



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 10:14 PM GMT

PDB ID : 1SPU  
Title : STRUCTURE OF OXIDOREDUCTASE  
Authors : Wilmot, C.M.; Phillips, S.E.V.  
Deposited on : 1996-11-13  
Resolution : 2.00 Å(reported)

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

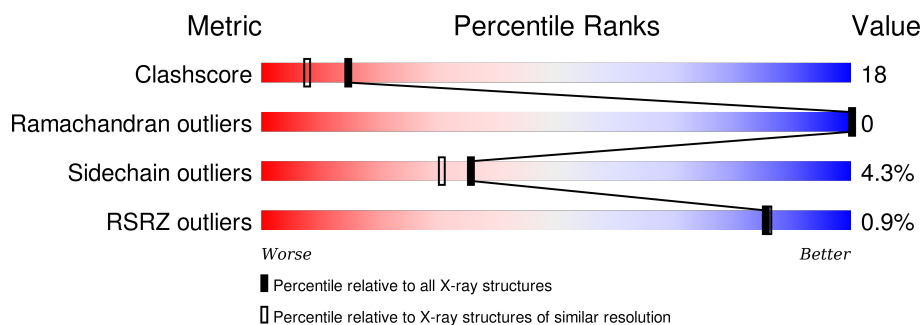
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	727	
1	B	727	

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
1	PAQ	A	466	X	-	-	-
1	PAQ	B	466	X	-	-	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12431 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 COPPER AMINE OXIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	718	Total	C	N	O	S	0	0	0
			5671	3607	967	1075	22			
1	B	720	Total	C	N	O	S	0	0	0
			5690	3619	972	1077	22			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	466	PAQ	TYR	MODIFIED RESIDUE	UNP P46883
B	466	PAQ	TYR	MODIFIED RESIDUE	UNP P46883

- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Cu	0	0
			1	1		
2	A	1	Total	Cu	0	0
			1	1		

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Ca	0	0
			2	2		
3	A	2	Total	Ca	0	0
			2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	539	Total	O	0	0
			539	539		

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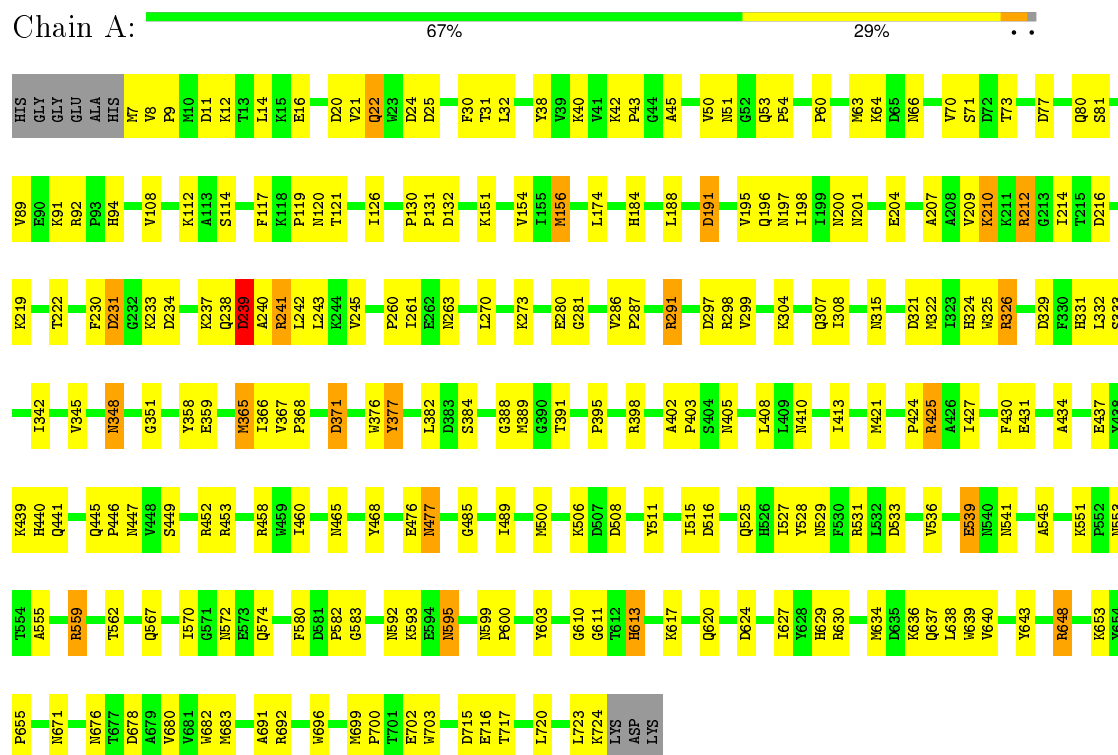
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	525	Total	O	0	0
			525	525		

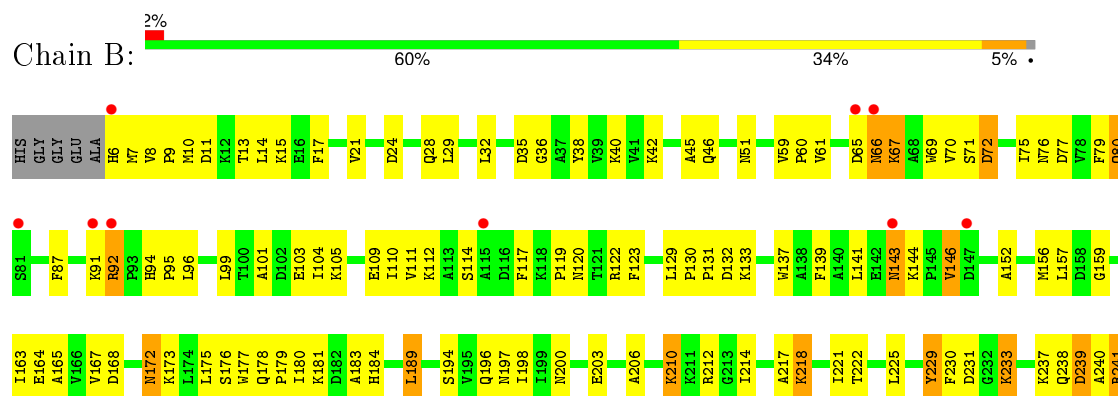
### 3 Residue-property plots

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

#### • Molecule 1: COPPER AMINE OXIDASE



#### • Molecule 1: COPPER AMINE OXIDASE



G665	Q578	Y466	P340	L242
K669	R579	D467	T346	L243
D670	F580	Y468	E359	I246
N671	D581	I469	I366	L249
E672	T584	E476	V367	D250
N676	L585	M477	P368	D253
A679	L587	A484	Y369	H259
M682	L588	K496	I374	P260
M683	M595	E503	R377	L261
R692	R596	R510	A380	E262
A693	H597	D516	Y381	N263
E694	G598	I519	L382	D269
P697	M599	Q525	D383	L270
I698	I605	H526	Y387	E271
M699	G610	R531	T391	Q272
P700	H613	L532	R398	K273
N712	F614	D533	G399	K274
N717	Y615	V536	K400	L275
L720	A616	D537	L408	V276
G721	A619	G538	M410	V286
L723	D624	E539	E411	P287
K724	E625	N540	T412	M288
K725	M626	N541	I413	T289
ASP	I627	A545	Y416	A290
LYS	Y628	M546	V419	R291
	H629	D547	P420	P292
	R630	P548	M421	R296
	L631	K551	P424	D297
	M634	P552	R425	R298
	D635	N553	R432	V299
	K636	T554	E437	A300
	D637	A555	H440	P301
	L638	P558	Q445	A302
	M639	R559	P446	V303
	R642	M563	R452	K304
	Y643	N566	R453	Q307
	H644	Q567	R458	I308
	E647	Y568	M459	K314
	R648	I570	E571	N315
	F649	M572	E573	I318
	K653	E574	Q574	M322
	M656			R326
	D661			F330
				R337
				V338
				G339

## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	134.46 Å   166.07 Å   79.41 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	20.00 – 2.00 18.59 – 1.99	Depositor EDS
% Data completeness (in resolution range)	83.7 (20.00-2.00) 80.3 (18.59-1.99)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.60 (at 1.99 Å)	Xtriage
Refinement program	PROLSQ	Depositor
R, $R_{free}$	0.206 , (Not available) 0.181 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	20.0	Xtriage
Anisotropy	0.665	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 97.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 100528 reflections	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	12431	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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: PAQ, CA, CU

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	0.80	0/5793	1.57	51/7886 (0.6%)
1	B	0.79	0/5813	1.62	51/7912 (0.6%)
All	All	0.79	0/11606	1.60	102/15798 (0.6%)

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	1	1
1	B	1	0
All	All	2	1

There are no bond length outliers.

All (102) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	291	ARG	NE-CZ-NH1	22.14	131.37	120.30
1	B	630	ARG	NE-CZ-NH1	15.28	127.94	120.30
1	B	291	ARG	CD-NE-CZ	14.99	144.59	123.60
1	B	291	ARG	NE-CZ-NH2	-13.27	113.67	120.30
1	A	648	ARG	NE-CZ-NH2	-12.95	113.82	120.30
1	B	692	ARG	NE-CZ-NH1	11.40	126.00	120.30
1	A	212	ARG	NE-CZ-NH1	11.24	125.92	120.30
1	B	458	ARG	NE-CZ-NH1	11.21	125.90	120.30
1	A	291	ARG	NE-CZ-NH1	11.18	125.89	120.30
1	B	122	ARG	NE-CZ-NH1	10.50	125.55	120.30
1	A	326	ARG	NE-CZ-NH1	10.50	125.55	120.30
1	B	241	ARG	NE-CZ-NH1	10.12	125.36	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	398	ARG	NE-CZ-NH1	9.80	125.20	120.30
1	B	296	ARG	NE-CZ-NH1	-9.72	115.44	120.30
1	A	239	ASP	CB-CG-OD1	9.69	127.02	118.30
1	B	212	ARG	NE-CZ-NH2	-9.64	115.48	120.30
1	A	648	ARG	NE-CZ-NH1	9.64	125.12	120.30
1	B	648	ARG	NE-CZ-NH2	-9.63	115.48	120.30
1	B	92	ARG	NE-CZ-NH1	9.54	125.07	120.30
1	A	212	ARG	NE-CZ-NH2	-9.20	115.70	120.30
1	B	337	ARG	NE-CZ-NH1	9.12	124.86	120.30
1	A	92	ARG	NE-CZ-NH2	-9.06	115.77	120.30
1	A	20	ASP	CB-CG-OD2	8.97	126.37	118.30
1	A	24	ASP	CB-CG-OD1	8.93	126.34	118.30
1	B	212	ARG	NE-CZ-NH1	8.76	124.68	120.30
1	A	630	ARG	NE-CZ-NH1	8.58	124.59	120.30
1	B	648	ARG	NE-CZ-NH1	8.40	124.50	120.30
1	A	453	ARG	NE-CZ-NH1	8.38	124.49	120.30
1	A	92	ARG	NE-CZ-NH1	8.25	124.42	120.30
1	A	458	ARG	NE-CZ-NH1	8.10	124.35	120.30
1	B	628	TYR	CB-CG-CD1	-7.85	116.29	121.00
1	B	241	ARG	NE-CZ-NH2	-7.52	116.54	120.30
1	B	453	ARG	NE-CZ-NH1	7.44	124.02	120.30
1	B	586	ARG	NE-CZ-NH1	7.17	123.89	120.30
1	B	630	ARG	CD-NE-CZ	7.12	133.56	123.60
1	B	359	GLU	CA-CB-CG	7.02	128.85	113.40
1	B	510	ARG	NE-CZ-NH1	7.01	123.81	120.30
1	A	291	ARG	CD-NE-CZ	6.94	133.32	123.60
1	A	559	ARG	NE-CZ-NH1	6.83	123.72	120.30
1	A	508	ASP	CB-CG-OD2	6.78	124.40	118.30
1	B	432	ARG	NE-CZ-NH1	6.77	123.68	120.30
1	A	241	ARG	NE-CZ-NH2	-6.66	116.97	120.30
1	A	425	ARG	NE-CZ-NH1	6.64	123.62	120.30
1	B	566	ASN	CB-CA-C	6.64	123.68	110.40
1	B	72	ASP	CB-CG-OD2	6.59	124.23	118.30
1	A	533	ASP	CB-CG-OD2	6.58	124.22	118.30
1	A	692	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	B	537	ASP	CB-CG-OD1	6.44	124.09	118.30
1	B	531	ARG	NE-CZ-NH2	6.43	123.51	120.30
1	A	440	HIS	N-CA-CB	6.42	122.17	110.60
1	A	398	ARG	NE-CZ-NH2	-6.36	117.12	120.30
1	A	431	GLU	CG-CD-OE1	6.36	131.01	118.30
1	A	191	ASP	CB-CG-OD1	-6.34	112.60	118.30
1	A	31	THR	O-C-N	6.29	132.77	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	510	ARG	NE-CZ-NH2	-6.29	117.15	120.30
1	B	526	HIS	N-CA-CB	6.28	121.91	110.60
1	B	146	VAL	CB-CA-C	6.27	123.31	111.40
1	A	231	ASP	CB-CG-OD1	6.12	123.81	118.30
1	A	234	ASP	CB-CG-OD1	6.11	123.80	118.30
1	B	183	ALA	O-C-N	5.99	132.29	122.70
1	B	122	ARG	CD-NE-CZ	5.91	131.87	123.60
1	B	432	ARG	NE-CZ-NH2	-5.89	117.35	120.30
1	A	458	ARG	NE-CZ-NH2	-5.83	117.39	120.30
1	A	191	ASP	CB-CG-OD2	5.82	123.54	118.30
1	B	624	ASP	CB-CG-OD1	5.75	123.48	118.30
1	B	326	ARG	NE-CZ-NH2	5.75	123.17	120.30
1	A	431	GLU	CG-CD-OE2	-5.68	106.95	118.30
1	A	184	HIS	N-CA-CB	5.63	120.73	110.60
1	B	229	TYR	CB-CG-CD1	-5.61	117.63	121.00
1	A	648	ARG	CD-NE-CZ	5.61	131.45	123.60
1	A	238	GLN	C-N-CA	5.59	135.68	121.70
1	B	377	TYR	CB-CG-CD2	-5.55	117.67	121.00
1	B	369	TYR	CB-CG-CD1	-5.53	117.68	121.00
1	A	643	TYR	CB-CG-CD2	-5.52	117.69	121.00
1	B	440	HIS	N-CA-CB	5.48	120.47	110.60
1	A	630	ARG	NE-CZ-NH2	-5.47	117.57	120.30
1	A	307	GLN	O-C-N	5.46	131.44	122.70
1	A	624	ASP	CB-CG-OD1	5.45	123.20	118.30
1	A	326	ARG	CD-NE-CZ	5.44	131.22	123.60
1	B	421	MET	CA-CB-CG	5.42	122.52	113.30
1	B	581	ASP	O-C-N	5.42	131.39	121.10
1	A	25	ASP	CB-CG-OD2	5.37	123.13	118.30
1	B	661	ASP	CB-CG-OD2	5.36	123.12	118.30
1	A	421	MET	N-CA-CB	-5.34	100.98	110.60
1	B	77	ASP	CB-CG-OD2	-5.33	113.50	118.30
1	B	35	ASP	CB-CG-OD2	5.31	123.08	118.30
1	B	239	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	22	GLN	N-CA-CB	5.25	120.06	110.60
1	A	539	GLU	CG-CD-OE1	5.24	128.77	118.30
1	A	410	ASN	O-C-N	5.23	131.06	122.70
1	A	326	ARG	NE-CZ-NH2	-5.22	117.69	120.30
1	A	624	ASP	CB-CG-OD2	-5.19	113.63	118.30
1	A	371	ASP	CB-CA-C	5.17	120.74	110.40
1	B	630	ARG	NH1-CZ-NH2	-5.16	113.73	119.40
1	A	30	PHE	O-C-N	5.15	130.94	122.70
1	B	596	ARG	NE-CZ-NH2	5.15	122.87	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	425	ARG	NE-CZ-NH2	-5.10	117.75	120.30
1	A	50	VAL	O-C-N	5.03	130.75	122.70
1	B	616	ALA	N-CA-CB	5.03	117.14	110.10
1	B	547	ASP	O-C-N	5.03	130.65	121.10
1	B	359	GLU	N-CA-CB	5.01	119.62	110.60
1	A	603	TYR	CB-CG-CD2	5.01	124.00	121.00

