



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:20 AM GMT

PDB ID : 2GP6  
Title : X-ray crystal structure of Mycobacterium tuberculosis beta-ketoacyl acyl carrier protein synthase II (mtKasB)  
Authors : Sridharan, S.; Sacchettini, J.; TB Structural Genomics Consortium (TBSGC)  
Deposited on : 2006-04-17  
Resolution : 2.40 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

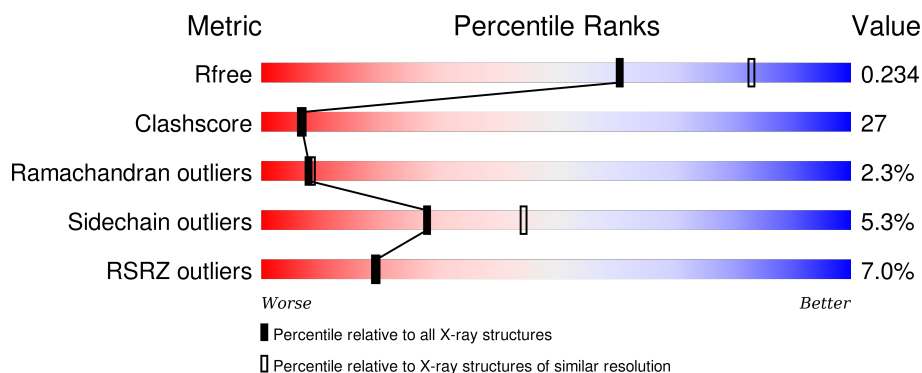
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


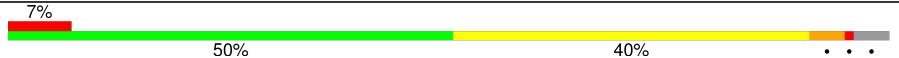
The reported resolution of this entry is 2.40 Å.

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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	434	 6% 53% 35% 5% . .
1	B	434	 7% 50% 40% . . .

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6421 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 3-oxoacyl-[acyl-carrier-protein] synthase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	415	Total	C	N	O	S	0	0	0
			3096	1932	561	587	16			
1	B	415	Total	C	N	O	S	0	0	0
			3096	1932	561	587	16			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	MET	-	CLONING ARTIFACT	UNP P63456
A	-15	GLY	-	CLONING ARTIFACT	UNP P63456
A	-14	SER	-	CLONING ARTIFACT	UNP P63456
A	-13	SER	-	CLONING ARTIFACT	UNP P63456
A	-12	HIS	-	EXPRESSION TAG	UNP P63456
A	-11	HIS	-	EXPRESSION TAG	UNP P63456
A	-10	HIS	-	EXPRESSION TAG	UNP P63456
A	-9	HIS	-	EXPRESSION TAG	UNP P63456
A	-8	HIS	-	EXPRESSION TAG	UNP P63456
A	-7	HIS	-	EXPRESSION TAG	UNP P63456
A	-6	SER	-	CLONING ARTIFACT	UNP P63456
A	-5	SER	-	CLONING ARTIFACT	UNP P63456
A	-4	GLY	-	CLONING ARTIFACT	UNP P63456
A	-3	LEU	-	CLONING ARTIFACT	UNP P63456
A	-2	VAL	-	CLONING ARTIFACT	UNP P63456
A	-1	PRO	-	CLONING ARTIFACT	UNP P63456
A	0	ARG	-	CLONING ARTIFACT	UNP P63456
A	1	GLY	-	CLONING ARTIFACT	UNP P63456
A	2	SER	-	CLONING ARTIFACT	UNP P63456
A	3	HIS	-	CLONING ARTIFACT	UNP P63456
A	4	MET	-	CLONING ARTIFACT	UNP P63456
B	-16	MET	-	CLONING ARTIFACT	UNP P63456
B	-15	GLY	-	CLONING ARTIFACT	UNP P63456
B	-14	SER	-	CLONING ARTIFACT	UNP P63456
B	-13	SER	-	CLONING ARTIFACT	UNP P63456

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-12	HIS	-	EXPRESSION TAG	UNP P63456
B	-11	HIS	-	EXPRESSION TAG	UNP P63456
B	-10	HIS	-	EXPRESSION TAG	UNP P63456
B	-9	HIS	-	EXPRESSION TAG	UNP P63456
B	-8	HIS	-	EXPRESSION TAG	UNP P63456
B	-7	HIS	-	EXPRESSION TAG	UNP P63456
B	-6	SER	-	CLONING ARTIFACT	UNP P63456
B	-5	SER	-	CLONING ARTIFACT	UNP P63456
B	-4	GLY	-	CLONING ARTIFACT	UNP P63456
B	-3	LEU	-	CLONING ARTIFACT	UNP P63456
B	-2	VAL	-	CLONING ARTIFACT	UNP P63456
B	-1	PRO	-	CLONING ARTIFACT	UNP P63456
B	0	ARG	-	CLONING ARTIFACT	UNP P63456
B	1	GLY	-	CLONING ARTIFACT	UNP P63456
B	2	SER	-	CLONING ARTIFACT	UNP P63456
B	3	HIS	-	CLONING ARTIFACT	UNP P63456
B	4	MET	-	CLONING ARTIFACT	UNP P63456

