.59
2	D	801	FAD	C4-C4X-C10	-5.80	116.23	119.94
2	B	801	FAD	C4-C4X-C10	-5.34	116.52	119.94
2	B	801	FAD	C4X-C4-N3	-4.14	117.92	123.59
2	D	801	FAD	C4B-O4B-C1B	-3.02	106.39	109.72
2	B	801	FAD	C4B-O4B-C1B	-2.77	106.68	109.72
2	B	801	FAD	C7-C6-C5X	-2.26	117.24	120.92
2	C	801	FAD	O5'-P-O1P	-2.14	101.32	109.62
3	C	903	MES	C6-O1-C2	2.02	116.68	109.89
2	A	801	FAD	C2A-N1A-C6A	2.06	122.45	118.77
2	B	801	FAD	O4'-C4'-C3'	2.07	114.22	109.02
2	D	801	FAD	O4B-C4B-C3B	2.08	109.33	105.15
2	D	801	FAD	C2A-N1A-C6A	2.17	122.65	118.77
2	B	801	FAD	C4-C4X-N5	2.19	121.37	118.72
2	C	801	FAD	O4B-C4B-C3B	2.19	109.55	105.15
2	C	801	FAD	O3P-PA-O5B	2.20	108.78	102.94
2	D	801	FAD	C5B-C4B-C3B	2.35	124.54	115.21
2	C	801	FAD	C2A-N1A-C6A	2.43	123.11	118.77
2	C	801	FAD	C5B-C4B-C3B	2.50	125.13	115.21
2	D	801	FAD	O3P-PA-O5B	2.55	109.70	102.94
2	B	801	FAD	O4B-C4B-C5B	2.61	118.67	109.32
2	C	801	FAD	C4X-N5-C5X	2.63	119.79	116.76
2	C	801	FAD	O2B-C2B-C3B	2.64	120.42	111.83
2	D	801	FAD	O2P-P-O1P	2.68	127.04	112.53
3	C	903	MES	O3S-S-O2S	2.75	118.02	111.61
2	A	801	FAD	C4X-N5-C5X	2.76	119.94	116.76

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	801	FAD	O3B-C3B-C2B	2.83	121.03	111.83
3	C	903	MES	O1-C2-C3	2.86	118.39	111.84
2	D	801	FAD	C4-C4X-N5	2.86	122.19	118.72
2	B	801	FAD	O2B-C2B-C3B	2.89	121.21	111.83
2	B	801	FAD	O4B-C4B-C3B	2.92	111.04	105.15
2	C	801	FAD	O4B-C4B-C5B	2.99	120.01	109.32
3	C	903	MES	C7-N4-C3	3.28	119.68	111.27
2	D	801	FAD	O4B-C4B-C5B	3.31	121.14	109.32
2	A	801	FAD	O2B-C2B-C3B	3.31	122.60	111.83
2	C	801	FAD	C4-C4X-C10	3.39	122.11	119.94
2	D	801	FAD	O2B-C2B-C3B	3.51	123.25	111.83
2	C	801	FAD	O4B-C1B-N9A	3.56	115.56	108.10
2	D	801	FAD	C4X-N5-C5X	3.59	120.89	116.76
2	B	801	FAD	O4B-C1B-N9A	3.63	115.69	108.10
2	A	801	FAD	O3B-C3B-C4B	3.67	122.05	111.05
2	C	801	FAD	O3B-C3B-C4B	3.78	122.39	111.05
2	D	801	FAD	O4B-C1B-N9A	4.08	116.64	108.10
2	A	801	FAD	O4B-C1B-N9A	4.14	116.76	108.10
2	D	801	FAD	O3B-C3B-C4B	4.19	123.61	111.05
3	C	903	MES	C7-N4-C5	4.22	122.09	111.27
3	C	903	MES	C5-N4-C3	4.24	118.08	108.90
3	C	903	MES	O3S-S-O1S	4.66	122.45	111.61
2	C	801	FAD	C1'-N10-C9A	4.73	124.17	118.86
2	A	801	FAD	C1'-N10-C9A	5.18	124.68	118.86
2	B	801	FAD	C1'-N10-C9A	5.24	124.75	118.86
2	A	801	FAD	C4-C4X-N5	6.07	126.09	118.72
2	A	801	FAD	C2B-C1B-N9A	6.69	124.51	114.29
2	B	801	FAD	C4-N3-C2	7.57	121.79	115.25
2	B	801	FAD	C2B-C1B-N9A	8.23	126.86	114.29