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	466	PAQ	CG
1	B	466	PAQ	CG

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	648	ARG	Sidechain

## 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	5671	0	5545	188	0
1	B	5690	0	5563	242	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	2	0	0	0	0
3	B	2	0	0	0	0
4	A	539	0	0	17	0
4	B	525	0	0	20	0
All	All	12431	0	11108	400	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 18.

All (400) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:210:LYS:HE3	1:B:217:ALA:HB2	1.24	1.14
1:B:368:PRO:HB2	1:B:621:PHE:HZ	1.09	1.12
1:B:92:ARG:HB2	1:B:92:ARG:HH11	1.24	1.00
1:B:368:PRO:HB2	1:B:621:PHE:CZ	1.97	0.98
1:A:297:ASP:HB2	1:B:725:LYS:HE3	1.46	0.98
1:A:592:ASN:HD21	1:A:676:ASN:HD21	1.03	0.97
1:B:644:HIS:HB3	4:B:1413:HOH:O	1.67	0.91
1:A:304:LYS:H	1:B:315:ASN:HD21	1.20	0.90
1:A:38:TYR:H	1:A:51:ASN:ND2	1.70	0.89
1:A:38:TYR:H	1:A:51:ASN:HD21	1.21	0.85
1:A:699:MET:SD	4:A:1422:HOH:O	2.34	0.85
1:B:92:ARG:HB2	1:B:92:ARG:NH1	1.91	0.85
1:A:315:ASN:HD21	1:B:304:LYS:H	1.26	0.84
1:A:216:ASP:HB3	1:A:219:LYS:HD2	1.60	0.82
1:B:269:ASP:HB2	1:B:276:VAL:HG11	1.62	0.81
1:A:592:ASN:HD21	1:A:676:ASN:ND2	1.80	0.78
1:B:38:TYR:H	1:B:51:ASN:HD21	1.31	0.78
1:A:545:ALA:HB2	1:A:570:ILE:HD11	1.66	0.78
1:B:6:HIS:HB3	1:B:72:ASP:OD1	1.84	0.77
1:B:139:PHE:O	1:B:143:ASN:HA	1.83	0.77
1:A:297:ASP:CB	1:B:725:LYS:HE3	2.15	0.77
1:B:38:TYR:H	1:B:51:ASN:ND2	1.84	0.76
1:B:38:TYR:HE1	1:B:40:LYS:HE3	1.49	0.76
1:B:445:GLN:HB3	1:B:446:PRO:CD	2.16	0.74
1:A:326:ARG:HH22	1:B:303:VAL:CG1	2.00	0.74
1:B:200:ASN:ND2	4:B:1597:HOH:O	2.16	0.74
1:B:445:GLN:HB3	1:B:446:PRO:HD2	1.70	0.73
1:A:198:ILE:HD11	1:A:273:LYS:HD3	1.70	0.72
1:A:536:VAL:H	1:A:541:ASN:HD21	1.37	0.71
1:A:525:GLN:NE2	1:A:620:GLN:H	1.87	0.71
1:A:237:LYS:HE2	1:A:239:ASP:HB2	1.71	0.70
1:A:525:GLN:HE22	1:A:620:GLN:H	1.39	0.70
1:A:326:ARG:HH22	1:B:303:VAL:HG11	1.57	0.70
1:A:12:LYS:O	1:A:16:GLU:HB2	1.92	0.70
1:B:65:ASP:O	1:B:66:ASN:HB2	1.91	0.70
1:A:214:ILE:HD11	1:A:261:ILE:HG12	1.74	0.69
1:B:239:ASP:HB2	4:B:1388:HOH:O	1.91	0.69
1:A:325:TRP:CE2	1:A:326:ARG:HD2	2.28	0.69
1:B:237:LYS:HE2	1:B:240:ALA:HB2	1.75	0.68
1:A:21:VAL:HG13	1:A:32:LEU:CD2	2.23	0.68
1:A:260:PRO:HD2	1:A:287:PRO:HG2	1.75	0.68
1:A:368:PRO:HG3	1:A:634:MET:CE	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:LEU:O	1:B:189:LEU:HD22	1.95	0.67
1:B:94:HIS:HD2	1:B:96:LEU:H	1.42	0.67
1:B:322:MET:HE3	1:B:330:PHE:O	1.94	0.67
1:B:109:GLU:HG2	4:B:1514:HOH:O	1.94	0.66
1:A:723:LEU:HD23	1:B:298:ARG:HD3	1.76	0.66
1:B:723:LEU:HD11	1:B:725:LYS:HD2	1.76	0.66
1:A:126:ILE:HG12	1:A:154:VAL:HG13	1.76	0.65
1:B:272:GLN:HE21	1:B:274:LYS:HG2	1.62	0.65
1:A:237:LYS:HG2	4:A:1146:HOH:O	1.97	0.64
1:B:241:ARG:HG2	1:B:270:LEU:HB2	1.80	0.64
1:A:7:MET:HA	1:A:70:VAL:O	1.98	0.64
1:B:503:GLU:HG2	4:B:1569:HOH:O	1.97	0.64
1:B:644:HIS:HB2	1:B:647:GLU:HG3	1.79	0.64
1:B:65:ASP:O	1:B:66:ASN:CB	2.45	0.64
1:A:260:PRO:HD2	1:A:287:PRO:CD	2.29	0.63
1:B:359:GLU:CD	1:B:648:ARG:HH22	2.01	0.63
1:B:572:ASN:ND2	1:B:671:ASN:HD21	1.96	0.63
1:A:298:ARG:HA	1:B:722:ALA:O	1.99	0.62
1:A:38:TYR:N	1:A:51:ASN:HD21	1.93	0.62
1:A:572:ASN:HB2	1:A:671:ASN:ND2	2.13	0.62
1:A:260:PRO:HD2	1:A:287:PRO:HD2	1.82	0.62
1:A:299:VAL:HG23	1:B:724:LYS:HG2	1.82	0.62
1:B:272:GLN:NE2	1:B:274:LYS:HD3	2.15	0.62
1:B:7:MET:HE2	1:B:70:VAL:HA	1.82	0.61
1:A:233:LYS:HG3	4:A:1370:HOH:O	2.00	0.61
1:B:307:GLN:NE2	4:B:1533:HOH:O	2.33	0.61
1:B:580:PHE:H	1:B:637:GLN:HE21	1.47	0.61
1:B:581:ASP:HB3	1:B:584:THR:HG23	1.83	0.61
1:A:553:ASN:ND2	1:A:555:ALA:H	1.98	0.61
1:A:439:LYS:NZ	1:A:447:ASN:ND2	2.47	0.61
1:A:439:LYS:HZ1	1:A:447:ASN:ND2	1.99	0.61
1:A:574:GLN:H	1:A:671:ASN:ND2	1.99	0.60
1:A:539:GLU:HG2	1:A:678:ASP:HB2	1.83	0.60
1:B:101:ALA:O	1:B:105:LYS:HG3	2.00	0.60
1:A:322:MET:HG2	4:A:1278:HOH:O	2.01	0.60
1:B:221:ILE:CD1	1:B:250:ASP:HB2	2.32	0.60
1:A:368:PRO:CG	1:A:634:MET:CE	2.80	0.59
1:A:600:PRO:HB3	4:A:1136:HOH:O	2.02	0.59
1:B:574:GLN:H	1:B:671:ASN:HD22	1.50	0.59
1:A:595:ASN:ND2	1:A:599:ASN:H	2.01	0.59
1:B:477:ASN:HD22	1:B:477:ASN:C	2.06	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:ASN:HD22	1:A:477:ASN:C	2.07	0.58
1:B:229:TYR:CD1	1:B:238:GLN:NE2	2.70	0.58
1:A:209:VAL:HG13	1:A:214:ILE:HB	1.85	0.58
1:B:539:GLU:HB2	4:B:1352:HOH:O	2.03	0.58
1:A:260:PRO:HD2	1:A:287:PRO:CG	2.34	0.58
1:B:259:HIS:HE1	1:B:289:THR:O	1.86	0.58
1:B:545:ALA:O	1:B:567:GLN:HA	2.04	0.58
1:A:63:MET:HE3	1:A:66:ASN:HA	1.83	0.58
1:B:40:LYS:HE2	4:B:1501:HOH:O	2.03	0.58
1:B:95:PRO:HB3	1:B:146:VAL:HG21	1.86	0.58