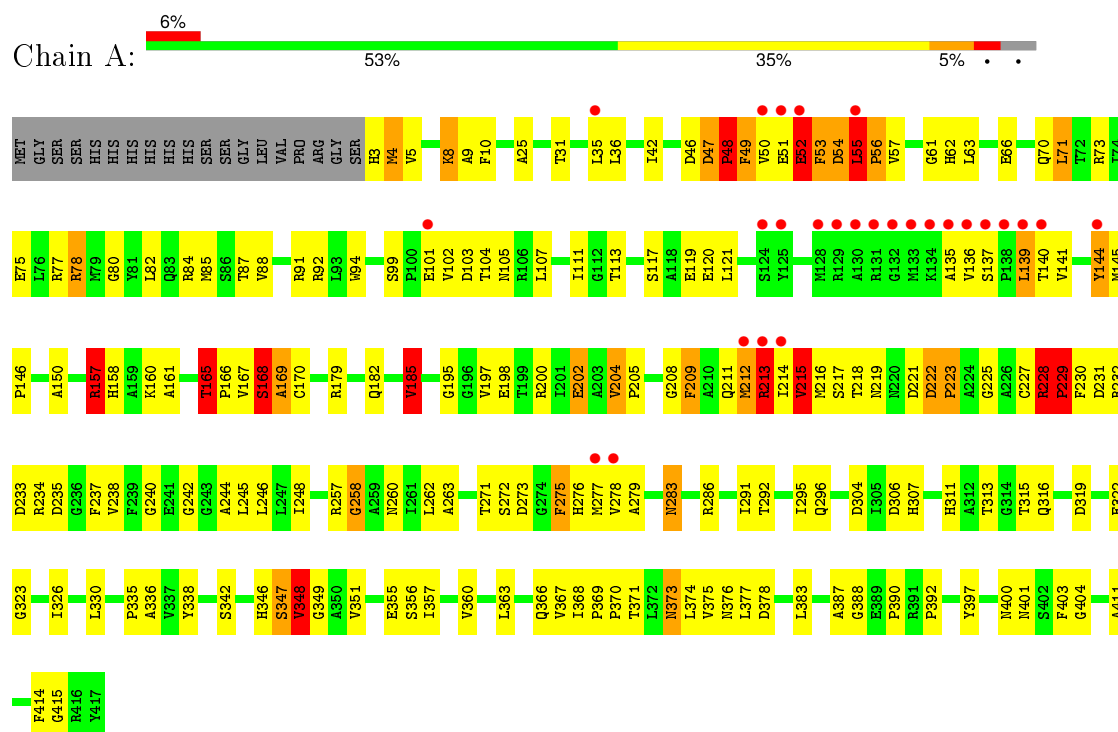
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	104	Total O 104 104	0	0
2	B	125	Total O 125 125	0	0

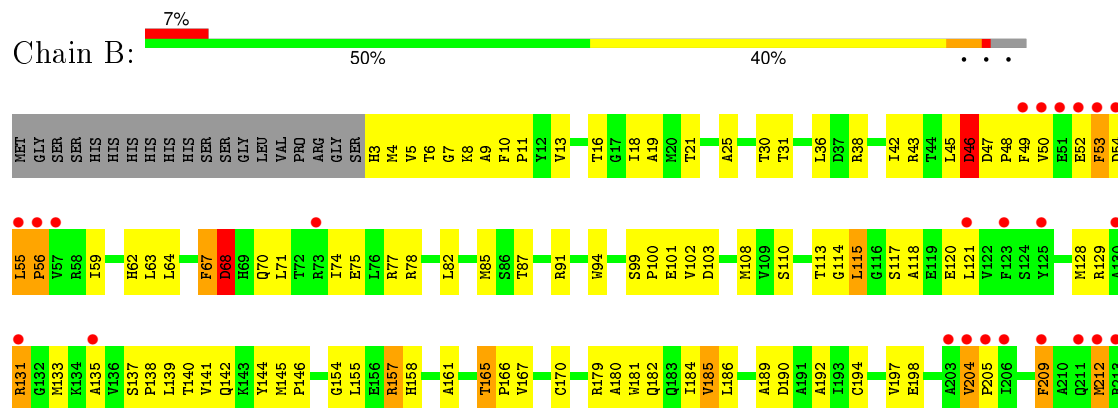
### 3 Residue-property plots [i](#)

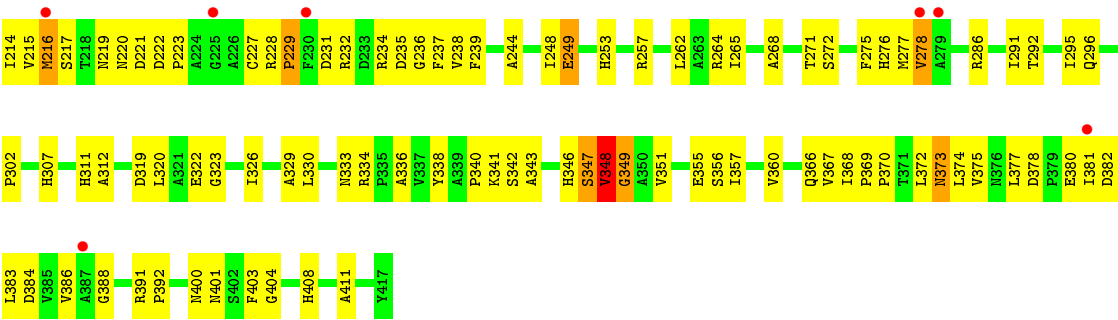
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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: 3-oxoacyl-[acyl-carrier-protein] synthase 2



- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 2





## 4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	198.68 Å   198.68 Å   71.83 Å 90.00°   90.00°   120.00°	Depositor
Resolution (Å)	50.00 – 2.40 37.55 – 2.40	Depositor EDS
% Data completeness (in resolution range)	91.4 (50.00-2.40) 93.7 (37.55-2.40)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.55 (at 2.39 Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.177 , 0.232 0.184 , 0.234	Depositor DCC
$R_{free}$ test set	1911 reflections (5.19%)	DCC
Wilson B-factor (Å <sup>2</sup> )	53.6	Xtriage
Anisotropy	0.247	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.408 for h,-h-k,-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.21$	Xtriage
Outliers	0 of 38767 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	6421	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 3.21% 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

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	0.67	3/3153 (0.1%)	1.20	35/4281 (0.8%)
1	B	0.54	0/3153	0.92	15/4281 (0.4%)
All	All	0.61	3/6306 (0.0%)	1.07	50/8562 (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	2	14
1	B	1	4
All	All	3	18

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	165	THR	C-N	5.30	1.44	1.34
1	A	222	ASP	C-N	5.09	1.44	1.34
1	A	56	PRO	N-CD	5.07	1.54	1.47