2	C	801	FAD	C2B-C1B-N9A	9.31	128.52	114.29
2	D	801	FAD	C2B-C1B-N9A	10.17	129.83	114.29
2	D	801	FAD	C4-N3-C2	11.22	124.94	115.25
2	A	801	FAD	C4-N3-C2	14.13	127.46	115.25
2	C	801	FAD	C4-N3-C2	17.60	130.46	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	FAD	2	0
2	B	801	FAD	2	0
2	C	801	FAD	2	0
3	C	903	MES	1	0
2	D	801	FAD	4	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	576/623 (92%)	0.01	18 (3%) 52 56	15, 22, 44, 71	0
1	B	576/623 (92%)	-0.05	10 (1%) 73 76	14, 21, 38, 58	0
1	C	575/623 (92%)	0.11	19 (3%) 50 53	17, 27, 48, 72	0
1	D	574/623 (92%)	0.29	27 (4%) 35 38	19, 34, 56, 74	0
All	All	2301/2492 (92%)	0.09	74 (3%) 51 54	14, 26, 49, 74	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	389	LEU	7.8
1	D	618	PHE	6.6
1	A	459	VAL	6.3
1	B	459	VAL	6.3
1	C	619	THR	6.2
1	D	343	ALA	6.0
1	A	388	GLU	5.8
1	D	459	VAL	5.6
1	C	389	LEU	5.5
1	A	400	SER	5.3
1	C	343	ALA	5.2
1	C	459	VAL	4.9
1	B	618	PHE	4.9
1	A	343	ALA	4.8
1	D	617	PRO	4.6
1	C	390	THR	4.5
1	D	458	ALA	4.5
1	C	458	ALA	4.3
1	A	458	ALA	4.2
1	A	344	ASN	3.7
1	D	342	PRO	3.7

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Mol	Chain	Res	Type	RSRZ
1	C	457	GLY	3.6
1	C	385	THR	3.6
1	D	270	ALA	3.6
1	D	45	ILE	3.6
1	C	186	ASP	3.5
1	A	186	ASP	3.4
1	C	388	GLU	3.4
1	D	307	ASP	3.3
1	B	343	ALA	3.3
1	D	269	ASP	3.3
1	C	383	ARG	3.1
1	C	344	ASN	3.1
1	A	385	THR	3.0
1	B	345	PRO	3.0
1	A	384	GLY	3.0
1	B	344	ASN	2.9
1	A	401	THR	2.9
1	B	458	ALA	2.9
1	A	45	ILE	2.9
1	D	186	ASP	2.8
1	D	400	SER	2.8
1	D	457	GLY	2.8
1	C	345	PRO	2.8
1	D	317	VAL	2.7
1	D	344	ASN	2.7
1	D	309	PHE	2.7
1	C	232	GLY	2.6
1	A	44	ASP	2.6
1	D	185	LYS	2.5
1	A	345	PRO	2.5
1	C	318	LEU	2.5
1	A	390	THR	2.4
1	D	188	ALA	2.4
1	B	232	GLY	2.3
1	D	490	LYS	2.3
1	B	44	ASP	2.3
1	D	345	PRO	2.3
1	B	341	ASN	2.3
1	C	185	LYS	2.3
1	A	387	GLY	2.3
1	D	582	GLY	2.3
1	C	618	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	389	LEU	2.2
1	A	460	GLN	2.2
1	D	322	ALA	2.2
1	A	618	PHE	2.2
1	C	269	ASP	2.1
1	D	385	THR	2.1
1	C	490	LYS	2.1
1	D	602	ALA	2.1
1	D	339	ARG	2.0
1	D	321	GLY	2.0
1	D	347	GLU	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
3	MES	C	903	12/12	0.95	0.12	1.37	40,41,43,47	0
2	FAD	D	801	53/53	0.96	0.11	-0.31	23,28,32,34	0
2	FAD	B	801	53/53	0.98	0.10	-0.52	12,15,20,21	0
2	FAD	A	801	53/53	0.98	0.10	-0.53	12,17,21,22	0
2	FAD	C	801	53/53	0.98	0.10	-0.69	17,22,25,27	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.