1:A:326:ARG:HH12	1:B:303:VAL:HG21	1.69	0.57
1:A:574:GLN:HG2	1:A:671:ASN:HB2	1.85	0.57
1:B:669:LYS:O	1:B:669:LYS:HE3	2.04	0.57
1:B:263:ASN:CA	1:B:374:ILE:HD11	2.34	0.57
1:B:38:TYR:CE1	1:B:40:LYS:HE3	2.37	0.57
1:B:7:MET:HE2	1:B:70:VAL:CA	2.34	0.57
1:B:366:ILE:HA	1:B:381:TYR:O	2.04	0.57
1:A:121:THR:HG23	1:A:156:MET:HB2	1.87	0.57
1:B:210:LYS:CE	1:B:217:ALA:HB2	2.16	0.57
1:B:578:GLN:HA	1:B:636:LYS:HD3	1.86	0.57
1:A:366:ILE:HG23	1:A:527:ILE:HB	1.86	0.57
1:A:377:TYR:CE1	1:B:558:PRO:HG2	2.40	0.57
1:B:271:GLU:OE1	1:B:271:GLU:HA	2.05	0.57
1:B:196:GLN:HE22	1:B:222:THR:H	1.51	0.57
1:B:595:ASN:HB3	1:B:712:ASN:O	2.05	0.57
1:A:117:PHE:CZ	1:A:121:THR:HB	2.40	0.56
1:A:332:LEU:HD21	1:A:427:ILE:HG21	1.88	0.56
1:A:237:LYS:CE	1:A:239:ASP:HB2	2.35	0.56
1:B:10:MET:HG2	1:B:14:LEU:HD12	1.88	0.56
1:A:348:ASN:HD21	1:A:351:GLY:CA	2.19	0.56
1:B:168:ASP:HB2	1:B:175:LEU:HD11	1.87	0.56
1:B:111:VAL:O	1:B:114:SER:HB3	2.05	0.56
1:A:717:THR:HG21	1:B:698:ILE:HG23	1.88	0.56
1:A:368:PRO:HG3	1:A:634:MET:HE3	1.88	0.55
1:B:596:ARG:HB3	1:B:597:MET:CE	2.35	0.55
1:B:133:LYS:NZ	1:B:533:ASP:OD2	2.39	0.55
1:B:540:ASN:HB3	1:B:676:ASN:ND2	2.20	0.55
1:A:331:HIS:CE1	1:A:333:SER:HB3	2.41	0.55
1:A:243:LEU:HD12	1:A:270:LEU:HD11	1.89	0.55
1:B:17:PHE:HB2	1:B:75:ILE:HD13	1.89	0.55
1:A:326:ARG:NH1	1:B:303:VAL:HG21	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:539:GLU:HB2	4:A:1423:HOH:O	2.05	0.55
1:A:324:HIS:HD2	1:A:329:ASP:OD1	1.90	0.55
1:A:308:ILE:HG12	1:B:308:ILE:HG12	1.88	0.55
1:A:610:GLY:HA3	1:B:610:GLY:HA3	1.89	0.55
1:B:111:VAL:O	1:B:117:PHE:HB2	2.06	0.55
1:B:7:MET:HE1	1:B:59:VAL:HG12	1.88	0.54
1:B:541:ASN:ND2	4:B:1496:HOH:O	2.41	0.54
4:A:1438:HOH:O	1:B:46:GLN:HG2	2.07	0.54
1:A:368:PRO:CG	1:A:634:MET:HE1	2.38	0.54
1:B:642:ARG:HD2	1:B:672:GLU:HB2	1.90	0.54
1:A:299:VAL:HG23	1:B:724:LYS:CG	2.37	0.54
1:A:403:PRO:HG3	1:A:430:PHE:CD2	2.43	0.54
1:B:263:ASN:HA	1:B:374:ILE:HD11	1.89	0.53
1:B:143:ASN:ND2	1:B:143:ASN:O	2.41	0.53
1:B:596:ARG:NH2	4:B:1112:HOH:O	2.42	0.53
1:B:13:THR:HG22	1:B:75:ILE:HD11	1.90	0.53
1:B:269:ASP:CB	1:B:276:VAL:HG11	2.36	0.53
1:B:7:MET:HE2	1:B:70:VAL:C	2.29	0.53
1:A:89:VAL:HG12	4:A:909:HOH:O	2.08	0.53
1:B:8:VAL:HG12	1:B:13:THR:OG1	2.09	0.53
1:A:582:PRO:C	1:B:615:VAL:HG12	2.30	0.53
1:A:8:VAL:HB	1:A:9:PRO:HD2	1.91	0.52
1:B:629:HIS:C	1:B:629:HIS:CD2	2.82	0.52
1:B:286:VAL:O	1:B:288:MET:HG2	2.09	0.52
1:B:574:GLN:H	1:B:671:ASN:ND2	2.07	0.52
1:B:36:GLY:HA2	1:B:314:LYS:HE2	1.92	0.52
1:A:38:TYR:N	1:A:51:ASN:ND2	2.51	0.52
1:B:628:TYR:C	1:B:628:TYR:CD1	2.83	0.52
1:B:10:MET:CG	1:B:14:LEU:HD12	2.39	0.52
1:A:222:THR:HB	1:A:245:VAL:HG13	1.92	0.52
1:B:272:GLN:HE21	1:B:274:LYS:CG	2.22	0.52
1:B:7:MET:HE3	1:B:71:SER:N	2.24	0.51
1:B:263:ASN:C	1:B:374:ILE:HD11	2.30	0.51
1:A:263:ASN:HB3	1:A:281:GLY:HA3	1.93	0.51
1:A:724:LYS:HE3	1:B:298:ARG:O	2.10	0.51
1:B:221:ILE:HD11	1:B:250:ASP:HB2	1.92	0.51
1:A:291:ARG:NH2	1:B:596:ARG:HH12	2.09	0.51
1:A:196:GLN:HE22	1:A:222:THR:H	1.59	0.51
1:B:642:ARG:HD2	1:B:672:GLU:CB	2.40	0.51
1:B:7:MET:CE	1:B:71:SER:N	2.74	0.51
1:A:42:LYS:HZ2	1:A:42:LYS:HB3	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:ARG:HD2	1:B:516:ASP:OD2	2.11	0.51
1:B:13:THR:HG22	1:B:75:ILE:CD1	2.41	0.51
1:A:559:ARG:HG2	1:B:377:TYR:HB2	1.93	0.51
1:B:536:VAL:H	1:B:541:ASN:HD21	1.59	0.50
1:A:439:LYS:NZ	1:A:447:ASN:HD21	2.08	0.50
1:A:43:PRO:HB3	1:A:63:MET:HG2	1.93	0.50
1:B:460:ILE:HA	1:B:468:TYR:O	2.12	0.50
1:B:322:MET:CE	1:B:330:PHE:C	2.80	0.50
1:A:572:ASN:CG	1:A:671:ASN:HD21	2.15	0.50
1:A:723:LEU:HD23	1:B:298:ARG:CD	2.42	0.50
1:B:243:LEU:CD1	1:B:270:LEU:HD11	2.42	0.50
1:B:21:VAL:HG22	1:B:32:LEU:HD22	1.92	0.50
1:A:365:MET:HE3	1:A:528:TYR:CD1	2.47	0.50
1:A:592:ASN:ND2	1:A:676:ASN:HD21	1.87	0.49
1:A:321:ASP:HB3	1:A:332:LEU:O	2.12	0.49
1:B:152:ALA:HB3	1:B:167:VAL:HG22	1.95	0.49
1:B:157:LEU:HG	1:B:159:GLY:O	2.13	0.49
1:A:121:THR:CG2	1:A:156:MET:HB2	2.42	0.49
1:B:243:LEU:HD12	1:B:270:LEU:HD11	1.93	0.49
1:A:580:PHE:HA	4:A:1387:HOH:O	2.12	0.49
1:A:384:SER:HB3	1:A:389:MET:SD	2.53	0.49
1:A:342:ILE:HG22	1:A:345:VAL:CG2	2.43	0.49
1:B:366:ILE:HD11	1:B:380:ALA:HB1	1.95	0.49
1:A:204:GLU:O	1:A:207:ALA:HB3	2.12	0.49
1:B:387:TYR:CZ	1:B:466:PAQ:H5	2.48	0.49
1:B:91:LYS:HE3	4:B:1507:HOH:O	2.12	0.49
1:A:511:TYR:HB3	4:A:1311:HOH:O	2.14	0.48
1:B:588:LEU:HB2	1:B:605:ILE:HD11	1.94	0.48
1:B:210:LYS:N	1:B:210:LYS:HD2	2.28	0.48
1:B:229:TYR:CZ	1:B:231:ASP:HA	2.49	0.48
1:B:525:GLN:HE22	1:B:620:GLN:H	1.59	0.48
1:A:613:HIS:CE1	1:A:702:GLU:HG3	2.48	0.48
1:B:112:LYS:HG2	1:B:117:PHE:CE2	2.49	0.48
1:B:639:TRP:HB2	1:B:682:TRP:HB2	1.96	0.48
