



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:34 AM GMT

PDB ID : 2ANL  
Title : X-ray crystal structure of the aspartic protease plasmepsin 4 from the malarial parasite plasmodium malariae bound to an allophenylnorstatine based inhibitor  
Authors : Clemente, J.C.; Govindasamy, L.; Madabushi, A.; Fisher, S.Z.; Moose, R.E.; Yowell, C.A.; Hidaka, K.; Kimura, T.; Hayashi, Y.; Kiso, Y.; Agbandje-McKenna, M.; Dame, J.B.; Dunn, B.M.; McKenna, R.  
Deposited on : 2005-08-11  
Resolution : 3.30 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

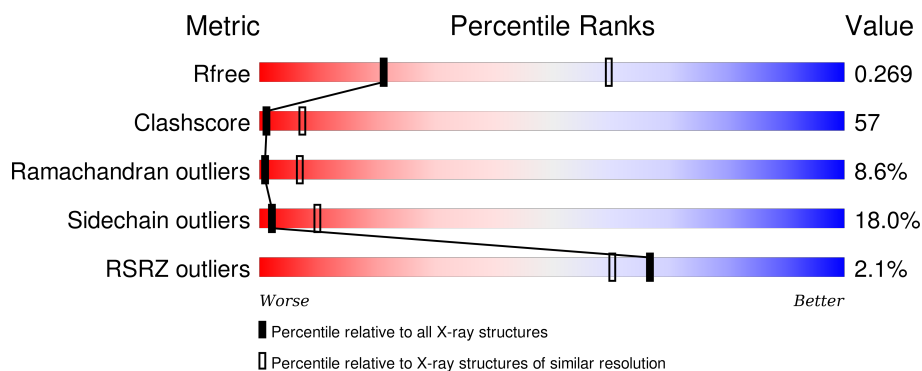
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.30 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	2060 (3.40-3.20)
Clashscore	102246	1058 (3.38-3.22)
Ramachandran outliers	100387	1038 (3.38-3.22)
Sidechain outliers	100360	1037 (3.38-3.22)
RSRZ outliers	91569	2070 (3.40-3.20)

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	327	<div> <div>33%</div> <div>48%</div> <div>15%</div> <div>5%</div> </div>
1	B	327	<div> <div>3%</div> <div>31%</div> <div>50%</div> <div>15%</div> <div>5%</div> </div>

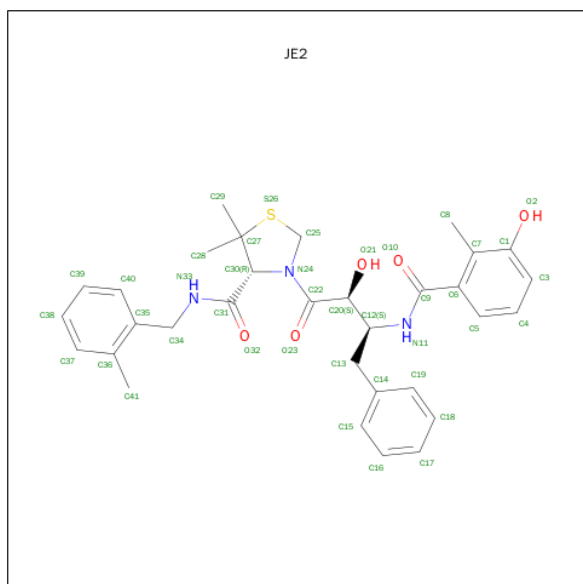


In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called plasmepsin IV.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total 2617	C 1696	N 395	O 515	S 11	0	0	0
1	B	327	Total 2617	C 1696	N 395	O 515	S 11	0	0	0

- Molecule 2 is (4R)-3-{(2S,3S)-2-HYDROXY-3-[(3-HYDROXY-2-METHYLBENZOYL)AMINO]-4-PHENYLBUTANOYL}-5,5-DIMETHYL-N-(2-METHYLBENZYL)-1,3-THIAZOLIDINE-4-CARBOXAMIDE (three-letter code: JE2) (formula:  $C_{32}H_{37}N_3O_5S$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 41	C 32	N 3	O 5	S 1	0	0
2	B	1	Total 41	C 32	N 3	O 5	S 1	0	0

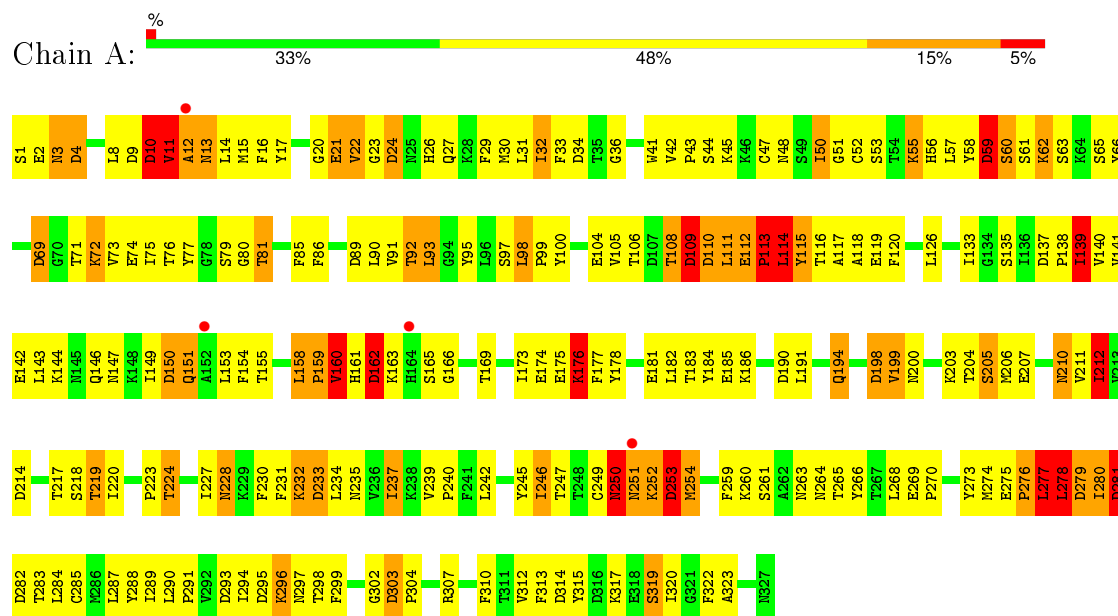
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	7	Total 7	O 7	0	0
3	B	7	Total 7	O 7	0	0

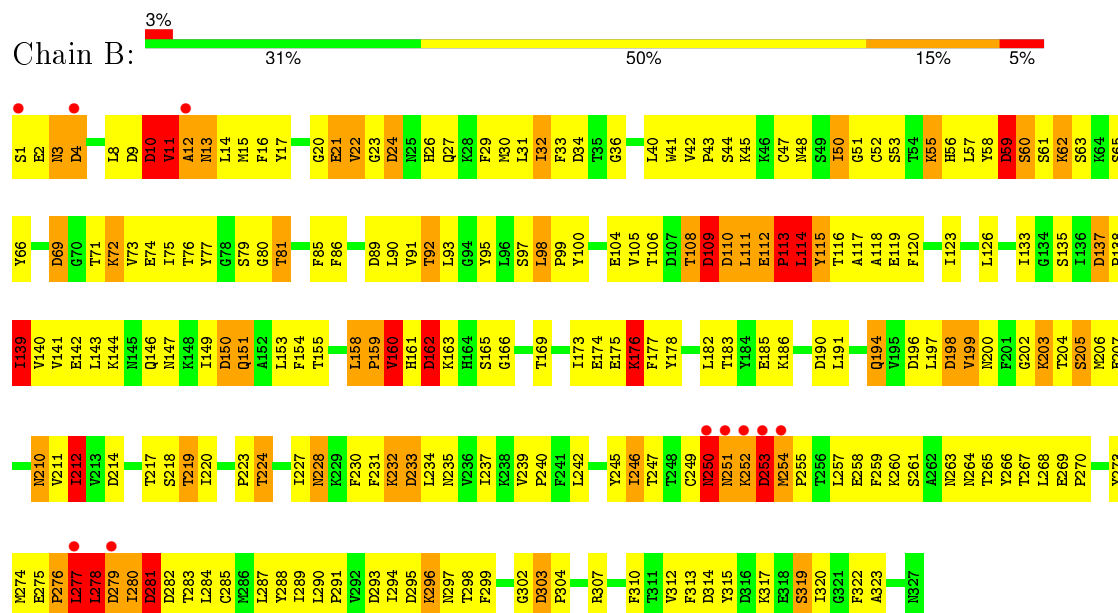
### 3 Residue-property plots

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

#### • Molecule 1: plasmepsin IV



#### • Molecule 1: plasmepsin IV



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	95.88 Å 112.58 Å 90.40 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	25.00 – 3.30 24.33 – 3.30	Depositor EDS
% Data completeness (in resolution range)	(Not available) (25.00-3.30) 79.4 (24.33-3.30)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.04 (at 3.30 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.247 , 0.298 0.254 , 0.269	Depositor DCC
$R_{free}$ test set	719 reflections (5.31%)	DCC
Wilson B-factor (Å <sup>2</sup> )	51.3	Xtriage
Anisotropy	0.087	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 3.3	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 14320 reflections	Xtriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	5330	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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: JE2