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	55	LEU	C-N-CD	11.37	152.28	128.40
1	A	228	ARG	C-N-CD	11.31	152.16	128.40
1	A	165	THR	C-N-CD	11.20	151.92	128.40
1	A	222	ASP	C-N-CD	10.93	151.35	128.40
1	A	204	VAL	C-N-CD	10.53	150.52	128.40
1	A	47	ASP	C-N-CD	10.52	150.50	128.40
1	B	165	THR	C-N-CD	10.47	150.39	128.40
1	A	78	ARG	NE-CZ-NH1	10.05	125.33	120.30
1	A	57	VAL	O-C-N	-8.68	108.81	122.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	46	ASP	CB-CG-OD2	8.59	126.03	118.30
1	A	229	PRO	CA-N-CD	-8.51	99.58	111.50
1	A	55	LEU	C-N-CD	8.06	145.32	128.40
1	A	222	ASP	CB-CG-OD2	8.04	125.53	118.30
1	B	67	PHE	CB-CG-CD1	-7.85	115.31	120.80
1	B	56	PRO	CA-N-CD	-7.50	100.99	111.50
1	A	47	ASP	CB-CG-OD1	7.49	125.04	118.30
1	B	54	ASP	CB-CG-OD2	7.46	125.02	118.30
1	B	373	ASN	O-C-N	-7.27	111.07	122.70
1	B	46	ASP	CB-CG-OD2	7.23	124.81	118.30
1	B	158	HIS	O-C-N	-7.13	111.29	122.70
1	A	229	PRO	O-C-N	-7.09	111.36	122.70
1	A	275	PHE	CB-CG-CD2	-7.01	115.90	120.80
1	A	56	PRO	CA-N-CD	-6.93	101.79	111.50
1	A	223	PRO	CA-N-CD	-6.48	102.43	111.50
1	A	166	PRO	CA-N-CD	-6.46	102.46	111.50
1	A	9	ALA	O-C-N	6.39	132.93	122.70
1	A	275	PHE	CB-CG-CD1	6.33	125.23	120.80
1	A	78	ARG	CD-NE-CZ	6.31	132.43	123.60
1	A	48	PRO	CA-N-CD	-6.29	102.70	111.50
1	B	166	PRO	CA-N-CD	-6.25	102.75	111.50
1	A	230	PHE	CB-CG-CD1	6.21	125.14	120.80
1	A	205	PRO	CA-N-CD	-6.14	102.90	111.50
1	A	53	PHE	CB-CG-CD2	6.09	125.06	120.80
1	B	68	ASP	CB-CG-OD1	6.08	123.78	118.30
1	A	9	ALA	CA-C-N	-6.00	104.01	117.20
1	A	53	PHE	O-C-N	-5.92	113.23	122.70
1	A	53	PHE	CA-C-O	5.86	132.41	120.10
1	A	185	VAL	CA-CB-CG1	5.82	119.63	110.90
1	B	165	THR	CA-CB-CG2	5.54	120.15	112.40
1	B	53	PHE	C-N-CA	5.32	134.99	121.70
1	A	215	VAL	CA-CB-CG2	5.30	118.86	110.90
1	B	346	HIS	C-N-CA	5.30	134.95	121.70
1	A	221	ASP	CB-CG-OD2	5.29	123.06	118.30
1	A	248	ILE	CA-CB-CG2	5.28	121.47	110.90
1	A	57	VAL	CA-C-N	5.28	128.82	117.20
1	A	51	GLU	C-N-CA	5.19	134.68	121.70
1	A	78	ARG	O-C-N	-5.18	114.41	122.70
1	B	53	PHE	N-CA-CB	5.09	119.76	110.60
1	A	169	ALA	O-C-N	-5.08	114.57	122.70
1	B	347	SER	C-N-CA	5.06	134.35	121.70

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	A	53	PHE	CA
1	A	54	ASP	CA
1	B	53	PHE	CA

All (18) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	157	ARG	Mainchain
1	A	165	THR	Mainchain
1	A	185	VAL	Mainchain
1	A	202	GLU	Mainchain
1	A	213	ARG	Mainchain
1	A	228	ARG	Mainchain
1	A	229	PRO	Mainchain
1	A	283	ASN	Mainchain
1	A	348	VAL	Mainchain
1	A	373	ASN	Mainchain
1	A	388	GLY	Mainchain
1	A	48	PRO	Mainchain
1	A	52	GLU	Mainchain
1	A	55	LEU	Mainchain
1	B	249	GLU	Mainchain
1	B	348	VAL	Mainchain
1	B	349	GLY	Mainchain
1	B	67	PHE	Mainchain

## 5.2 Too-close contacts [i](#)

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	3096	0	3064	168	0
1	B	3096	0	3063	176	0
2	A	104	0	0	0	0
2	B	125	0	0	4	0
All	All	6421	0	6127	327	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 27.