1:A:367:VAL:HG13	1:A:525:GLN:O	2.14	0.48
1:B:119:PRO:O	1:B:120:ASN:HB2	2.12	0.48
1:B:99:LEU:HA	1:B:103:GLU:OE1	2.14	0.48
1:A:326:ARG:HD3	1:A:476:GLU:CD	2.34	0.48
1:A:348:ASN:ND2	1:A:351:GLY:H	2.12	0.48
1:A:716:GLU:HA	1:B:693:ALA:O	2.13	0.48
1:B:629:HIS:CD2	1:B:630:ARG:N	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:639:TRP:HB2	1:A:682:TRP:HB2	1.96	0.48
1:A:119:PRO:O	1:A:120:ASN:HB2	2.14	0.48
1:A:209:VAL:CG1	1:A:214:ILE:HB	2.44	0.48
1:B:164:GLU:OE2	1:B:653:LYS:HE2	2.14	0.48
1:A:439:LYS:HZ2	1:A:447:ASN:HD21	1.60	0.47
1:A:515:ILE:HG21	1:A:691:ALA:HB1	1.96	0.47
1:A:620:GLN:HB3	1:B:563:MET:HG2	1.96	0.47
1:B:262:GLU:O	1:B:263:ASN:HB2	2.14	0.47
1:B:717:THR:HB	1:B:720:LEU:HG	1.97	0.47
1:B:76:ASN:OD1	1:B:80:GLN:NE2	2.48	0.47
1:B:383:ASP:OD1	1:B:466:PAQ:N3	2.47	0.47
1:A:368:PRO:HG3	1:A:634:MET:HE1	1.93	0.47
1:B:61:VAL:HG22	1:B:70:VAL:HG12	1.97	0.47
1:A:188:LEU:O	1:A:191:ASP:HB2	2.15	0.47
1:B:326:ARG:HH11	1:B:326:ARG:HG3	1.78	0.47
1:B:87:PHE:HA	1:B:318:ILE:O	2.15	0.47
1:B:410:ASN:OD1	1:B:424:PRO:HA	2.15	0.47
1:A:545:ALA:O	1:A:567:GLN:HA	2.15	0.47
1:A:485:GLY:HA2	1:A:702:GLU:O	2.15	0.47
1:B:95:PRO:CB	1:B:146:VAL:HG21	2.44	0.47
1:A:574:GLN:HG2	1:A:671:ASN:CB	2.44	0.47
1:B:460:ILE:HG12	1:B:469:ILE:HG23	1.96	0.47
1:B:368:PRO:CB	1:B:621:PHE:CZ	2.86	0.47
1:A:516:ASP:HB2	1:A:696:TRP:CD1	2.50	0.47
1:A:441:GLN:NE2	1:A:445:GLN:O	2.46	0.47
1:A:460:ILE:HA	1:A:468:TYR:O	2.14	0.46
1:B:197:ASN:ND2	4:B:1521:HOH:O	2.43	0.46
1:A:14:LEU:HD11	1:A:32:LEU:HD13	1.97	0.46
1:A:402:ALA:HB1	1:A:403:PRO:HD2	1.97	0.46
1:A:40:LYS:HE2	1:A:40:LYS:HB2	1.80	0.46
1:A:574:GLN:CG	1:A:671:ASN:HB2	2.45	0.46
1:A:617:LYS:O	1:A:637:GLN:NE2	2.47	0.46
1:A:53:GLN:HA	1:A:54:PRO:HD3	1.81	0.46
1:A:408:LEU:HD12	1:A:425:ARG:HD2	1.96	0.46
1:B:218:LYS:N	1:B:218:LYS:HD3	2.31	0.46
1:A:629:HIS:HD2	4:A:1264:HOH:O	1.98	0.46
1:B:210:LYS:HE2	1:B:214:ILE:O	2.15	0.46
1:A:551:LYS:O	1:A:562:THR:N	2.41	0.46
1:B:476:GLU:OE1	4:B:1301:HOH:O	2.21	0.46
1:A:391:THR:HA	1:A:413:ILE:CD1	2.46	0.46
1:B:629:HIS:HD2	1:B:630:ARG:N	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:24:ASP:O	1:B:28:GLN:N	2.49	0.46
1:B:67:LYS:HD2	1:B:69:TRP:CZ2	2.51	0.45
1:B:253:ASP:O	1:B:292:PRO:HB3	2.16	0.45
1:B:129:LEU:HA	1:B:130:PRO:HD2	1.68	0.45
1:B:545:ALA:HB3	1:B:568:TYR:CE2	2.52	0.45
1:B:67:LYS:HD2	1:B:69:TRP:CE2	2.51	0.45
1:B:164:GLU:HG3	1:B:180:ILE:CG1	2.47	0.45
1:B:110:ILE:HD11	1:B:172:ASN:HA	1.97	0.45
1:A:365:MET:HB2	1:A:365:MET:HE3	1.76	0.45
1:A:595:ASN:HB2	1:A:715:ASP:OD1	2.17	0.45
1:B:699:MET:HA	1:B:700:PRO:HD3	1.71	0.45
1:A:326:ARG:NH2	1:B:303:VAL:CG1	2.75	0.45
1:B:469:ILE:O	1:B:484:ALA:HA	2.17	0.45
1:B:679:ALA:HB2	4:B:1380:HOH:O	2.17	0.45
1:B:229:TYR:CE1	1:B:238:GLN:NE2	2.85	0.45
1:B:559:ARG:HD2	1:B:559:ARG:HA	1.86	0.45
1:A:377:TYR:HB2	1:B:559:ARG:HG2	1.98	0.45
1:B:29:LEU:HD12	1:B:42:LYS:HG3	1.98	0.45
1:A:595:ASN:C	1:A:595:ASN:HD22	2.20	0.45
1:A:222:THR:HB	1:A:245:VAL:CG1	2.46	0.45
1:B:130:PRO:HA	1:B:131:PRO:HD3	1.88	0.45
1:A:371:ASP:HB3	1:A:376:TRP:HB3	1.98	0.45
1:B:225:LEU:CD1	1:B:246:ILE:HG12	2.47	0.45
1:B:619:ALA:HB1	1:B:634:MET:HE2	1.99	0.44
1:B:445:GLN:CB	1:B:446:PRO:CD	2.85	0.44
1:B:322:MET:HE1	1:B:330:PHE:C	2.38	0.44
1:A:723:LEU:HA	1:A:723:LEU:HD23	1.81	0.44
1:A:636:LYS:HB2	1:A:639:TRP:CE2	2.51	0.44
1:B:547:ASP:HA	1:B:548:PRO:HD3	1.74	0.44
1:A:94:HIS:HD2	1:A:322:MET:CE	2.31	0.44
1:B:9:PRO:HB3	1:B:67:LYS:HD3	1.99	0.44
1:A:434:ALA:HB3	1:A:452:ARG:HG2	2.00	0.44
1:A:358:TYR:CD2	1:A:359:GLU:HG3	2.52	0.44
1:A:291:ARG:HH21	1:A:516:ASP:CG	2.20	0.44
1:A:45:ALA:O	1:A:60:PRO:HB3	2.16	0.44
1:B:38:TYR:N	1:B:51:ASN:HD21	2.08	0.44
1:B:225:LEU:HD12	1:B:246:ILE:HG12	1.99	0.44
1:A:653:LYS:O	1:A:655:PRO:HD3	2.18	0.44
1:B:553:ASN:ND2	1:B:555:ALA:H	2.14	0.44
1:B:123:PHE:O	1:B:416:TYR:HA	2.17	0.44
1:B:322:MET:HE2	4:B:1195:HOH:O	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:8:VAL:CG1	1:B:9:PRO:HD2	2.48	0.44
1:A:240:ALA:HB1	1:A:242:LEU:HD21	1.99	0.44
1:A:273:LYS:HD2	4:A:1250:HOH:O	2.17	0.44
1:A:243:LEU:CD1	1:A:270:LEU:HD11	2.48	0.44
1:B:165:ALA:HA	1:B:176:SER:O	2.18	0.44
1:B:437:GLU:HA	1:B:452:ARG:HB2	2.00	0.44
1:B:496:LYS:NZ	4:B:1519:HOH:O	2.41	0.44
1:B:644:HIS:HB2	1:B:647:GLU:CG	2.48	0.44
1:B:387:TYR:CE1	1:B:466:PAQ:H5	2.52	0.44
1:A:77:ASP:O	1:A:81:SER:HB3	2.18	0.44
1:A:449:SER:O	1:B:400:LYS:HE2	2.18	0.44
1:A:388:GLY:HA3	4:A:1137:HOH:O	2.17	0.44
1:A:286:VAL:HA	1:A:287:PRO:HD3	1.78	0.43
1:B:574:GLN:CG	1:B:671:ASN:HB2	2.48	0.43
1:A:71:SER:C	1:A:73:THR:H	2.21	0.43
1:B:419:VAL:HA	1:B:420:PRO:HD3	1.91	0.43