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	1.09	1/2681 (0.0%)	1.14	16/3636 (0.4%)
1	B	1.08	0/2681	1.13	16/3636 (0.4%)
All	All	1.09	1/5362 (0.0%)	1.13	32/7272 (0.4%)

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	8
1	B	0	8
All	All	0	16

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	279	ASP	CA-CB	-6.08	1.40	1.53

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	253	ASP	N-CA-CB	16.09	139.56	110.60
1	A	253	ASP	N-CA-CB	16.09	139.56	110.60
1	A	279	ASP	CB-CA-C	-15.07	80.26	110.40
1	B	279	ASP	CB-CA-C	-8.75	92.90	110.40
1	A	4	ASP	CB-CG-OD2	8.05	125.54	118.30
1	B	198	ASP	CB-CG-OD2	8.01	125.51	118.30
1	B	4	ASP	CB-CG-OD2	8.00	125.50	118.30
1	A	198	ASP	CB-CG-OD2	7.98	125.48	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	24	ASP	CB-CG-OD2	7.21	124.78	118.30
1	B	24	ASP	CB-CG-OD2	7.20	124.78	118.30
1	A	150	ASP	CB-CG-OD2	7.17	124.76	118.30
1	B	150	ASP	CB-CG-OD2	7.17	124.75	118.30
1	B	303	ASP	CB-CG-OD2	7.02	124.62	118.30
1	A	303	ASP	CB-CG-OD2	6.98	124.58	118.30
1	B	109	ASP	CB-CG-OD2	6.59	124.23	118.30
1	A	109	ASP	CB-CG-OD2	6.58	124.22	118.30
1	B	111	LEU	N-CA-C	-6.29	94.01	111.00
1	A	111	LEU	N-CA-C	-6.29	94.02	111.00
1	B	10	ASP	CB-CG-OD2	6.02	123.72	118.30
1	A	10	ASP	CB-CG-OD2	5.98	123.68	118.30
1	A	9	ASP	CB-CG-OD2	5.67	123.41	118.30
1	B	9	ASP	CB-CG-OD2	5.62	123.36	118.30
1	A	158	LEU	C-N-CD	-5.34	108.85	120.60
1	B	158	LEU	C-N-CD	-5.33	108.86	120.60
1	A	69	ASP	CB-CG-OD2	5.28	123.05	118.30
1	B	69	ASP	CB-CG-OD2	5.27	123.05	118.30
1	A	281	ASP	CB-CG-OD2	5.23	123.01	118.30
1	A	162	ASP	CB-CG-OD2	5.22	123.00	118.30
1	B	162	ASP	CB-CG-OD2	5.21	122.98	118.30
1	B	281	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	282	ASP	CB-CG-OD2	5.20	122.98	118.30
1	B	282	ASP	CB-CG-OD2	5.16	122.94	118.30

There are no chirality outliers.

All (16) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	11	VAL	Peptide
1	A	112	GLU	Peptide
1	A	113	PRO	Peptide
1	A	114	LEU	Peptide
1	A	212	ILE	Peptide
1	A	277	LEU	Peptide
1	A	278	LEU	Peptide
1	A	59	ASP	Peptide
1	B	11	VAL	Peptide
1	B	112	GLU	Peptide
1	B	113	PRO	Peptide
1	B	114	LEU	Peptide
1	B	212	ILE	Peptide

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Mol	Chain	Res	Type	Group
1	B	277	LEU	Peptide
1	B	278	LEU	Peptide
1	B	59	ASP	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	2617	0	2539	305	1
1	B	2617	0	2539	308	1
2	A	41	0	37	6	0
2	B	41	0	37	6	0
3	A	7	0	0	2	0
3	B	7	0	0	2	0
All	All	5330	0	5152	595	1

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 57.