All (327) 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:10:PHE:HB3	1:B:185:VAL:HG22	1.25	1.09
1:A:10:PHE:HB3	1:A:185:VAL:HG22	1.31	1.07
1:A:229:PRO:HD2	1:A:342:SER:HB3	1.37	1.05
1:A:146:PRO:HG2	1:B:167:VAL:HG11	1.42	0.99
1:A:167:VAL:HG11	1:B:146:PRO:HG2	1.45	0.97
1:B:180:ALA:HB1	1:B:248:ILE:HD11	1.49	0.95
1:B:180:ALA:CB	1:B:248:ILE:HD11	1.95	0.95
1:A:214:ILE:HG22	1:A:237:PHE:CD2	2.03	0.93
1:A:229:PRO:CD	1:A:342:SER:HB3	1.99	0.91
1:B:10:PHE:HB3	1:B:185:VAL:CG2	2.01	0.91
1:B:117:SER:HB2	1:B:144:TYR:HA	1.52	0.90
1:A:36:LEU:HD23	1:A:369:PRO:HB3	1.54	0.88
1:B:320:LEU:HA	1:B:381:ILE:HD11	1.56	0.88
1:A:367:VAL:HG22	1:A:392:PRO:HB3	1.58	0.85
1:B:312:ALA:HB1	1:B:319:ASP:OD1	1.77	0.84
1:A:82:LEU:HD22	1:A:197:VAL:HG12	1.61	0.82
1:A:71:LEU:HB2	1:A:75:GLU:OE2	1.81	0.81
1:B:170:CYS:HB2	1:B:404:GLY:HA3	1.62	0.80
1:B:45:LEU:HD23	1:B:50:VAL:HG11	1.64	0.79
1:B:82:LEU:HD22	1:B:197:VAL:HG12	1.65	0.78
1:A:212:MET:HE1	1:B:139:LEU:HD11	1.66	0.78
1:A:228:ARG:HH12	1:A:233:ASP:HB2	1.50	0.76
1:A:260:ASN:O	1:A:262:LEU:HD12	1.86	0.76
1:B:271:THR:HG22	1:B:272:SER:N	2.01	0.75
1:A:214:ILE:HG22	1:A:237:PHE:HD2	1.51	0.74
1:A:78:ARG:HD2	1:A:139:LEU:HD23	1.67	0.74
1:A:229:PRO:HD2	1:A:342:SER:CB	2.15	0.74
1:A:10:PHE:HB3	1:A:185:VAL:CG2	2.16	0.74
1:B:271:THR:HG22	1:B:272:SER:H	1.50	0.74
1:A:271:THR:HG22	1:A:272:SER:N	2.02	0.74
1:A:212:MET:CE	1:B:139:LEU:HD11	2.17	0.73
1:B:137:SER:HB3	1:B:140:THR:HG23	1.69	0.73
1:B:170:CYS:HB2	1:B:404:GLY:CA	2.19	0.72
1:A:104:THR:HB	1:A:158:HIS:O	1.88	0.72
1:A:158:HIS:HB3	2:B:436:HOH:O	1.89	0.72
1:A:311:HIS:HB2	1:A:401:ASN:O	1.89	0.72
1:B:307:HIS:HD2	1:B:336:ALA:O	1.71	0.72
1:A:214:ILE:HG22	1:A:237:PHE:CE2	2.25	0.72
1:A:78:ARG:HD2	1:A:139:LEU:CD2	2.19	0.72
1:A:52:GLU:HB3	1:A:53:PHE:CD2	2.25	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:ILE:O	1:A:165:THR:HG23	1.89	0.71
1:B:180:ALA:HB3	1:B:248:ILE:HD11	1.74	0.69
1:A:94:TRP:CD1	1:A:99:SER:HA	2.28	0.68
1:A:228:ARG:NH1	1:A:233:ASP:HB2	2.08	0.68
1:A:215:VAL:HG22	1:A:237:PHE:CE2	2.27	0.68
1:B:186:LEU:O	1:B:186:LEU:HD23	1.93	0.67
1:A:374:LEU:HD23	1:A:387:ALA:HB2	1.74	0.67
1:A:25:ALA:HB3	1:A:31:THR:OG1	1.95	0.67
1:A:102:VAL:HG12	1:A:103:ASP:N	2.10	0.67
1:B:3:HIS:ND1	1:B:8:LYS:HD2	2.09	0.67
1:A:311:HIS:CD2	1:A:403:PHE:H	2.13	0.66
1:B:216:MET:HB2	1:B:235:ASP:O	1.94	0.66
1:A:351:VAL:O	1:A:355:GLU:HG3	1.96	0.66
1:B:340:PRO:HG2	1:B:355:GLU:OE2	1.97	0.65
1:B:198:GLU:OE1	1:B:348:VAL:HG23	1.97	0.65
1:A:214:ILE:HG23	1:A:315:THR:HG21	1.79	0.65
1:B:338:TYR:CZ	1:B:369:PRO:HG2	2.32	0.64
1:B:228:ARG:HG2	1:B:373:ASN:HB3	1.79	0.64
1:B:214:ILE:C	1:B:216:MET:H	2.01	0.64
1:A:78:ARG:NH1	1:A:139:LEU:HD11	2.13	0.64
1:A:145:MET:HE1	1:B:115:LEU:HB3	1.79	0.63
1:B:85:MET:SD	1:B:197:VAL:HG13	2.38	0.63
1:B:141:VAL:O	1:B:145:MET:HG2	1.98	0.63
1:A:144:TYR:CE2	1:A:145:MET:HE2	2.34	0.63
1:A:3:HIS:HB3	1:A:8:LYS:HD2	1.80	0.62
1:A:78:ARG:NH1	1:A:139:LEU:HD21	2.13	0.62
1:B:320:LEU:HD12	1:B:381:ILE:HD11	1.80	0.62
1:B:351:VAL:O	1:B:355:GLU:HG3	1.98	0.62
1:A:137:SER:HB3	1:A:140:THR:HG23	1.80	0.62
1:B:128:MET:HB3	1:B:133:MET:HE1	1.81	0.62
1:B:367:VAL:HG22	1:B:392:PRO:HB3	1.82	0.61
1:A:85:MET:SD	1:A:197:VAL:HG13	2.40	0.61
1:A:229:PRO:HG2	1:A:371:THR:CG2	2.31	0.61
1:B:209:PHE:HD1	1:B:214:ILE:HD11	1.65	0.61
1:B:59:ILE:HG21	1:B:220:ASN:HA	1.82	0.61
1:A:375:VAL:HG23	1:A:376:ASN:N	2.15	0.61
1:A:48:PRO:C	1:A:50:VAL:H	2.05	0.60
1:B:117:SER:CB	1:B:144:TYR:HA	2.30	0.60
1:A:368:ILE:O	1:A:390:PRO:HA	2.00	0.60
1:B:322:GLU:O	1:B:326:ILE:HG12	2.02	0.60
1:A:277:MET:HB3	1:B:155:LEU:HD11	1.82	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:146:PRO:O	1:B:165:THR:HG21	2.01	0.59
1:A:271:THR:HG22	1:A:272:SER:H	1.65	0.59
1:A:322:GLU:O	1:A:326:ILE:HG12	2.03	0.59
1:A:144:TYR:CD2	1:A:145:MET:HE2	2.38	0.59
1:B:343:ALA:HB2	1:B:372:LEU:HD13	1.84	0.59
1:B:94:TRP:O	1:B:99:SER:HA	2.03	0.59
1:B:102:VAL:HG12	1:B:103:ASP:N	2.17	0.59
1:A:48:PRO:HG2	1:A:49:PHE:H	1.67	0.59
1:B:184:ILE:HD13	1:B:189:ALA:HB3	1.85	0.58
1:B:13:VAL:O	1:B:264:ARG:HG3	2.01	0.58
1:B:209:PHE:CD1	1:B:214:ILE:HD11	2.38	0.58
1:A:78:ARG:HH11	1:A:139:LEU:HD21	1.68	0.58
1:A:113:THR:HG23	1:A:197:VAL:O	2.02	0.58
1:B:129:ARG:NH1	2:B:434:HOH:O	2.35	0.58
1:A:119:GLU:HB3	1:A:202:GLU:OE1	2.04	0.58
1:B:311:HIS:HB2	1:B:401:ASN:O	2.03	0.58
1:A:217:SER:C	1:A:219:ASN:H	2.07	0.57
1:A:144:TYR:HE2	1:A:145:MET:CE	2.17	0.57
1:A:42:ILE:HD13	1:A:238:VAL:HG11	1.87	0.57
1:B:120:GLU:CG	1:B:144:TYR:HB3	2.35	0.56
1:B:42:ILE:HD13	1:B:238:VAL:HG11	1.87	0.56
1:B:8:LYS:HG3	1:B:9:ALA:H	1.71	0.56
1:B:128:MET:HB3	1:B:133:MET:CE	2.36	0.56
1:B:179:ARG:HH11	1:B:182:GLN:HE21	1.54	0.56
1:B:71:LEU:HB3	1:B:75:GLU:OE2	2.05	0.56
1:A:70:GLN:HE22	1:A:92:ARG:HH21	1.54	0.56
1:B:215:VAL:O	1:B:217:SER:N	2.38	0.56
1:A:198:GLU:HG2	1:A:348:VAL:HG13	1.88	0.56