1:B:7:MET:HE1	1:B:59:VAL:CG1	2.47	0.43
1:A:91:LYS:HG3	4:A:1405:HOH:O	2.18	0.43
1:A:395:PRO:HB3	1:A:424:PRO:O	2.17	0.43
1:A:595:ASN:C	1:A:595:ASN:ND2	2.71	0.43
1:B:578:GLN:OE1	4:B:1483:HOH:O	2.21	0.43
1:B:595:ASN:ND2	1:B:595:ASN:C	2.72	0.43
1:A:382:LEU:HD13	1:A:655:PRO:HB2	2.01	0.43
1:A:230:PHE:O	1:A:231:ASP:HB3	2.18	0.43
1:B:206:ALA:O	1:B:210:LYS:CD	2.66	0.43
1:A:331:HIS:HE1	1:A:333:SER:HB3	1.81	0.43
1:B:398:ARG:HG3	1:B:408:LEU:HD11	2.01	0.43
1:A:130:PRO:HA	1:A:131:PRO:HD3	1.78	0.43
1:B:723:LEU:HG	1:B:725:LYS:HG3	2.01	0.43
1:A:214:ILE:HD11	1:A:261:ILE:CG1	2.46	0.43
1:A:14:LEU:CD1	1:A:32:LEU:HD22	2.49	0.43
1:A:308:ILE:O	1:A:405:ASN:HB3	2.19	0.43
1:A:699:MET:HB3	4:A:1421:HOH:O	2.18	0.42
1:A:593:LYS:O	1:A:600:PRO:HA	2.18	0.42
1:A:348:ASN:HD22	1:A:348:ASN:C	2.23	0.42
1:A:324:HIS:CD2	1:A:329:ASP:OD1	2.72	0.42
1:B:286:VAL:HA	1:B:287:PRO:HD3	1.85	0.42
1:B:210:LYS:HE3	1:B:217:ALA:CB	2.18	0.42
1:B:619:ALA:HB1	1:B:621:PHE:CD2	2.55	0.42
1:B:621:PHE:HE2	1:B:634:MET:CE	2.33	0.42
1:B:627:ILE:CD1	1:B:631:LEU:HD12	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:194:SER:O	1:B:198:ILE:HG13	2.19	0.42
1:A:437:GLU:HA	1:A:452:ARG:HB2	2.02	0.42
1:B:337:ARG:HD3	1:B:649:PHE:CE1	2.54	0.42
1:A:500:MET:HG3	1:B:599:ASN:ND2	2.34	0.42
1:A:366:ILE:CG2	1:A:527:ILE:HB	2.47	0.42
1:A:391:THR:HA	1:A:413:ILE:HD11	2.01	0.42
1:A:131:PRO:HA	4:A:1245:HOH:O	2.19	0.42
1:B:692:ARG:HG3	1:B:694:GLU:OE1	2.19	0.42
1:A:366:ILE:HG13	1:A:368:PRO:HG3	2.02	0.42
1:B:595:ASN:ND2	1:B:597:MET:H	2.17	0.42
1:B:260:PRO:HD2	1:B:287:PRO:HD2	2.01	0.42
1:A:640:VAL:HA	1:A:680:VAL:O	2.20	0.42
1:A:241:ARG:HB2	4:A:1317:HOH:O	2.19	0.42
1:B:665:GLY:HA2	4:B:1441:HOH:O	2.19	0.42
1:A:63:MET:HB3	1:A:63:MET:HE3	1.97	0.42
1:B:366:ILE:HD11	1:B:627:ILE:HD11	2.01	0.42
1:B:366:ILE:HG12	1:B:367:VAL:N	2.35	0.42
1:B:516:ASP:HB3	1:B:519:ILE:HB	2.01	0.42
1:B:525:GLN:NE2	1:B:620:GLN:H	2.18	0.42
1:A:529:ASN:HA	1:A:683:MET:O	2.20	0.42
1:A:611:GLY:HA2	1:A:703:TRP:O	2.20	0.42
1:A:216:ASP:HB3	1:A:219:LYS:CD	2.43	0.42
1:B:629:HIS:HD2	1:B:630:ARG:HA	1.85	0.42
1:A:207:ALA:O	1:A:210:LYS:HB3	2.20	0.42
1:B:272:GLN:HB3	1:B:274:LYS:HG2	2.02	0.41
1:B:596:ARG:HB3	1:B:597:MET:HE2	2.02	0.41
1:A:531:ARG:HD2	1:A:682:TRP:CH2	2.55	0.41
1:B:45:ALA:O	1:B:60:PRO:HB3	2.20	0.41
1:B:391:THR:HA	1:B:413:ILE:HD11	2.02	0.41
1:B:644:HIS:CD2	4:B:1279:HOH:O	2.73	0.41
1:A:326:ARG:NH2	1:B:303:VAL:HG13	2.34	0.41
1:B:238:GLN:NE2	1:B:238:GLN:HA	2.35	0.41
1:B:249:LEU:O	1:B:259:HIS:HB2	2.19	0.41
1:B:178:GLN:HA	1:B:179:PRO:HD3	1.66	0.41
1:B:230:PHE:HB3	1:B:233:LYS:HB2	2.02	0.41
1:B:229:TYR:HD1	1:B:238:GLN:HE22	1.67	0.41
1:B:231:ASP:HB2	1:B:626:TRP:CZ2	2.55	0.41
1:A:445:GLN:HB3	1:A:446:PRO:HD2	2.02	0.41
1:A:465:ASN:HB2	1:A:489:ILE:O	2.21	0.41
1:A:574:GLN:H	1:A:671:ASN:HD22	1.68	0.41
1:B:104:ILE:HB	1:B:420:PRO:HG3	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:339:GLY:HA3	1:B:340:PRO:HD2	1.87	0.41
1:B:532:LEU:HD11	1:B:683:MET:HE2	2.02	0.41
1:A:108:VAL:HG12	1:A:112:LYS:HD2	2.03	0.41
1:B:75:ILE:O	1:B:79:PHE:HB2	2.20	0.41
1:B:141:LEU:HD21	1:B:346:THR:HG21	2.02	0.41
1:A:200:ASN:HA	1:A:200:ASN:HD22	1.63	0.41
1:B:163:ILE:HG21	1:B:177:TRP:CE2	2.56	0.41
1:B:723:LEU:HD11	1:B:725:LYS:CD	2.49	0.41
1:B:269:ASP:HB2	1:B:276:VAL:CG1	2.43	0.41
1:B:322:MET:HE3	1:B:330:PHE:C	2.41	0.41
1:B:572:ASN:CB	1:B:672:GLU:O	2.69	0.41
1:B:8:VAL:HG12	1:B:9:PRO:HD2	2.02	0.41
1:A:191:ASP:O	1:A:195:VAL:HG23	2.20	0.41
1:A:212:ARG:NH2	1:A:280:GLU:HB3	2.36	0.41
1:B:545:ALA:HB2	1:B:570:ILE:HD11	2.02	0.41
1:A:720:LEU:HD11	1:B:697:PRO:HG2	2.03	0.41
1:A:699:MET:HA	1:A:700:PRO:HD3	1.94	0.40
1:B:627:ILE:HG23	1:B:628:TYR:N	2.36	0.40
1:B:129:LEU:HD23	1:B:129:LEU:C	2.42	0.40
1:B:412:THR:HA	1:B:421:MET:O	2.21	0.40
1:A:114:SER:HB2	1:A:174:LEU:HD22	2.02	0.40
1:B:581:ASP:HB3	1:B:584:THR:CG2	2.50	0.40
1:A:583:GLY:N	1:B:615:VAL:HG12	2.36	0.40
1:B:300:ALA:HA	1:B:301:PRO:HD2	1.95	0.40
1:B:619:ALA:HB2	1:B:634:MET:HB3	2.03	0.40
1:B:46:GLN:NE2	4:B:1505:HOH:O	2.54	0.40
1:A:210:LYS:HA	1:A:210:LYS:HE3	2.03	0.40
1:B:184:HIS:HB2	1:B:656:ASN:O	2.22	0.40
1:A:627:ILE:HD12	1:A:627:ILE:HA	1.80	0.40
1:A:197:ASN:HA	1:A:197:ASN:HD22	1.58	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	715/727 (98%)	684 (96%)	31 (4%)	0	100	100
1	B	717/727 (99%)	691 (96%)	26 (4%)	0	100	100
All	All	1432/1454 (98%)	1375 (96%)	57 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	609/615 (99%)	591 (97%)	18 (3%)	48	47
1	B	611/615 (99%)	576 (94%)	35 (6%)	25	19
All	All	1220/1230 (99%)	1167 (96%)	53 (4%)	35	30