All (595) 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:280:ILE:CD1	1:A:281:ASP:HB3	1.57	1.34
1:B:280:ILE:CD1	1:B:281:ASP:HB3	1.57	1.33
1:B:92:THR:C	1:B:93:LEU:HD23	1.63	1.19
1:A:181:GLU:HG2	1:B:202:GLY:O	1.43	1.18
1:A:92:THR:C	1:A:93:LEU:HD23	1.63	1.17
1:A:159:PRO:O	1:A:160:VAL:HG22	1.44	1.16
1:B:159:PRO:O	1:B:160:VAL:HG22	1.45	1.16
1:B:280:ILE:HD13	1:B:281:ASP:N	1.62	1.15
1:A:280:ILE:HD13	1:A:281:ASP:N	1.62	1.14
1:A:160:VAL:HB	1:A:163:LYS:HG3	1.28	1.13
1:B:280:ILE:HD13	1:B:281:ASP:HB3	1.35	1.09
1:B:160:VAL:HB	1:B:163:LYS:HG3	1.28	1.07
1:B:280:ILE:C	1:B:280:ILE:HD13	1.76	1.05
1:A:280:ILE:C	1:A:280:ILE:HD13	1.76	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:110:ASP:C	1:A:112:GLU:H	1.51	1.04
1:A:109:ASP:O	1:A:110:ASP:HB2	1.57	1.04
1:A:280:ILE:HD13	1:A:281:ASP:HB3	1.35	1.03
1:A:80:GLY:HA3	1:A:111:LEU:HD12	1.41	1.02
1:A:252:LYS:HD2	1:A:252:LYS:O	1.59	1.01
1:B:252:LYS:HD2	1:B:252:LYS:O	1.59	1.01
1:B:109:ASP:O	1:B:110:ASP:HB2	1.57	1.00
1:A:280:ILE:HD11	1:A:281:ASP:HB3	1.42	0.99
1:A:181:GLU:OE1	1:B:258:GLU:HG3	1.60	0.99
1:B:110:ASP:C	1:B:112:GLU:H	1.51	0.99
1:B:280:ILE:HD11	1:B:281:ASP:HB3	1.42	0.99
1:B:80:GLY:HA3	1:B:111:LEU:HD12	1.41	0.98
1:A:280:ILE:HD13	1:A:281:ASP:CB	1.94	0.97
1:B:280:ILE:HD13	1:B:281:ASP:CB	1.94	0.97
1:A:314:ASP:OD2	1:A:317:LYS:HD2	1.64	0.96
1:A:159:PRO:C	1:A:160:VAL:HG22	1.85	0.96
1:A:112:GLU:OE2	1:A:116:THR:HG23	1.66	0.96
1:A:175:GLU:HB3	1:B:203:LYS:NZ	1.80	0.96
1:B:280:ILE:CD1	1:B:281:ASP:CB	2.44	0.96
1:B:159:PRO:C	1:B:160:VAL:HG22	1.85	0.95
1:B:45:LYS:HD2	1:B:59:ASP:HB2	1.48	0.95
1:A:280:ILE:CD1	1:A:281:ASP:CB	2.44	0.95
1:A:45:LYS:HD2	1:A:59:ASP:HB2	1.48	0.95
1:A:281:ASP:OD2	1:A:283:THR:HG22	1.67	0.94
1:B:110:ASP:C	1:B:112:GLU:N	2.18	0.94
1:A:279:ASP:CG	1:A:279:ASP:O	1.98	0.94
1:B:112:GLU:OE2	1:B:116:THR:HG23	1.66	0.94
1:A:110:ASP:H	1:A:112:GLU:HB2	1.33	0.93
1:B:281:ASP:OD2	1:B:283:THR:HG22	1.67	0.93
1:A:109:ASP:O	1:A:110:ASP:CB	2.15	0.93
1:B:110:ASP:H	1:B:112:GLU:HB2	1.33	0.93
1:A:110:ASP:C	1:A:112:GLU:N	2.18	0.93
1:A:92:THR:O	1:A:93:LEU:HD23	1.68	0.92
1:B:275:GLU:O	1:B:276:PRO:O	1.87	0.92
1:B:92:THR:O	1:B:93:LEU:HD23	1.68	0.92
1:A:275:GLU:O	1:A:276:PRO:O	1.87	0.91
1:A:44:SER:HB2	1:A:104:GLU:HG2	1.53	0.90
1:B:159:PRO:C	1:B:160:VAL:CG2	2.39	0.90
1:A:159:PRO:C	1:A:160:VAL:CG2	2.40	0.90
1:B:114:LEU:HD23	1:B:114:LEU:H	1.37	0.90
1:B:109:ASP:O	1:B:110:ASP:CB	2.15	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:SER:HB2	1:B:104:GLU:HG2	1.53	0.89
1:A:160:VAL:CB	1:A:163:LYS:HG3	2.03	0.88
1:B:160:VAL:CB	1:B:163:LYS:HG3	2.03	0.88
1:A:114:LEU:HD23	1:A:114:LEU:H	1.37	0.88
1:A:181:GLU:OE1	1:B:200:ASN:HB2	1.75	0.87
1:B:232:LYS:HE2	1:B:233:ASP:N	1.92	0.85
1:A:232:LYS:HE2	1:A:233:ASP:N	1.92	0.84
1:A:181:GLU:CG	1:B:202:GLY:O	2.26	0.84
1:A:280:ILE:HD13	1:A:281:ASP:CA	2.11	0.81
1:B:280:ILE:HD13	1:B:281:ASP:CA	2.11	0.81
1:A:110:ASP:H	1:A:112:GLU:CB	1.94	0.80
1:A:93:LEU:HD23	1:A:93:LEU:N	1.87	0.80
1:B:275:GLU:C	1:B:276:PRO:O	2.19	0.80
1:B:93:LEU:HD23	1:B:93:LEU:N	1.87	0.79
1:B:110:ASP:H	1:B:112:GLU:CB	1.94	0.79
1:A:77:TYR:HA	2:A:3151:JE2:HC83	1.65	0.79
1:B:270:PRO:HA	1:B:273:TYR:CE2	2.19	0.78
1:A:251:ASN:O	1:A:254:MET:HG2	1.85	0.77
1:B:77:TYR:HA	2:B:3152:JE2:HC83	1.65	0.77
1:A:270:PRO:HA	1:A:273:TYR:CE2	2.19	0.77
1:B:279:ASP:OD1	1:B:279:ASP:O	2.03	0.77
1:B:251:ASN:O	1:B:254:MET:HG2	1.85	0.77
1:A:111:LEU:O	1:A:114:LEU:HB2	1.84	0.77
1:B:111:LEU:O	1:B:114:LEU:HB2	1.84	0.77
1:A:175:GLU:HB3	1:B:203:LYS:HZ3	1.47	0.76
1:A:181:GLU:HB3	1:B:200:ASN:ND2	1.99	0.76
1:A:275:GLU:C	1:A:276:PRO:O	2.19	0.76
1:A:199:VAL:HG11	1:A:299:PHE:CE1	2.21	0.76
1:B:36:GLY:HA3	2:B:3152:JE2:O21	1.85	0.76
1:B:199:VAL:HG11	1:B:299:PHE:CE1	2.21	0.75
1:A:36:GLY:HA3	2:A:3151:JE2:O21	1.86	0.75
1:B:113:PRO:HD2	1:B:114:LEU:HD23	1.69	0.75
1:A:113:PRO:HD2	1:A:114:LEU:HD23	1.69	0.74
1:B:114:LEU:HD23	1:B:114:LEU:N	2.03	0.73
1:B:13:ASN:O	1:B:14:LEU:HD13	1.89	0.72
1:A:144:LYS:HD3	1:A:151:GLN:HA	1.72	0.72
1:A:234:LEU:H	1:A:234:LEU:HD23	1.53	0.72
1:B:22:VAL:O	1:B:22:VAL:CG2	2.38	0.72
1:B:234:LEU:HD23	1:B:234:LEU:H	1.53	0.72
1:A:13:ASN:O	1:A:14:LEU:HD13	1.89	0.71
1:B:144:LYS:HD3	1:B:151:GLN:HA	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:VAL:CG2	1:A:22:VAL:O	2.38	0.71
1:B:280:ILE:C	1:B:280:ILE:CD1	2.49	0.71
1:A:114:LEU:CD2	1:A:114:LEU:H	2.03	0.71
1:B:114:LEU:CD2	1:B:114:LEU:H	2.03	0.71
1:A:10:ASP:OD1	1:A:10:ASP:C	2.30	0.70
1:B:175:GLU:HA	1:B:178:TYR:CE2	2.26	0.70
1:A:114:LEU:HD23	1:A:114:LEU:N	2.03	0.70
1:A:175:GLU:HA	1:A:178:TYR:CE2	2.26	0.70
1:B:22:VAL:O	1:B:22:VAL:HG23	1.91	0.70
1:A:22:VAL:HG23	1:A:22:VAL:O	1.91	0.70
1:A:41:TRP:CE3	1:A:105:VAL:HG21	2.27	0.70
1:B:41:TRP:CE3	1:B:105:VAL:HG21	2.27	0.70
1:A:175:GLU:HB3	1:B:203:LYS:HZ1	1.56	0.69
1:A:108:THR:O	1:A:109:ASP:O	2.10	0.69
1:B:108:THR:O	1:B:109:ASP:O	2.10	0.69
1:A:278:LEU:HG	1:A:278:LEU:O	1.91	0.69
1:A:159:PRO:O	1:A:160:VAL:CG2	2.33	0.69
1:B:10:ASP:C	1:B:10:ASP:OD1	2.30	0.69
1:B:278:LEU:HG	1:B:278:LEU:O	1.91	0.69
1:A:294:ILE:HD12	1:A:294:ILE:H	1.58	0.68
1:A:181:GLU:OE1	1:B:258:GLU:CG	2.38	0.68
1:A:114:LEU:CD2	1:A:114:LEU:N	2.57	0.68
1:B:150:ASP:HB3	1:B:151:GLN:NE2	2.09	0.68
1:A:150:ASP:HB3	1:A:151:GLN:NE2	2.09	0.68
1:B:294:ILE:H	1:B:294:ILE:HD12	1.58	0.68
1:A:97:SER:O	1:A:98:LEU:HB2	1.94	0.67
1:B:114:LEU:CD2	1:B:114:LEU:N	2.57	0.67
1:A:1:SER:HB2	1:A:3:ASN:OD1	1.93	0.67
1:A:21:GLU:OE2	1:A:26:HIS:HB3	1.95	0.67
1:B:1:SER:HB2	1:B:3:ASN:OD1	1.93	0.67
1:B:11:VAL:HG23	1:B:15:MET:O	1.95	0.67
1:B:278:LEU:CG	1:B:278:LEU:O	2.43	0.67
1:A:108:THR:O	1:A:109:ASP:C	2.32	0.67
1:B:275:GLU:O	1:B:276:PRO:C	2.32	0.67
1:B:21:GLU:OE2	1:B:26:HIS:HB3	1.95	0.67
1:B:1:SER:HB3	3:B:410:HOH:O	1.95	0.66
1:A:278:LEU:CG	1:A:278:LEU:O	2.43	0.66
1:A:224:THR:HG22	1:A:293:ASP:OD1	1.96	0.66
1:A:138:PRO:HG2	1:A:141:VAL:CG2	2.26	0.66
1:B:108:THR:O	1:B:109:ASP:C	2.32	0.66
1:A:144:LYS:H	1:A:149:ILE:HD11	1.61	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:VAL:HG23	1:A:15:MET:O	1.95	0.66
1:B:47:CYS:SG	1:B:106:THR:O	2.55	0.66
1:A:1:SER:HB3	3:A:403:HOH:O	1.95	0.66
1:B:224:THR:HG22	1:B:293:ASP:OD1	1.96	0.66
1:A:199:VAL:HG11	1:A:299:PHE:HE1	1.61	0.65
1:B:11:VAL:O	1:B:13:ASN:N	2.30	0.65
1:B:138:PRO:HG2	1:B:141:VAL:CG2	2.25	0.65
1:A:22:VAL:HG21	1:A:58:TYR:CD2	2.31	0.65
1:B:312:VAL:O	1:B:320:ILE:HG13	1.97	0.65
1:B:97:SER:O	1:B:98:LEU:HB2	1.94	0.65