1:B:49:PHE:CD1	1:B:50:VAL:HG23	2.41	0.56
1:A:52:GLU:HB3	1:A:53:PHE:HD2	1.67	0.56
1:B:234:ARG:HH12	1:B:378:ASP:HB2	1.70	0.56
1:B:212:MET:HE3	2:B:521:HOH:O	2.06	0.55
1:A:179:ARG:HH11	1:A:182:GLN:HE21	1.53	0.55
1:A:228:ARG:O	1:A:229:PRO:C	2.42	0.55
1:A:139:LEU:HD22	1:A:139:LEU:H	1.71	0.55
1:B:36:LEU:HD23	1:B:369:PRO:HB3	1.87	0.55
1:A:366:GLN:O	1:A:392:PRO:HA	2.06	0.55
1:A:271:THR:CG2	1:A:272:SER:N	2.67	0.55
1:B:74:ILE:O	1:B:78:ARG:HG3	2.07	0.55
1:A:216:MET:HB3	1:A:235:ASP:O	2.06	0.55
1:A:375:VAL:HG23	1:A:376:ASN:H	1.72	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:VAL:C	1:B:217:SER:H	2.10	0.55
1:B:231:ASP:OD2	1:B:232:ARG:N	2.40	0.55
1:A:213:ARG:HA	1:A:216:MET:CE	2.37	0.55
1:B:198:GLU:HG2	1:B:347:SER:O	2.06	0.55
1:A:277:MET:HB3	1:B:155:LEU:CD1	2.37	0.54
1:A:363:LEU:HD11	1:A:414:PHE:O	2.07	0.54
1:A:144:TYR:CE2	1:A:145:MET:CE	2.91	0.54
1:B:214:ILE:HG13	1:B:215:VAL:N	2.23	0.54
1:B:21:THR:HG23	1:B:21:THR:O	2.07	0.54
1:B:220:ASN:C	1:B:222:ASP:H	2.11	0.54
1:B:113:THR:HG22	1:B:114:GLY:H	1.72	0.54
1:A:55:LEU:HD23	1:A:56:PRO:HD3	1.90	0.53
1:A:215:VAL:HG22	1:A:237:PHE:CZ	2.43	0.53
1:B:275:PHE:CD1	1:B:276:HIS:HB2	2.43	0.53
1:A:102:VAL:HG12	1:A:103:ASP:H	1.74	0.53
1:B:320:LEU:HD12	1:B:381:ILE:CD1	2.38	0.53
1:B:113:THR:HG22	1:B:114:GLY:N	2.23	0.53
1:A:271:THR:CG2	1:A:272:SER:H	2.21	0.53
1:A:338:TYR:CZ	1:A:369:PRO:HG2	2.44	0.53
1:A:63:LEU:HD21	1:A:242:GLY:HA2	1.90	0.53
1:B:5:VAL:HG12	1:B:7:GLY:H	1.73	0.53
1:A:107:LEU:O	1:A:161:ALA:HB3	2.09	0.53
1:A:276:HIS:HB3	1:A:279:ALA:O	2.08	0.53
1:B:271:THR:CG2	1:B:272:SER:N	2.72	0.52
1:B:205:PRO:O	1:B:209:PHE:HB2	2.10	0.52
1:B:11:PRO:HD2	1:B:185:VAL:HG22	1.91	0.52
1:A:278:VAL:HG21	1:B:139:LEU:CD1	2.40	0.52
1:B:68:ASP:C	1:B:70:GLN:H	2.13	0.52
1:A:146:PRO:CG	1:B:167:VAL:HG11	2.29	0.51
1:A:160:LYS:HD2	2:B:436:HOH:O	2.10	0.51
1:A:271:THR:HG21	1:A:286:ARG:HB3	1.92	0.51
1:B:291:ILE:O	1:B:295:ILE:HG13	2.10	0.51
1:A:55:LEU:HD23	1:A:56:PRO:CD	2.40	0.51
1:A:307:HIS:CD2	1:A:368:ILE:HD13	2.45	0.51
1:B:262:LEU:HD12	1:B:262:LEU:N	2.26	0.51
1:A:121:LEU:HD13	1:B:118:ALA:HB1	1.93	0.51
1:A:78:ARG:CD	1:A:139:LEU:HD21	2.42	0.50
1:B:204:VAL:N	1:B:205:PRO:HD2	2.26	0.50
1:B:87:THR:O	1:B:91:ARG:HG3	2.12	0.50
1:A:87:THR:O	1:A:91:ARG:HG3	2.12	0.50
1:B:48:PRO:O	1:B:52:GLU:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:135:ALA:O	1:A:136:VAL:HG13	2.11	0.50
1:A:307:HIS:HD2	1:A:336:ALA:O	1.94	0.49
1:A:291:ILE:O	1:A:295:ILE:HG13	2.11	0.49
1:B:100:PRO:HB3	1:B:257:ARG:NH1	2.28	0.49
1:B:271:THR:HG21	1:B:286:ARG:HB3	1.93	0.49
1:B:4:MET:HA	1:B:9:ALA:CB	2.42	0.49
1:B:338:TYR:CE2	1:B:369:PRO:HG2	2.47	0.49
1:B:370:PRO:HB3	1:B:386:VAL:HG12	1.94	0.49
1:A:73:ARG:HG3	1:A:77:ARG:HH11	1.78	0.49
1:A:397:TYR:HD1	1:A:415:GLY:HA2	1.77	0.49
1:B:271:THR:CG2	1:B:272:SER:H	2.21	0.49
1:A:4:MET:HB2	1:A:10:PHE:CZ	2.48	0.49
1:A:370:PRO:HD3	1:A:390:PRO:HG3	1.95	0.49
1:B:214:ILE:HD12	1:B:237:PHE:HE2	1.77	0.49
1:A:35:LEU:HD22	1:A:338:TYR:OH	2.13	0.48
1:B:227:CYS:HB2	1:B:238:VAL:HG23	1.95	0.48
1:A:102:VAL:CG1	1:A:103:ASP:N	2.75	0.48
1:B:219:ASN:ND2	1:B:222:ASP:HB3	2.28	0.48
1:A:119:GLU:HB3	1:A:202:GLU:CD	2.33	0.48
1:A:229:PRO:O	1:A:319:ASP:OD1	2.32	0.48
1:B:25:ALA:HB3	1:B:31:THR:OG1	2.13	0.48
1:B:46:ASP:O	1:B:47:ASP:CG	2.52	0.48
1:B:229:PRO:HG2	1:B:342:SER:HB3	1.96	0.48
1:A:215:VAL:O	1:A:217:SER:N	2.47	0.48
1:B:214:ILE:C	1:B:216:MET:N	2.67	0.48
1:A:323:GLY:HA2	1:A:383:LEU:HD11	1.94	0.48
1:A:73:ARG:CG	1:A:77:ARG:HH11	2.26	0.48
1:A:52:GLU:CB	1:A:53:PHE:HD2	2.27	0.48
1:A:214:ILE:C	1:A:216:MET:H	2.17	0.48
1:B:154:GLY:O	1:B:157:ARG:O	2.32	0.48
1:B:333:ASN:O	1:B:334:ARG:HG2	2.14	0.47
1:B:244:ALA:HB1	1:B:357:ILE:HD12	1.96	0.47
1:A:227:CYS:SG	1:A:342:SER:HA	2.54	0.47
1:A:347:SER:HB3	1:A:351:VAL:N	2.29	0.47
1:B:43:ARG:HH22	1:B:64:LEU:HD21	1.79	0.47
1:A:168:SER:O	1:A:169:ALA:C	2.49	0.47
1:A:348:VAL:O	1:A:351:VAL:HG12	2.15	0.47
1:B:131:ARG:HB3	1:B:135:ALA:HB3	1.96	0.47
1:A:229:PRO:HG2	1:A:371:THR:HG21	1.96	0.47
1:B:55:LEU:O	1:B:56:PRO:C	2.50	0.47
1:B:215:VAL:C	1:B:217:SER:N	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:ARG:NH1	1:A:182:GLN:HE21	2.12	0.47
1:B:5:VAL:CG1	1:B:6:THR:N	2.76	0.47
1:A:291:ILE:HD13	1:A:411:ALA:HB2	1.97	0.47
1:A:36:LEU:HD23	1:A:369:PRO:CB	2.37	0.47
1:A:356:SER:O	1:A:360:VAL:HG23	2.15	0.47
1:A:144:TYR:HE2	1:A:145:MET:HE3	1.79	0.47
1:A:78:ARG:CD	1:A:139:LEU:CD2	2.89	0.47
1:A:271:THR:CG2	1:A:286:ARG:HB3	2.45	0.47
1:B:198:GLU:CD	1:B:348:VAL:HG23	2.35	0.46
1:B:403:PHE:HA	1:B:408:HIS:O	2.15	0.46
1:A:141:VAL:HG11	1:B:209:PHE:HE2	1.80	0.46
1:B:374:LEU:HD11	1:B:377:LEU:HB2	1.97	0.46
1:A:80:GLY:O	1:A:84:ARG:HG3	2.16	0.46
1:A:222:ASP:O	1:A:223:PRO:C	2.47	0.46
1:A:209:PHE:HB3	1:A:215:VAL:CG2	2.46	0.46
1:A:94:TRP:CZ3	1:A:157:ARG:HD3	2.51	0.46