All (53) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	ASP
1	A	22	GLN
1	A	64	LYS
1	A	80	GLN
1	A	132	ASP
1	A	151	LYS
1	A	156	MET
1	A	201	ASN
1	A	210	LYS
1	A	239	ASP
1	A	348	ASN
1	A	365	MET
1	A	377	TYR
1	A	477	ASN
1	A	506	LYS

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Mol	Chain	Res	Type
1	A	595	ASN
1	A	613	HIS
1	A	638	LEU
1	B	11	ASP
1	B	15	LYS
1	B	66	ASN
1	B	67	LYS
1	B	80	GLN
1	B	132	ASP
1	B	137	TRP
1	B	143	ASN
1	B	144	LYS
1	B	156	MET
1	B	172	ASN
1	B	173	LYS
1	B	181	LYS
1	B	189	LEU
1	B	203	GLU
1	B	210	LYS
1	B	218	LYS
1	B	233	LYS
1	B	322	MET
1	B	377	TYR
1	B	477	ASN
1	B	551	LYS
1	B	566	ASN
1	B	572	ASN
1	B	574	GLN
1	B	595	ASN
1	B	599	ASN
1	B	613	HIS
1	B	620	GLN
1	B	629	HIS
1	B	635	ASP
1	B	636	LYS
1	B	648	ARG
1	B	669	LYS
1	B	692	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (59) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	97	ASN
1	A	170	GLN
1	A	196	GLN
1	A	197	ASN
1	A	200	ASN
1	A	201	ASN
1	A	263	ASN
1	A	272	GLN
1	A	315	ASN
1	A	324	HIS
1	A	348	ASN
1	A	447	ASN
1	A	477	ASN
1	A	517	HIS
1	A	525	GLN
1	A	529	ASN
1	A	541	ASN
1	A	553	ASN
1	A	566	ASN
1	A	567	GLN
1	A	595	ASN
1	A	599	ASN
1	A	604	GLN
1	A	671	ASN
1	A	676	ASN
1	B	46	GLN
1	B	51	ASN
1	B	66	ASN
1	B	76	ASN
1	B	80	GLN
1	B	94	HIS
1	B	143	ASN
1	B	178	GLN
1	B	196	GLN
1	B	197	ASN
1	B	200	ASN
1	B	238	GLN
1	B	263	ASN
1	B	272	GLN
1	B	315	ASN
1	B	350	ASN
1	B	477	ASN