1:B:22:VAL:HG21	1:B:58:TYR:CD2	2.31	0.64
1:B:279:ASP:CG	1:B:279:ASP:O	2.34	0.64
1:A:47:CYS:SG	1:A:106:THR:O	2.55	0.64
1:A:275:GLU:O	1:A:276:PRO:C	2.32	0.64
1:B:158:LEU:HD23	1:B:159:PRO:HD2	1.79	0.64
1:A:114:LEU:O	1:A:116:THR:N	2.31	0.64
1:A:11:VAL:O	1:A:13:ASN:N	2.30	0.64
1:B:159:PRO:O	1:B:160:VAL:CG2	2.33	0.64
1:A:112:GLU:OE2	1:A:116:THR:CG2	2.44	0.64
1:A:312:VAL:O	1:A:320:ILE:HG13	1.97	0.64
1:B:144:LYS:H	1:B:149:ILE:HD11	1.61	0.64
1:A:158:LEU:HD23	1:A:159:PRO:HD2	1.79	0.64
1:A:90:LEU:HD12	1:A:98:LEU:O	1.98	0.64
1:B:21:GLU:HA	1:B:27:GLN:O	1.98	0.63
1:A:140:VAL:HB	1:A:315:TYR:HE1	1.63	0.63
1:A:59:ASP:OD2	1:A:59:ASP:C	2.36	0.63
1:B:114:LEU:O	1:B:116:THR:N	2.31	0.63
1:B:59:ASP:C	1:B:59:ASP:OD2	2.36	0.63
1:B:280:ILE:HD11	1:B:281:ASP:CB	2.23	0.63
1:B:283:THR:HG23	1:B:284:LEU:N	2.14	0.63
1:B:90:LEU:HD12	1:B:98:LEU:O	1.98	0.63
1:A:21:GLU:HA	1:A:27:GLN:O	1.98	0.63
1:B:278:LEU:HD12	1:B:278:LEU:O	1.99	0.62
1:A:153:LEU:HB2	1:A:313:PHE:O	2.00	0.62
1:B:140:VAL:HB	1:B:315:TYR:HE1	1.63	0.62
1:A:278:LEU:O	1:A:278:LEU:HD12	1.99	0.62
1:A:283:THR:HG23	1:A:284:LEU:N	2.14	0.62
1:B:89:ASP:CG	1:B:90:LEU:H	2.04	0.61
1:A:23:GLY:N	1:A:90:LEU:O	2.33	0.61
1:B:153:LEU:HB2	1:B:313:PHE:O	2.00	0.61
1:B:295:ASP:HB2	1:B:298:THR:OG1	2.00	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:LYS:HA	1:A:319:SER:HB2	1.83	0.60
1:A:295:ASP:HB2	1:A:298:THR:OG1	2.00	0.60
1:A:98:LEU:HD23	1:A:99:PRO:N	2.17	0.60
1:B:199:VAL:HG11	1:B:299:PHE:HE1	1.61	0.60
1:A:89:ASP:CG	1:A:90:LEU:H	2.04	0.60
1:B:23:GLY:N	1:B:90:LEU:O	2.33	0.60
1:B:98:LEU:HD23	1:B:99:PRO:N	2.17	0.60
1:B:112:GLU:OE2	1:B:116:THR:CG2	2.44	0.60
1:B:186:LYS:HA	1:B:319:SER:HB2	1.83	0.60
1:A:80:GLY:CA	1:A:111:LEU:HD12	2.26	0.60
1:B:22:VAL:HG21	1:B:58:TYR:CE2	2.36	0.60
1:A:13:ASN:C	1:A:14:LEU:HD22	2.22	0.60
1:A:22:VAL:HG21	1:A:58:TYR:CE2	2.36	0.60
1:B:13:ASN:C	1:B:14:LEU:HD22	2.22	0.60
1:B:92:THR:O	1:B:93:LEU:CD2	2.46	0.59
1:A:92:THR:O	1:A:93:LEU:CD2	2.46	0.59
1:A:314:ASP:OD2	1:A:317:LYS:CD	2.45	0.59
1:B:278:LEU:O	1:B:280:ILE:HG23	2.02	0.59
1:A:314:ASP:HB3	1:A:317:LYS:HB2	1.83	0.59
1:A:280:ILE:HD11	1:A:281:ASP:CB	2.23	0.59
1:B:227:ILE:O	1:B:230:PHE:N	2.36	0.59
1:A:278:LEU:O	1:A:280:ILE:HG23	2.02	0.58
1:A:211:VAL:C	1:A:212:ILE:CG2	2.72	0.58
1:A:278:LEU:HD23	3:A:401:HOH:O	2.03	0.58
1:A:160:VAL:HB	1:A:163:LYS:CG	2.19	0.58
1:B:304:PRO:HA	1:B:307:ARG:HD2	1.86	0.58
1:B:275:GLU:HG3	1:B:288:TYR:OH	2.04	0.58
1:B:278:LEU:HD23	3:B:408:HOH:O	2.03	0.58
1:A:181:GLU:HB3	1:B:200:ASN:HD22	1.68	0.58
1:A:184:TYR:CB	1:B:207:GLU:OE2	2.52	0.58
1:B:199:VAL:O	1:B:205:SER:OG	2.22	0.58
1:A:275:GLU:HG3	1:A:288:TYR:OH	2.04	0.58
1:A:227:ILE:O	1:A:230:PHE:N	2.36	0.58
1:B:22:VAL:CG2	1:B:58:TYR:CE2	2.87	0.58
1:A:22:VAL:CG2	1:A:58:TYR:CE2	2.87	0.58
1:A:198:ASP:OD1	1:A:207:GLU:HG3	2.04	0.58
1:A:59:ASP:OD2	1:A:60:SER:N	2.37	0.57
1:A:217:THR:HG22	1:A:219:THR:HG23	1.86	0.57
1:B:55:LYS:HD3	1:B:120:PHE:O	2.05	0.57
1:A:98:LEU:C	1:A:98:LEU:HD23	2.25	0.57
1:B:211:VAL:C	1:B:212:ILE:CG2	2.72	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:59:ASP:OD2	1:B:60:SER:N	2.37	0.57
1:A:199:VAL:O	1:A:205:SER:OG	2.22	0.57
1:A:304:PRO:HA	1:A:307:ARG:HD2	1.86	0.57
1:A:69:ASP:HB3	1:A:86:PHE:O	2.05	0.57
1:A:91:VAL:N	1:A:98:LEU:O	2.31	0.56
1:B:278:LEU:CD1	1:B:278:LEU:O	2.53	0.56
1:B:98:LEU:HD23	1:B:98:LEU:C	2.25	0.56
1:B:89:ASP:OD2	1:B:90:LEU:N	2.38	0.56
1:A:111:LEU:O	1:A:114:LEU:CB	2.54	0.56
1:A:77:TYR:CD2	2:A:3151:JE2:HC82	2.41	0.56
1:B:217:THR:HG22	1:B:219:THR:HG23	1.86	0.56
1:B:69:ASP:HB3	1:B:86:PHE:O	2.05	0.56
1:A:278:LEU:CD1	1:A:278:LEU:O	2.53	0.56
1:B:198:ASP:OD1	1:B:207:GLU:HG3	2.04	0.56
1:A:55:LYS:HD3	1:A:120:PHE:O	2.04	0.56
1:B:91:VAL:N	1:B:98:LEU:O	2.31	0.56
1:A:80:GLY:HA3	1:A:111:LEU:CD1	2.28	0.56
1:B:110:ASP:N	1:B:112:GLU:HB2	2.13	0.56
1:B:92:THR:HB	1:B:97:SER:HA	1.88	0.56
1:B:98:LEU:HD23	1:B:99:PRO:C	2.26	0.56
1:A:302:GLY:C	1:A:304:PRO:HD2	2.27	0.56
1:A:175:GLU:C	1:A:177:PHE:H	2.10	0.56
1:B:138:PRO:HG2	1:B:141:VAL:HG21	1.88	0.56
1:B:277:LEU:HB3	1:B:278:LEU:HB3	1.88	0.55
1:B:175:GLU:C	1:B:177:PHE:H	2.10	0.55
1:B:10:ASP:OD1	1:B:11:VAL:N	2.39	0.55
1:B:302:GLY:C	1:B:304:PRO:HD2	2.27	0.55
1:B:77:TYR:CD2	2:B:3152:JE2:HC82	2.41	0.55
1:B:280:ILE:CD1	1:B:281:ASP:N	2.54	0.55
1:A:138:PRO:HG2	1:A:141:VAL:HG21	1.88	0.55
1:B:161:HIS:CG	1:B:162:ASP:N	2.73	0.55
1:A:277:LEU:HB3	1:A:278:LEU:HB3	1.88	0.55
1:B:75:ILE:HG12	1:B:133:ILE:HD12	1.89	0.55
1:A:85:PHE:N	1:A:85:PHE:CD1	2.74	0.55
1:B:85:PHE:N	1:B:85:PHE:CD1	2.74	0.55
1:B:259:PHE:HB2	1:B:266:TYR:HB2	1.89	0.55
1:A:10:ASP:OD1	1:A:11:VAL:N	2.39	0.55
1:A:92:THR:HB	1:A:97:SER:HA	1.88	0.54
1:A:259:PHE:HB2	1:A:266:TYR:HB2	1.89	0.54
1:A:161:HIS:CG	1:A:162:ASP:N	2.73	0.54
1:A:322:PHE:CD1	1:A:322:PHE:N	2.76	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:98:LEU:HD23	1:A:99:PRO:C	2.26	0.54
1:A:89:ASP:OD2	1:A:90:LEU:N	2.38	0.54
1:A:75:ILE:HG12	1:A:133:ILE:HD12	1.89	0.54
1:A:110:ASP:N	1:A:112:GLU:HB2	2.14	0.54
1:A:161:HIS:CG	1:A:162:ASP:H	2.26	0.54
1:B:173:ILE:HD12	1:B:173:ILE:N	2.23	0.54
1:B:239:VAL:HB	1:B:242:LEU:CD1	2.38	0.54
1:A:173:ILE:N	1:A:173:ILE:HD12	2.23	0.54
1:A:275:GLU:CG	1:A:288:TYR:OH	2.56	0.53
1:A:198:ASP:OD1	1:A:207:GLU:CG	2.56	0.53
1:B:234:LEU:CD2	1:B:234:LEU:H	2.21	0.53
1:A:227:ILE:O	1:A:228:ASN:C	2.46	0.53
1:B:227:ILE:O	1:B:228:ASN:C	2.46	0.53
1:B:80:GLY:HA3	1:B:111:LEU:CD1	2.28	0.53
1:B:322:PHE:CD1	1:B:322:PHE:N	2.76	0.53
1:B:198:ASP:OD1	1:B:207:GLU:CG	2.56	0.53
1:B:50:ILE:O	1:B:51:GLY:C	2.47	0.53
1:A:247:THR:O	1:A:285:CYS:N	2.39	0.53
1:B:320:ILE:HG12	1:B:322:PHE:CE1	2.44	0.53
1:A:211:VAL:C	1:A:212:ILE:HG22	2.29	0.53
1:B:275:GLU:CG	1:B:288:TYR:OH	2.56	0.53
1:A:31:LEU:O	1:A:32:ILE:HG13	2.09	0.53
1:A:263:ASN:ND2	1:B:263:ASN:HA	2.24	0.53
1:B:247:THR:O	1:B:285:CYS:N	2.39	0.53
1:A:320:ILE:HG12	1:A:322:PHE:CE1	2.44	0.53
1:A:239:VAL:HB	1:A:242:LEU:CD1	2.38	0.53
1:B:160:VAL:HB	1:B:163:LYS:CG	2.19	0.52
1:A:62:LYS:N	1:A:62:LYS:HD2	2.23	0.52
1:A:194:GLN:HB2	1:A:210:ASN:HD21	1.75	0.52
1:A:50:ILE:O	1:A:51:GLY:C	2.47	0.52
1:A:154:PHE:CE2	1:A:313:PHE:CD2	2.98	0.52
1:A:155:THR:OG1	1:A:169:THR:HB	2.10	0.52
1:B:161:HIS:CG	1:B:162:ASP:H	2.26	0.52
1:A:223:PRO:HD2	1:A:299:PHE:CE2	2.45	0.52
1:B:194:GLN:HB2	1:B:210:ASN:HD21	1.75	0.52
1:A:217:THR:HG22	1:A:218:SER:N	2.25	0.52
1:A:251:ASN:O	1:A:254:MET:CG	2.55	0.52