1:B:347:SER:HB2	1:B:351:VAL:N	2.31	0.46
1:A:5:VAL:HB	1:A:8:LYS:HG2	1.96	0.46
1:B:108:MET:HB3	1:B:161:ALA:HB3	1.97	0.46
1:A:94:TRP:CE3	1:A:157:ARG:CD	2.98	0.46
1:B:348:VAL:HG23	1:B:349:GLY:H	1.80	0.46
1:B:128:MET:HB3	1:B:133:MET:SD	2.56	0.46
1:B:356:SER:O	1:B:360:VAL:HG23	2.17	0.45
1:A:212:MET:SD	1:A:278:VAL:HG11	2.55	0.45
1:B:121:LEU:HD21	1:B:144:TYR:CE1	2.51	0.45
1:B:50:VAL:HA	1:B:55:LEU:HD23	1.98	0.45
1:A:400:ASN:HD22	1:A:401:ASN:N	2.14	0.45
1:A:198:GLU:OE1	1:A:349:GLY:HA3	2.16	0.45
1:B:179:ARG:NH1	1:B:182:GLN:HE21	2.14	0.45
1:B:216:MET:O	1:B:235:ASP:HB2	2.16	0.45
1:A:204:VAL:HG22	1:B:128:MET:HE2	1.98	0.45
1:B:108:MET:CG	1:B:192:ALA:HB2	2.46	0.45
1:A:195:GLY:HA3	1:A:244:ALA:O	2.17	0.45
1:A:400:ASN:ND2	1:A:401:ASN:N	2.65	0.45
1:B:320:LEU:HD11	1:B:380:GLU:HG3	1.98	0.45
1:B:341:LYS:HE3	1:B:351:VAL:HG21	1.98	0.45
1:B:100:PRO:HB3	1:B:257:ARG:CZ	2.47	0.45
1:B:190:ASP:HB3	1:B:253:HIS:CD2	2.52	0.44
1:A:273:ASP:C	1:A:275:PHE:H	2.20	0.44
1:A:263:ALA:CB	1:A:360:VAL:HG13	2.47	0.44
1:B:170:CYS:HB2	1:B:404:GLY:HA2	1.97	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:82:LEU:HD22	1:B:197:VAL:CG1	2.43	0.44
1:B:307:HIS:CD2	1:B:336:ALA:O	2.61	0.44
1:A:212:MET:HE3	1:B:139:LEU:HD11	1.97	0.44
1:B:102:VAL:HG12	1:B:103:ASP:H	1.79	0.44
1:B:198:GLU:HG2	1:B:348:VAL:HG22	1.99	0.44
1:A:245:LEU:C	1:A:246:LEU:HD12	2.38	0.44
1:B:323:GLY:HA2	1:B:383:LEU:HD11	2.00	0.44
1:A:82:LEU:HD22	1:A:197:VAL:CG1	2.41	0.43
1:B:366:GLN:O	1:B:392:PRO:HA	2.18	0.43
1:B:102:VAL:CG1	1:B:103:ASP:N	2.80	0.43
1:B:198:GLU:HG2	1:B:348:VAL:CG2	2.48	0.43
1:A:144:TYR:HD2	1:A:144:TYR:C	2.21	0.43
1:A:170:CYS:HB2	1:A:404:GLY:HA2	1.99	0.43
1:B:367:VAL:HA	1:B:392:PRO:HA	2.00	0.43
1:B:302:PRO:O	1:B:330:LEU:HD22	2.18	0.43
1:A:291:ILE:HD13	1:A:411:ALA:CB	2.49	0.43
1:A:273:ASP:C	1:A:275:PHE:N	2.71	0.43
1:A:158:HIS:O	1:A:160:LYS:HD3	2.18	0.43
1:A:102:VAL:CG1	1:A:103:ASP:H	2.32	0.43
1:A:225:GLY:HA2	1:A:373:ASN:ND2	2.33	0.43
1:A:212:MET:HE3	1:B:139:LEU:CD1	2.48	0.43
1:B:275:PHE:CD1	1:B:276:HIS:N	2.86	0.43
1:B:292:THR:HG22	1:B:296:GLN:HE21	1.84	0.43
1:B:16:THR:HG21	1:B:249:GLU:CD	2.39	0.43
1:A:55:LEU:CD2	1:A:56:PRO:HD2	2.48	0.43
1:A:244:ALA:HB1	1:A:357:ILE:CD1	2.49	0.43
1:B:292:THR:O	1:B:296:GLN:HG3	2.19	0.43
1:B:38:ARG:HD2	1:B:388:GLY:O	2.19	0.43
1:B:276:HIS:CD2	1:B:277:MET:H	2.37	0.43
1:B:334:ARG:NH1	1:B:382:ASP:OD2	2.51	0.43
1:B:268:ALA:HA	1:B:411:ALA:O	2.19	0.43
1:A:144:TYR:CD2	1:A:144:TYR:C	2.91	0.42
1:B:370:PRO:O	1:B:372:LEU:HD12	2.19	0.42
1:B:18:ILE:CG2	1:B:19:ALA:N	2.83	0.42
1:A:231:ASP:HB2	1:A:374:LEU:HD12	2.01	0.42
1:B:63:LEU:HB3	1:B:64:LEU:H	1.70	0.42
1:B:108:MET:HG2	1:B:192:ALA:HB2	2.01	0.42
1:B:307:HIS:CD2	1:B:368:ILE:HD13	2.54	0.42
1:A:304:ASP:HB3	1:A:397:TYR:HD2	1.83	0.42
1:B:110:SER:O	1:B:194:CYS:HA	2.19	0.42
1:B:139:LEU:N	1:B:139:LEU:HD22	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:400:ASN:ND2	1:B:401:ASN:N	2.68	0.42
1:A:208:GLY:HA2	1:A:211:GLN:HE21	1.85	0.42
1:B:49:PHE:HD1	1:B:50:VAL:HG23	1.85	0.42
1:B:343:ALA:CB	1:B:372:LEU:HD22	2.50	0.42
1:B:25:ALA:HB1	1:B:30:THR:HB	2.02	0.42
1:B:244:ALA:HB1	1:B:357:ILE:CD1	2.50	0.42
1:B:4:MET:HA	1:B:9:ALA:HB2	2.02	0.42
1:B:142:GLN:HA	1:B:145:MET:HG3	2.01	0.42
1:A:94:TRP:CD2	1:A:157:ARG:NE	2.88	0.42
1:A:48:PRO:C	1:A:50:VAL:N	2.73	0.42
1:A:84:ARG:O	1:A:88:VAL:HG23	2.19	0.42
1:A:330:LEU:HD13	1:A:335:PRO:HD3	2.02	0.42
1:A:160:LYS:HB3	1:B:286:ARG:HG3	2.02	0.41
1:B:400:ASN:HD22	1:B:401:ASN:N	2.17	0.41
1:B:120:GLU:HG2	1:B:144:TYR:HB3	2.02	0.41
1:A:111:ILE:HD12	1:A:150:ALA:HA	2.02	0.41
1:A:257:ARG:O	1:A:258:GLY:C	2.56	0.41
1:B:217:SER:HB2	1:B:236:GLY:C	2.40	0.41
1:A:347:SER:HB3	1:A:351:VAL:CA	2.50	0.41
1:B:5:VAL:HG12	1:B:6:THR:N	2.33	0.41
1:B:384:ASP:CG	1:B:391:ARG:HH12	2.23	0.41
1:B:21:THR:CG2	1:B:21:THR:O	2.68	0.41
1:B:291:ILE:HB	1:B:329:ALA:CB	2.51	0.41
1:A:105:ASN:OD1	1:A:160:LYS:HE3	2.20	0.41
1:B:59:ILE:CG2	1:B:220:ASN:HA	2.48	0.41
1:A:61:GLY:O	1:A:240:GLY:HA2	2.20	0.41
1:A:313:THR:HG22	1:A:346:HIS:HD2	1.85	0.41
1:B:137:SER:HA	1:B:138:PRO:HD3	1.92	0.41
1:B:220:ASN:O	1:B:222:ASP:N	2.54	0.41
1:A:66:GLU:HA	1:A:66:GLU:OE2	2.21	0.41
1:B:212:MET:CE	1:B:278:VAL:HG21	2.51	0.40
1:A:244:ALA:HB1	1:A:357:ILE:HD12	2.02	0.40
1:A:377:LEU:O	1:A:378:ASP:C	2.59	0.40
1:A:278:VAL:HG21	1:B:139:LEU:HD11	2.02	0.40
1:A:234:ARG:HG3	1:A:316:GLN:HE22	1.86	0.40
1:B:231:ASP:OD1	1:B:375:VAL:HG22	2.21	0.40
1:A:313:THR:CG2	1:A:346:HIS:HD2	2.34	0.40
1:A:232:ARG:HB2	1:A:378:ASP:HA	2.03	0.40
1:A:292:THR:O	1:A:296:GLN:HG3	2.22	0.40
1:A:121:LEU:CD1	1:B:118:ALA:HB1	2.52	0.40
1:B:181:TRP:HB2	1:B:265:ILE:HD13	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	413/434 (95%)	363 (88%)	38 (9%)	12 (3%)	6	5
1	B	413/434 (95%)	362 (88%)	44 (11%)	7 (2%)	11	14
All	All	826/868 (95%)	725 (88%)	82 (10%)	19 (2%)	8	8