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Mol	Chain	Res	Type
1	B	501	HIS
1	B	525	GLN
1	B	529	ASN
1	B	541	ASN
1	B	553	ASN
1	B	567	GLN
1	B	572	ASN
1	B	592	ASN
1	B	595	ASN
1	B	599	ASN
1	B	604	GLN
1	B	629	HIS
1	B	637	GLN
1	B	644	HIS
1	B	671	ASN
1	B	676	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z  > 2$
1	PAQ	A	466	1	17,22,23	2.03	4 (23%)	11,29,31	1.54	2 (18%)
1	PAQ	B	466	1	17,22,23	2.09	5 (29%)	11,29,31	1.26	1 (9%)

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
1	PAQ	A	466	1	1/1/5/10	0/7/27/29	0/2/2/2
1	PAQ	B	466	1	1/1/5/10	0/7/27/29	0/2/2/2

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	466	PAQ	CG-CD2	-4.63	1.40	1.50
1	B	466	PAQ	CG-CD2	-4.53	1.40	1.50
1	B	466	PAQ	C3-C2	-3.99	1.30	1.38
1	A	466	PAQ	C3-C2	-3.74	1.31	1.38
1	B	466	PAQ	OH-CZ	-3.13	1.25	1.34
1	A	466	PAQ	CE1-CD1	-3.07	1.39	1.45
1	B	466	PAQ	CE1-CD1	-2.41	1.41	1.45
1	A	466	PAQ	CE1-CZ	2.59	1.39	1.35
1	B	466	PAQ	CE1-CZ	2.67	1.40	1.35

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	466	PAQ	O2-CD1-CE1	-3.24	116.22	121.62
1	B	466	PAQ	O-C-CA	-2.86	118.05	125.49
1	A	466	PAQ	CB-CA-N	2.86	117.02	109.91

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	466	PAQ	CG
1	A	466	PAQ	CG

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	466	PAQ	3	0

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

Of 6 ligands modelled in this entry, 6 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	717/727 (98%)	-0.54	0 100 100	8, 21, 53, 82	0
1	B	719/727 (98%)	-0.43	13 (1%) 71 72	11, 24, 60, 99	0
All	All	1436/1454 (98%)	-0.48	13 (0%) 85 86	8, 23, 58, 99	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	301	PRO	5.2
1	B	65	ASP	4.8
1	B	302	ALA	4.5
1	B	6	HIS	3.8
1	B	143	ASN	2.8
1	B	115	ALA	2.7
1	B	92	ARG	2.6
1	B	91	LYS	2.4
1	B	628	TYR	2.3
1	B	66	ASN	2.3
1	B	147	ASP	2.2
1	B	81	SER	2.1
1	B	629	HIS	2.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [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( $\text{\AA}^2$ )	Q<0.9
1	PAQ	B	466	21/22	0.97	0.08	-	10,29,33,35	0
1	PAQ	A	466	21/22	0.96	0.09	-	9,23,34,38	0

### 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( $\text{\AA}^2$ )	Q<0.9
3	CA	B	802	1/1	0.61	0.19	0.87	71,71,71,71	0
3	CA	A	802	1/1	0.92	0.10	-0.27	56,56,56,56	0
3	CA	A	801	1/1	0.99	0.05	-2.25	19,19,19,19	0
3	CA	B	801	1/1	1.00	0.04	-2.40	20,20,20,20	0
2	CU	B	800	1/1	1.00	0.03	-	20,20,20,20	0
2	CU	A	800	1/1	0.99	0.03	-	25,25,25,25	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.