1:B:220:ILE:HD11	1:B:304:PRO:HB2	1.92	0.52
1:B:31:LEU:O	1:B:32:ILE:HG13	2.09	0.52
1:A:33:PHE:CD1	1:A:33:PHE:N	2.77	0.52
1:B:223:PRO:HD2	1:B:299:PHE:CE2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:LEU:O	1:B:114:LEU:CB	2.54	0.52
1:A:43:PRO:O	1:A:57:LEU:HA	2.10	0.52
1:A:140:VAL:HB	1:A:315:TYR:CE1	2.45	0.52
1:A:178:TYR:CE1	1:A:182:LEU:HD11	2.45	0.51
1:A:227:ILE:HD12	1:A:291:PRO:HB3	1.91	0.51
1:A:277:LEU:CB	1:A:278:LEU:HB3	2.40	0.51
1:A:280:ILE:CD1	1:A:281:ASP:N	2.54	0.51
1:B:211:VAL:C	1:B:212:ILE:HG22	2.29	0.51
1:B:303:ASP:HB2	1:B:304:PRO:HD3	1.93	0.51
1:B:217:THR:HG22	1:B:218:SER:N	2.25	0.51
1:B:154:PHE:CE2	1:B:313:PHE:CD2	2.98	0.51
1:A:220:ILE:HD11	1:A:304:PRO:HB2	1.92	0.51
1:B:33:PHE:N	1:B:33:PHE:CD1	2.77	0.51
1:B:43:PRO:O	1:B:57:LEU:HA	2.10	0.51
1:A:234:LEU:H	1:A:234:LEU:CD2	2.21	0.51
1:B:155:THR:OG1	1:B:169:THR:HB	2.10	0.51
1:B:17:TYR:CE1	1:B:30:MET:HG2	2.46	0.51
1:B:277:LEU:CB	1:B:278:LEU:HB3	2.40	0.51
1:B:227:ILE:HD12	1:B:291:PRO:HB3	1.91	0.51
1:B:251:ASN:O	1:B:254:MET:CG	2.56	0.51
1:B:80:GLY:CA	1:B:111:LEU:HD12	2.26	0.51
1:B:182:LEU:N	1:B:182:LEU:HD12	2.26	0.51
1:A:211:VAL:CG1	1:A:212:ILE:N	2.73	0.51
1:B:314:ASP:HB3	1:B:317:LYS:HB3	1.92	0.51
1:B:140:VAL:HB	1:B:315:TYR:CE1	2.45	0.51
1:B:283:THR:HG23	1:B:284:LEU:H	1.76	0.51
1:A:17:TYR:CE1	1:A:30:MET:HG2	2.46	0.51
1:B:62:LYS:HD2	1:B:62:LYS:N	2.22	0.50
1:B:281:ASP:C	1:B:281:ASP:OD2	2.49	0.50
1:A:182:LEU:HD12	1:A:182:LEU:N	2.26	0.50
1:A:230:PHE:O	1:A:233:ASP:HB2	2.11	0.50
1:B:178:TYR:CE1	1:B:182:LEU:HD11	2.45	0.50
1:A:1:SER:C	1:A:3:ASN:H	2.15	0.50
1:B:239:VAL:HB	1:B:242:LEU:HG	1.94	0.50
1:A:278:LEU:O	1:A:280:ILE:N	2.44	0.50
1:B:108:THR:O	1:B:110:ASP:HB3	2.11	0.50
1:A:314:ASP:CG	1:A:317:LYS:HB2	2.32	0.50
1:A:108:THR:O	1:A:110:ASP:HB3	2.11	0.50
1:A:281:ASP:OD2	1:A:281:ASP:C	2.49	0.50
1:A:113:PRO:O	1:A:114:LEU:O	2.30	0.50
1:A:279:ASP:O	1:A:279:ASP:OD2	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:230:PHE:O	1:B:233:ASP:HB2	2.11	0.50
1:B:278:LEU:O	1:B:280:ILE:N	2.44	0.50
1:B:50:ILE:O	1:B:53:SER:N	2.45	0.50
1:B:12:ALA:O	1:B:13:ASN:O	2.30	0.50
1:A:303:ASP:HB2	1:A:304:PRO:HD3	1.93	0.50
1:B:254:MET:CE	1:B:270:PRO:HB3	2.42	0.50
1:B:113:PRO:O	1:B:114:LEU:O	2.30	0.50
1:B:72:LYS:H	1:B:72:LYS:HD2	1.77	0.50
1:A:251:ASN:O	1:A:252:LYS:C	2.50	0.49
1:B:10:ASP:CG	1:B:11:VAL:N	2.66	0.49
1:A:254:MET:CE	1:A:270:PRO:HB3	2.42	0.49
1:B:60:SER:O	1:B:61:SER:C	2.51	0.49
1:A:98:LEU:HG	1:A:99:PRO:HD2	1.94	0.49
1:A:50:ILE:O	1:A:53:SER:N	2.45	0.49
1:B:138:PRO:O	1:B:139:ILE:C	2.51	0.49
1:B:155:THR:HB	1:B:310:PHE:CE2	2.47	0.49
1:A:55:LYS:HD2	1:A:115:TYR:CZ	2.48	0.49
1:B:1:SER:C	1:B:3:ASN:H	2.15	0.49
1:A:72:LYS:H	1:A:72:LYS:HD2	1.77	0.49
1:B:211:VAL:CG1	1:B:212:ILE:N	2.73	0.49
1:A:239:VAL:HB	1:A:242:LEU:HG	1.94	0.49
1:A:155:THR:HB	1:A:310:PHE:CE2	2.47	0.49
1:A:261:SER:HB3	1:A:264:ASN:HB2	1.95	0.49
1:B:98:LEU:HG	1:B:99:PRO:HD2	1.94	0.49
1:A:184:TYR:CZ	1:B:207:GLU:HB2	2.48	0.49
1:A:283:THR:HG23	1:A:284:LEU:H	1.76	0.49
1:B:217:THR:HG22	1:B:219:THR:H	1.77	0.49
1:B:261:SER:HB3	1:B:264:ASN:HB2	1.95	0.49
1:A:273:TYR:HA	1:A:288:TYR:HD1	1.78	0.48
1:A:60:SER:O	1:A:61:SER:C	2.51	0.48
1:A:139:ILE:O	1:A:142:GLU:N	2.41	0.48
1:A:12:ALA:O	1:A:13:ASN:O	2.30	0.48
1:A:296:LYS:H	1:A:296:LYS:HD3	1.78	0.48
1:A:110:ASP:N	1:A:112:GLU:CB	2.71	0.48
1:A:138:PRO:O	1:A:139:ILE:C	2.51	0.48
1:A:217:THR:HG22	1:A:219:THR:H	1.77	0.48
1:B:50:ILE:O	1:B:53:SER:OG	2.31	0.48
1:B:55:LYS:HD2	1:B:115:TYR:CZ	2.48	0.48
1:B:297:ASN:N	1:B:297:ASN:OD1	2.45	0.48
1:B:227:ILE:HD12	1:B:291:PRO:CA	2.44	0.48
1:A:184:TYR:CG	1:B:207:GLU:OE2	2.67	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:ASN:OD1	1:A:205:SER:OG	2.29	0.48
1:A:10:ASP:CG	1:A:11:VAL:N	2.65	0.48
1:A:160:VAL:CG2	1:A:163:LYS:HG3	2.44	0.48
1:A:227:ILE:HD12	1:A:291:PRO:CA	2.44	0.48
1:A:297:ASN:N	1:A:297:ASN:OD1	2.45	0.48
1:B:296:LYS:HD3	1:B:296:LYS:H	1.78	0.48
1:B:273:TYR:HA	1:B:288:TYR:HD1	1.78	0.48
1:A:246:ILE:HG13	1:A:247:THR:N	2.29	0.48
1:B:239:VAL:HB	1:B:242:LEU:HD11	1.96	0.47
1:A:239:VAL:HB	1:A:242:LEU:HD11	1.96	0.47
1:B:251:ASN:O	1:B:252:LYS:C	2.50	0.47
1:A:175:GLU:C	1:A:177:PHE:N	2.67	0.47
1:A:314:ASP:CB	1:A:317:LYS:HB2	2.42	0.47
1:B:50:ILE:HA	1:B:53:SER:OG	2.14	0.47
1:B:254:MET:HE2	1:B:254:MET:HB3	1.46	0.47
1:A:161:HIS:C	1:A:163:LYS:N	2.68	0.47
1:A:77:TYR:CD2	2:A:3151:JE2:C8	2.97	0.47
1:B:214:ASP:OD1	2:B:3152:JE2:O23	2.33	0.47
1:A:254:MET:HE2	1:A:270:PRO:HB3	1.96	0.47
1:A:211:VAL:HG22	1:A:299:PHE:HB2	1.97	0.47
1:B:304:PRO:HG3	1:B:307:ARG:NH1	2.30	0.47
1:B:211:VAL:HG22	1:B:299:PHE:HB2	1.96	0.47
1:B:161:HIS:C	1:B:163:LYS:N	2.68	0.47
1:A:200:ASN:HA	1:A:205:SER:OG	2.15	0.47
1:A:22:VAL:CG2	1:A:58:TYR:CD2	2.97	0.47
1:B:160:VAL:CG2	1:B:163:LYS:HG3	2.44	0.47
1:A:52:CYS:HB3	1:A:57:LEU:HD21	1.97	0.47
1:A:45:LYS:HA	1:A:57:LEU:HB3	1.97	0.47
1:B:246:ILE:HG13	1:B:247:THR:N	2.29	0.47
1:A:283:THR:CG2	1:A:284:LEU:N	2.78	0.47
1:B:52:CYS:HB3	1:B:57:LEU:HD21	1.97	0.47
1:A:214:ASP:OD1	2:A:3151:JE2:O23	2.33	0.47
1:A:304:PRO:HG3	1:A:307:ARG:NH1	2.30	0.47
1:A:50:ILE:HA	1:A:53:SER:OG	2.14	0.46
1:B:175:GLU:C	1:B:177:PHE:N	2.67	0.46
1:A:245:TYR:CD1	1:A:245:TYR:N	2.83	0.46
1:A:50:ILE:O	1:A:53:SER:OG	2.31	0.46
1:B:45:LYS:HA	1:B:57:LEU:HB3	1.97	0.46
1:B:100:TYR:CZ	1:B:139:ILE:HG23	2.50	0.46
1:B:200:ASN:HA	1:B:205:SER:OG	2.15	0.46
1:B:77:TYR:CD2	2:B:3152:JE2:C8	2.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:22:VAL:CG2	1:B:58:TYR:CD2	2.97	0.46
1:A:100:TYR:CZ	1:A:139:ILE:HG23	2.50	0.46
1:B:251:ASN:OD1	1:B:252:LYS:O	2.34	0.46
1:A:150:ASP:HB3	1:A:151:GLN:HE22	1.80	0.46
1:B:110:ASP:N	1:B:112:GLU:CB	2.71	0.46
1:B:153:LEU:HD12	1:B:153:LEU:C	2.36	0.46
1:A:118:ALA:O	1:A:120:PHE:N	2.46	0.46
1:B:283:THR:CG2	1:B:284:LEU:N	2.78	0.46
1:A:174:GLU:HB3	1:A:176:LYS:HG3	1.98	0.46
1:B:245:TYR:CD1	1:B:245:TYR:N	2.83	0.46
1:B:76:THR:HG23	1:B:81:THR:OG1	2.16	0.46
1:B:34:ASP:O	1:B:126:LEU:N	2.46	0.46
1:A:114:LEU:O	1:A:117:ALA:N	2.49	0.46
1:B:182:LEU:HA	1:B:323:ALA:HB2	1.98	0.46
1:B:182:LEU:H	1:B:182:LEU:HD12	1.81	0.46
1:B:150:ASP:HB3	1:B:151:GLN:HE22	1.80	0.45
1:A:76:THR:HG23	1:A:81:THR:OG1	2.16	0.45
1:A:251:ASN:OD1	1:A:252:LYS:O	2.34	0.45
1:B:313:PHE:CE1	1:B:320:ILE:HD12	2.52	0.45
1:B:277:LEU:HB3	1:B:278:LEU:CB	2.47	0.45
1:A:254:MET:HE2	1:A:254:MET:HB3	1.46	0.45
1:A:153:LEU:HD12	1:A:153:LEU:C	2.36	0.45
1:B:11:VAL:O	1:B:12:ALA:C	2.54	0.45