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	49	PHE
1	A	212	MET
1	A	229	PRO
1	A	54	ASP
1	A	117	SER
1	A	348	VAL
1	B	212	MET
1	B	216	MET
1	B	221	ASP
1	B	278	VAL
1	B	348	VAL
1	A	168	SER
1	A	213	ARG
1	A	218	THR
1	B	223	PRO
1	A	215	VAL
1	A	48	PRO
1	A	258	GLY
1	B	229	PRO

### 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	314/330 (95%)	294 (94%)	20 (6%)	22	34
1	B	314/330 (95%)	301 (96%)	13 (4%)	37	57
All	All	628/660 (95%)	595 (95%)	33 (5%)	28	44

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	MET
1	A	8	LYS
1	A	47	ASP
1	A	52	GLU
1	A	54	ASP
1	A	62	HIS
1	A	71	LEU
1	A	101	GLU
1	A	120	GLU
1	A	139	LEU
1	A	144	TYR
1	A	157	ARG
1	A	168	SER
1	A	185	VAL
1	A	200	ARG
1	A	209	PHE
1	A	228	ARG
1	A	283	ASN
1	A	306	ASP
1	A	347	SER
1	B	46	ASP
1	B	53	PHE
1	B	62	HIS
1	B	68	ASP
1	B	77	ARG
1	B	101	GLU
1	B	115	LEU