1:B:118:ALA:O	1:B:120:PHE:N	2.46	0.45
1:A:313:PHE:CE1	1:A:320:ILE:HD12	2.52	0.45
1:A:17:TYR:CD1	1:A:30:MET:HG2	2.52	0.45
1:A:185:GLU:OE1	1:A:261:SER:HB2	2.17	0.45
1:A:260:LYS:HE3	1:A:265:THR:HB	1.99	0.45
1:B:114:LEU:O	1:B:117:ALA:N	2.49	0.45
1:A:34:ASP:O	1:A:126:LEU:N	2.46	0.45
1:A:4:ASP:CG	1:A:95:TYR:HB3	2.37	0.45
1:B:79:SER:HB2	2:B:3152:JE2:C29	2.47	0.45
1:B:17:TYR:CD1	1:B:30:MET:HG2	2.52	0.45
1:B:8:LEU:HB2	1:B:166:GLY:HA3	1.99	0.45
1:B:4:ASP:CG	1:B:95:TYR:HB3	2.37	0.45
1:A:11:VAL:O	1:A:12:ALA:C	2.54	0.45
1:B:1:SER:C	1:B:3:ASN:N	2.71	0.45
1:B:62:LYS:N	1:B:62:LYS:CD	2.80	0.45
1:A:182:LEU:H	1:A:182:LEU:HD12	1.81	0.45
1:A:182:LEU:HA	1:A:323:ALA:HB2	1.98	0.45
1:A:79:SER:HB2	2:A:3151:JE2:C29	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:174:GLU:HB3	1:B:176:LYS:HG3	1.98	0.45
1:B:254:MET:HA	1:B:255:PRO:HD2	1.84	0.45
1:B:200:ASN:OD1	1:B:205:SER:OG	2.29	0.44
1:B:16:PHE:HE2	1:B:158:LEU:HD11	1.83	0.44
1:B:260:LYS:HE3	1:B:265:THR:HB	1.99	0.44
1:A:61:SER:O	1:A:63:SER:O	2.36	0.44
1:B:44:SER:CB	1:B:104:GLU:HG2	2.37	0.44
1:A:8:LEU:HB2	1:A:166:GLY:HA3	1.99	0.44
1:B:199:VAL:HG22	1:B:259:PHE:CD1	2.53	0.44
1:A:1:SER:C	1:A:3:ASN:N	2.71	0.44
1:B:61:SER:O	1:B:63:SER:O	2.36	0.44
1:A:184:TYR:HB3	1:B:207:GLU:OE2	2.18	0.44
1:B:185:GLU:OE1	1:B:261:SER:HB2	2.17	0.44
1:A:174:GLU:HB3	1:A:176:LYS:CG	2.47	0.44
1:A:268:LEU:HD12	1:A:268:LEU:HA	1.68	0.44
1:A:175:GLU:O	1:A:177:PHE:N	2.51	0.44
1:B:4:ASP:OD1	1:B:93:LEU:O	2.36	0.44
1:A:144:LYS:HA	1:A:144:LYS:HD2	1.83	0.44
1:A:184:TYR:CD2	1:B:207:GLU:OE2	2.71	0.44
1:B:174:GLU:HB3	1:B:176:LYS:CG	2.47	0.44
1:A:181:GLU:OE1	1:B:200:ASN:CB	2.57	0.44
1:A:97:SER:O	1:A:98:LEU:CB	2.64	0.44
1:A:161:HIS:C	1:A:161:HIS:CD2	2.90	0.44
1:A:16:PHE:CE2	1:A:158:LEU:HD11	2.53	0.44
1:A:277:LEU:HB3	1:A:278:LEU:CB	2.47	0.43
1:B:159:PRO:C	1:B:160:VAL:HG23	2.35	0.43
1:A:113:PRO:O	1:A:114:LEU:C	2.56	0.43
1:A:55:LYS:HD2	1:A:115:TYR:CE1	2.53	0.43
1:B:199:VAL:O	1:B:199:VAL:HG12	2.19	0.43
1:A:4:ASP:OD1	1:A:93:LEU:O	2.36	0.43
1:B:161:HIS:C	1:B:161:HIS:CD2	2.90	0.43
1:A:154:PHE:CE2	1:A:313:PHE:CG	3.07	0.43
1:B:47:CYS:O	1:B:48:ASN:OD1	2.37	0.43
1:B:204:THR:HG21	1:B:230:PHE:HB2	2.00	0.43
1:B:175:GLU:O	1:B:177:PHE:N	2.51	0.43
1:A:142:GLU:O	1:A:146:GLN:HG3	2.19	0.43
1:A:280:ILE:C	1:A:280:ILE:CD1	2.49	0.43
1:A:16:PHE:HE2	1:A:158:LEU:HD11	1.83	0.43
1:A:43:PRO:HG2	1:A:56:HIS:O	2.18	0.43
1:A:199:VAL:HG22	1:A:259:PHE:CD1	2.53	0.43
1:B:178:TYR:CZ	1:B:182:LEU:HD11	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:PRO:O	1:B:114:LEU:C	2.56	0.43
1:B:55:LYS:HD2	1:B:115:TYR:CE1	2.53	0.43
1:A:302:GLY:O	1:A:303:ASP:C	2.57	0.43
1:A:178:TYR:CZ	1:A:182:LEU:HD11	2.54	0.43
1:B:161:HIS:CD2	1:B:162:ASP:N	2.87	0.43
1:A:45:LYS:C	1:A:47:CYS:H	2.22	0.43
1:A:204:THR:HG21	1:A:230:PHE:HB2	2.01	0.43
1:B:242:LEU:HD12	1:B:242:LEU:O	2.19	0.43
1:B:16:PHE:CE2	1:B:158:LEU:HD11	2.53	0.43
1:B:43:PRO:HG2	1:B:56:HIS:O	2.18	0.43
1:B:161:HIS:C	1:B:163:LYS:H	2.22	0.42
1:B:45:LYS:C	1:B:47:CYS:H	2.22	0.42
1:B:142:GLU:O	1:B:146:GLN:HG3	2.19	0.42
1:B:302:GLY:O	1:B:303:ASP:C	2.57	0.42
1:A:62:LYS:N	1:A:62:LYS:CD	2.80	0.42
1:A:249:CYS:O	1:A:254:MET:SD	2.77	0.42
1:B:249:CYS:O	1:B:254:MET:SD	2.77	0.42
1:A:161:HIS:C	1:A:163:LYS:H	2.21	0.42
1:A:161:HIS:CD2	1:A:162:ASP:N	2.87	0.42
1:B:154:PHE:CE2	1:B:313:PHE:CG	3.07	0.42
1:A:303:ASP:N	1:A:304:PRO:CD	2.83	0.42
1:B:274:MET:HG2	1:B:287:LEU:HD23	2.01	0.42
1:A:50:ILE:O	1:A:53:SER:CB	2.68	0.42
1:B:191:LEU:HA	1:B:191:LEU:HD12	1.80	0.42
1:B:254:MET:HE2	1:B:270:PRO:HB3	2.00	0.42
1:A:242:LEU:O	1:A:242:LEU:HD12	2.19	0.42
1:A:47:CYS:O	1:A:48:ASN:OD1	2.37	0.42
1:B:97:SER:O	1:B:98:LEU:CB	2.64	0.42
1:A:99:PRO:HG2	1:A:99:PRO:O	2.20	0.42
1:B:139:ILE:O	1:B:142:GLU:N	2.41	0.42
1:B:93:LEU:HD22	1:B:93:LEU:HA	1.77	0.42
1:B:99:PRO:O	1:B:99:PRO:HG2	2.20	0.42
1:B:42:VAL:HG23	1:B:42:VAL:O	2.19	0.42
1:B:51:GLY:HA2	1:B:116:THR:HG22	2.02	0.42
1:A:153:LEU:HB3	1:A:314:ASP:HA	2.01	0.42
1:A:199:VAL:O	1:A:199:VAL:HG12	2.19	0.42
1:B:138:PRO:HG2	1:B:141:VAL:HB	2.02	0.42
1:B:111:LEU:HD12	1:B:111:LEU:HA	1.90	0.41
1:B:50:ILE:O	1:B:53:SER:CB	2.68	0.41
1:B:29:PHE:HE1	1:B:56:HIS:O	2.03	0.41
1:B:153:LEU:HB3	1:B:314:ASP:HA	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:VAL:O	1:A:42:VAL:HG23	2.19	0.41
1:A:227:ILE:HD12	1:A:291:PRO:CB	2.50	0.41
1:B:303:ASP:N	1:B:304:PRO:CD	2.83	0.41
1:B:239:VAL:HB	1:B:242:LEU:CG	2.50	0.41
1:B:250:ASN:O	1:B:252:LYS:N	2.54	0.41
1:A:138:PRO:HG2	1:A:141:VAL:HB	2.02	0.41
1:A:191:LEU:HA	1:A:191:LEU:HD12	1.79	0.41
1:B:227:ILE:HD12	1:B:291:PRO:CB	2.50	0.41
1:A:210:ASN:O	1:A:298:THR:HA	2.20	0.41
1:A:51:GLY:HA2	1:A:116:THR:HG22	2.02	0.41
1:A:250:ASN:O	1:A:252:LYS:N	2.53	0.41
1:B:113:PRO:HD2	1:B:114:LEU:CD2	2.46	0.41
1:A:43:PRO:HB2	1:A:57:LEU:HD23	2.03	0.41
1:A:29:PHE:HE1	1:A:56:HIS:O	2.04	0.41
1:B:210:ASN:O	1:B:298:THR:HA	2.20	0.41
1:A:283:THR:CG2	1:A:284:LEU:H	2.34	0.41
1:A:239:VAL:HB	1:A:242:LEU:CG	2.50	0.41
1:A:274:MET:HG2	1:A:287:LEU:HD23	2.01	0.41
1:A:289:ILE:O	1:A:290:LEU:HD23	2.20	0.41
1:B:98:LEU:HD12	1:B:143:LEU:CD2	2.51	0.41
1:A:98:LEU:HD12	1:A:143:LEU:CD2	2.51	0.41
1:B:20:GLY:O	1:B:29:PHE:N	2.54	0.41
1:B:45:LYS:HD2	1:B:59:ASP:CB	2.34	0.41
1:B:144:LYS:HA	1:B:144:LYS:HD2	1.83	0.41
1:B:137:ASP:HA	1:B:138:PRO:HD2	1.90	0.41
1:A:217:THR:HG22	1:A:219:THR:N	2.36	0.41
1:A:303:ASP:N	1:A:303:ASP:OD1	2.47	0.41
1:A:237:ILE:HD12	1:A:246:ILE:HD11	2.03	0.41
1:B:268:LEU:HA	1:B:268:LEU:HD12	1.68	0.41
1:B:231:PHE:O	1:B:234:LEU:HD23	2.21	0.40
1:A:231:PHE:O	1:A:234:LEU:HD23	2.21	0.40
1:B:43:PRO:HB2	1:B:57:LEU:HD23	2.03	0.40
1:A:20:GLY:O	1:A:29:PHE:N	2.54	0.40
1:A:22:VAL:HG23	1:A:58:TYR:HE2	1.86	0.40
1:B:155:THR:HB	1:B:310:PHE:CZ	2.56	0.40
1:B:99:PRO:O	1:B:99:PRO:CG	2.69	0.40
1:B:22:VAL:HG23	1:B:58:TYR:HE2	1.86	0.40
1:A:153:LEU:CB	1:A:313:PHE:O	2.67	0.40
1:A:175:GLU:OE1	1:B:203:LYS:HB3	2.21	0.40
1:B:217:THR:CG2	1:B:219:THR:HG23	2.49	0.40
1:B:257:LEU:O	1:B:267:THR:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:43:PRO:HA	1:A:105:VAL:HB	2.03	0.40
1:B:230:PHE:O	1:B:231:PHE:C	2.59	0.40
1:A:217:THR:CG2	1:A:219:THR:HG23	2.49	0.40
1:A:155:THR:HB	1:A:310:PHE:CZ	2.56	0.40
1:B:40:LEU:HA	1:B:123:ILE:O	2.22	0.40
1:B:289:ILE:O	1:B:290:LEU:HD23	2.20	0.40
1:B:196:ASP:O	1:B:197:LEU:HD23	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:LEU:N	1:B:279:ASP:CB[3_645]	1.93	0.27

## 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	325/327 (99%)	240 (74%)	57 (18%)	28 (9%)	1	7
1	B	325/327 (99%)	240 (74%)	57 (18%)	28 (9%)	1	7
All	All	650/654 (99%)	480 (74%)	114 (18%)	56 (9%)	1	7

All (56) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	113	PRO
1	A	114	LEU
1	A	159	PRO
1	A	160	VAL
1	A	240	PRO

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Mol	Chain	Res	Type
1	A	276	PRO
1	A	278	LEU
1	B	13	ASN
1	B	113	PRO
1	B	114	LEU
1	B	159	PRO
1	B	160	VAL
1	B	240	PRO
1	B	276	PRO
1	B	278	LEU
1	A	50	ILE
1	A	109	ASP
1	A	110	ASP
1	A	115	TYR
1	A	162	ASP
1	A	176	LYS
1	A	251	ASN
1	A	253	ASP
1	B	50	ILE
1	B	109	ASP
1	B	110	ASP
1	B	115	TYR
1	B	162	ASP
1	B	176	LYS
1	B	251	ASN
1	B	253	ASP
1	A	2	GLU
1	A	3	ASN
1	A	32	ILE
1	A	66	TYR
1	A	98	LEU
1	A	135	SER
1	A	250	ASN
1	B	2	GLU
1	B	3	ASN
1	B	32	ILE
1	B	66	TYR
1	B	98	LEU
1	B	135	SER
1	B	250	ASN
1	A	12	ALA
1	A	65	SER