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Mol	Chain	Res	Type
1	B	131	ARG
1	B	157	ARG
1	B	185	VAL
1	B	204	VAL
1	B	209	PHE
1	B	239	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	GLN
1	A	70	GLN
1	A	182	GLN
1	A	211	GLN
1	A	296	GLN
1	A	307	HIS
1	A	316	GLN
1	A	327	ASN
1	A	346	HIS
1	A	400	ASN
1	B	39	GLN
1	B	70	GLN
1	B	96	ASN
1	B	182	GLN
1	B	211	GLN
1	B	276	HIS
1	B	296	GLN
1	B	307	HIS
1	B	316	GLN
1	B	327	ASN
1	B	400	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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	415/434 (95%)	0.35	27 (6%)	22 22	19, 53, 76, 87	0
1	B	415/434 (95%)	0.36	31 (7%)	17 17	18, 53, 76, 84	0
All	All	830/868 (95%)	0.36	58 (6%)	19 19	18, 53, 76, 87	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	132	GLY	7.5
1	A	135	ALA	5.6
1	A	214	ILE	5.4
1	A	133	MET	5.0
1	A	131	ARG	4.6
1	B	135	ALA	4.6
1	A	136	VAL	4.5
1	B	50	VAL	4.5
1	A	144	TYR	4.4
1	A	128	MET	4.3
1	A	213	ARG	4.2
1	A	134	LYS	3.9
1	B	211	GLN	3.9
1	B	123	PHE	3.9
1	B	121	LEU	3.6
1	B	278	VAL	3.6
1	A	125	TYR	3.5
1	A	51	GLU	3.5
1	A	140	THR	3.4
1	A	50	VAL	3.4
1	A	138	PRO	3.3
1	B	53	PHE	3.3
1	A	124	SER	3.2
1	B	130	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	279	ALA	3.2
1	A	137	SER	3.1
1	B	51	GLU	3.1
1	B	54	ASP	3.0
1	B	56	PRO	3.0
1	A	139	LEU	2.9
1	B	213	ARG	2.9
1	B	49	PHE	2.9
1	B	125	TYR	2.8
1	B	212	MET	2.8
1	B	55	LEU	2.8
1	A	129	ARG	2.7
1	B	203	ALA	2.7
1	B	206	ILE	2.6
1	B	204	VAL	2.5
1	B	57	VAL	2.5
1	B	73	ARG	2.4
1	A	52	GLU	2.3
1	B	131	ARG	2.3
1	B	205	PRO	2.3
1	A	101	GLU	2.3
1	A	212	MET	2.3
1	B	387	ALA	2.3
1	A	35	LEU	2.3
1	B	230	PHE	2.2
1	A	277	MET	2.2
1	B	52	GLU	2.2
1	B	209	PHE	2.1
1	B	225	GLY	2.1
1	B	216	MET	2.1
1	A	55	LEU	2.1
1	A	130	ALA	2.1
1	B	381	ILE	2.0
1	A	278	VAL	2.0

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

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



### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

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

There are no such residues in this entry.