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Mol	Chain	Res	Type
1	B	12	ALA
1	B	65	SER
1	A	119	GLU
1	B	119	GLU
1	A	228	ASN
1	B	228	ASN
1	A	139	ILE
1	B	139	ILE

### 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	295/295 (100%)	242 (82%)	53 (18%)	2	10
1	B	295/295 (100%)	242 (82%)	53 (18%)	2	10
All	All	590/590 (100%)	484 (82%)	106 (18%)	2	10

All (106) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASP
1	A	11	VAL
1	A	21	GLU
1	A	22	VAL
1	A	24	ASP
1	A	55	LYS
1	A	59	ASP
1	A	60	SER
1	A	62	LYS
1	A	71	THR
1	A	72	LYS
1	A	73	VAL
1	A	74	GLU
1	A	81	THR
1	A	92	THR

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Mol	Chain	Res	Type
1	A	93	LEU
1	A	108	THR
1	A	109	ASP
1	A	114	LEU
1	A	137	ASP
1	A	139	ILE
1	A	147	ASN
1	A	151	GLN
1	A	160	VAL
1	A	165	SER
1	A	176	LYS
1	A	183	THR
1	A	190	ASP
1	A	194	GLN
1	A	199	VAL
1	A	203	LYS
1	A	205	SER
1	A	206	MET
1	A	210	ASN
1	A	212	ILE
1	A	219	THR
1	A	224	THR
1	A	232	LYS
1	A	233	ASP
1	A	235	ASN
1	A	237	ILE
1	A	246	ILE
1	A	250	ASN
1	A	252	LYS
1	A	253	ASP
1	A	254	MET
1	A	269	GLU
1	A	277	LEU
1	A	278	LEU
1	A	280	ILE
1	A	281	ASP
1	A	296	LYS
1	A	319	SER
1	B	10	ASP
1	B	11	VAL
1	B	21	GLU
1	B	22	VAL

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Mol	Chain	Res	Type
1	B	24	ASP
1	B	55	LYS
1	B	59	ASP
1	B	60	SER
1	B	62	LYS
1	B	71	THR
1	B	72	LYS
1	B	73	VAL
1	B	74	GLU
1	B	81	THR
1	B	92	THR
1	B	108	THR
1	B	109	ASP
1	B	114	LEU
1	B	137	ASP
1	B	139	ILE
1	B	147	ASN
1	B	151	GLN
1	B	160	VAL
1	B	162	ASP
1	B	165	SER
1	B	176	LYS
1	B	183	THR
1	B	190	ASP
1	B	194	GLN
1	B	199	VAL
1	B	203	LYS
1	B	205	SER
1	B	206	MET
1	B	210	ASN
1	B	212	ILE
1	B	219	THR
1	B	224	THR
1	B	232	LYS
1	B	233	ASP
1	B	235	ASN
1	B	237	ILE
1	B	246	ILE
1	B	250	ASN
1	B	252	LYS
1	B	253	ASP
1	B	254	MET

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Mol	Chain	Res	Type
1	B	269	GLU
1	B	277	LEU
1	B	278	LEU
1	B	280	ILE
1	B	281	ASP
1	B	296	LYS
1	B	319	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	13	ASN
1	A	151	GLN
1	A	161	HIS
1	A	194	GLN
1	A	210	ASN
1	B	13	ASN
1	B	151	GLN
1	B	161	HIS
1	B	194	GLN
1	B	200	ASN
1	B	210	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

2 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	JE2	A	3151	-	44,44,44	1.83	8 (18%)	57,63,63	1.97	12 (21%)
2	JE2	B	3152	-	44,44,44	1.83	8 (18%)	57,63,63	1.97	12 (21%)

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	JE2	A	3151	-	-	0/33/49/49	0/4/4/4
2	JE2	B	3152	-	-	0/33/49/49	0/4/4/4

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	3151	JE2	C27-S26	-6.30	1.72	1.85
2	B	3152	JE2	C27-S26	-6.27	1.72	1.85
2	B	3152	JE2	C20-C22	-4.87	1.48	1.53
2	A	3151	JE2	C20-C22	-4.84	1.48	1.53
2	A	3151	JE2	C6-C7	-3.38	1.36	1.40
2	B	3152	JE2	C6-C7	-3.37	1.36	1.40
2	B	3152	JE2	C9-N11	-3.37	1.26	1.34
2	A	3151	JE2	C9-N11	-3.37	1.26	1.34
2	A	3151	JE2	C25-S26	-3.01	1.75	1.82
2	B	3152	JE2	C25-S26	-2.99	1.75	1.82
2	A	3151	JE2	C20-C12	-2.12	1.52	1.54
2	B	3152	JE2	C20-C12	-2.10	1.52	1.54
2	A	3151	JE2	C30-N24	2.52	1.48	1.46
2	B	3152	JE2	C30-N24	2.57	1.48	1.46
2	B	3152	JE2	O10-C9	4.92	1.33	1.23
2	A	3151	JE2	O10-C9	4.92	1.33	1.23

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3151	JE2	C13-C12-N11	-6.31	103.23	110.14
2	B	3152	JE2	C13-C12-N11	-6.28	103.27	110.14
2	B	3152	JE2	C29-C27-S26	-5.03	100.79	109.18
2	A	3151	JE2	C29-C27-S26	-5.02	100.81	109.18
2	B	3152	JE2	C5-C6-C7	-4.67	117.31	120.78
2	A	3151	JE2	C5-C6-C7	-4.62	117.34	120.78
2	A	3151	JE2	C14-C13-C12	-3.29	108.25	113.48
2	B	3152	JE2	C14-C13-C12	-3.28	108.26	113.48
2	B	3152	JE2	C8-C7-C6	-3.13	117.70	122.27
2	A	3151	JE2	C8-C7-C6	-3.13	117.70	122.27
2	B	3152	JE2	C27-C30-C31	-3.09	106.89	113.28
2	A	3151	JE2	C27-C30-C31	-3.09	106.91	113.28
2	B	3152	JE2	O10-C9-N11	-2.34	118.21	122.44
2	A	3151	JE2	O10-C9-N11	-2.32	118.24	122.44
2	A	3151	JE2	C35-C34-N33	-2.22	108.59	113.08
2	B	3152	JE2	C35-C34-N33	-2.20	108.62	113.08
2	B	3152	JE2	C37-C36-C35	2.17	121.48	118.57
2	A	3151	JE2	C37-C36-C35	2.19	121.51	118.57
2	B	3152	JE2	C29-C27-C28	2.23	114.44	110.88
2	A	3151	JE2	C29-C27-C28	2.25	114.46	110.88
2	A	3151	JE2	C29-C27-C30	3.83	120.15	111.56
2	B	3152	JE2	C29-C27-C30	3.84	120.17	111.56
2	B	3152	JE2	C7-C6-C9	3.85	123.45	120.56
2	A	3151	JE2	C7-C6-C9	3.85	123.45	120.56

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3151	JE2	6	0
2	B	3152	JE2	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 [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	327/327 (100%)	-0.07	4 (1%) 81 76	24, 55, 57, 58	0
1	B	327/327 (100%)	0.08	10 (3%) 52 46	24, 55, 57, 58	0
All	All	654/654 (100%)	0.01	14 (2%) 67 60	24, 55, 57, 58	0

All (14) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	12	ALA	6.3
1	B	253	ASP	4.3
1	B	1	SER	3.7
1	A	12	ALA	3.6
1	B	250	ASN	3.4
1	B	251	ASN	3.3
1	A	164	HIS	3.1
1	A	152	ALA	2.5
1	B	252	LYS	2.4
1	B	279	ASP	2.3
1	A	251	ASN	2.2
1	B	277	LEU	2.1
1	B	254	MET	2.0
1	B	4	ASP	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( $\text{\AA}^2$ )	Q<0.9
2	JE2	B	3152	41/41	0.92	0.30	1.59	44,52,56,57	0
2	JE2	A	3151	41/41	0.94	0.25	0.73	44,52,56,57	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.