



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 01:18 AM GMT

PDB ID : 1RXX  
Title : Structure of arginine deiminase  
Authors : Galkin, A.; Kulakova, L.; Sarikaya, E.; Lim, K.; Howard, A.; Herzberg, O.;  
Structure 2 Function Project (S2F)  
Deposited on : 2003-12-18  
Resolution : 2.45 Å(reported)

This is a full wwPDB 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/ValidationPDFNotes.html>

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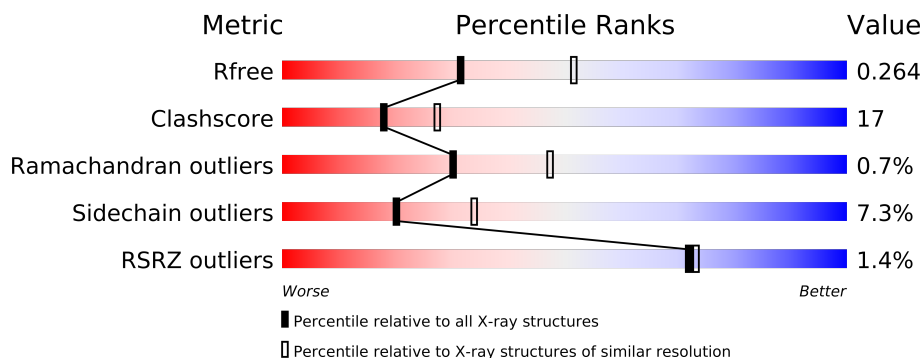
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.45 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))
$R_{free}$	66092	3566 (2.50-2.42)
Clashscore	79885	4471 (2.50-2.42)
Ramachandran outliers	78287	4383 (2.50-2.42)
Sidechain outliers	78261	4385 (2.50-2.42)
RSRZ outliers	66119	3568 (2.50-2.42)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	421	
1	B	421	
1	C	421	
1	D	421	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13187 atoms, of which 0 are hydrogen and 0 are deuterium.

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 Arginine deiminase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	408	Total	C	N	O	S	Se	0	0	0
			3185	2015	553	600	7	10			
1	B	404	Total	C	N	O	S	Se	0	0	0
			3160	2001	549	593	7	10			
1	C	412	Total	C	N	O	S	Se	0	0	0
			3214	2033	557	607	7	10			
1	D	402	Total	C	N	O	S	Se	0	0	0
			3136	1986	543	590	7	10			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	CLONING ARTIFACT	UNP P13981
A	-1	SER	-	CLONING ARTIFACT	UNP P13981
A	0	HIS	-	CLONING ARTIFACT	UNP P13981
A	1	MSE	-	CLONING ARTIFACT	UNP P13981
A	21	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	62	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	72	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	143	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	180	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	229	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	240	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	277	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	316	MSE	MET	MODIFIED RESIDUE	UNP P13981
A	407	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	-2	GLY	-	CLONING ARTIFACT	UNP P13981
B	-1	SER	-	CLONING ARTIFACT	UNP P13981
B	0	HIS	-	CLONING ARTIFACT	UNP P13981
B	1	MSE	-	CLONING ARTIFACT	UNP P13981
B	21	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	62	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	72	MSE	MET	MODIFIED RESIDUE	UNP P13981

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Chain	Residue	Modelled	Actual	Comment	Reference
B	143	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	180	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	229	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	240	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	277	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	316	MSE	MET	MODIFIED RESIDUE	UNP P13981
B	407	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	-2	GLY	-	CLONING ARTIFACT	UNP P13981
C	-1	SER	-	CLONING ARTIFACT	UNP P13981
C	0	HIS	-	CLONING ARTIFACT	UNP P13981
C	1	MSE	-	CLONING ARTIFACT	UNP P13981
C	21	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	62	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	72	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	143	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	180	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	229	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	240	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	277	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	316	MSE	MET	MODIFIED RESIDUE	UNP P13981
C	407	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	-2	GLY	-	CLONING ARTIFACT	UNP P13981
D	-1	SER	-	CLONING ARTIFACT	UNP P13981
D	0	HIS	-	CLONING ARTIFACT	UNP P13981
D	1	MSE	-	CLONING ARTIFACT	UNP P13981
D	21	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	62	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	72	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	143	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	180	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	229	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	240	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	277	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	316	MSE	MET	MODIFIED RESIDUE	UNP P13981
D	407	MSE	MET	MODIFIED RESIDUE	UNP P13981

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	113	Total O 113 113	0	0
2	B	147	Total O 147 147	0	0

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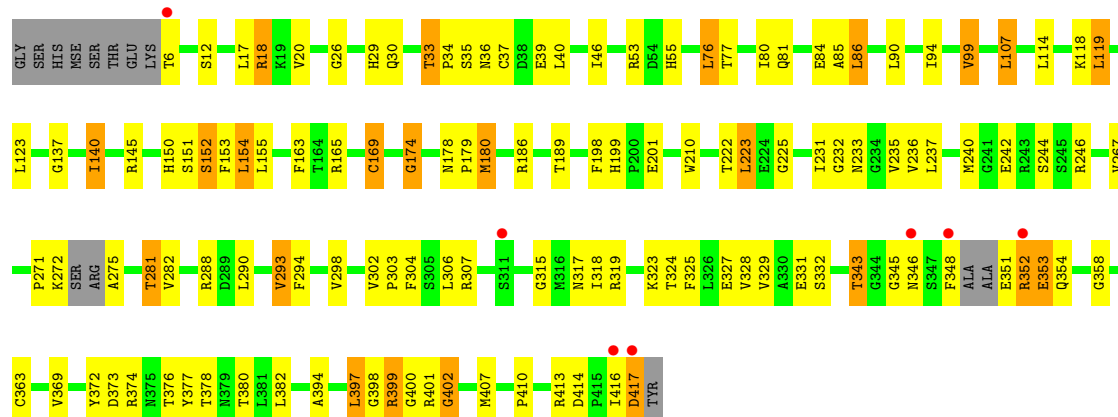
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	144	Total 144	O 144	0	0
2	D	88	Total 88	O 88	0	0

### 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.

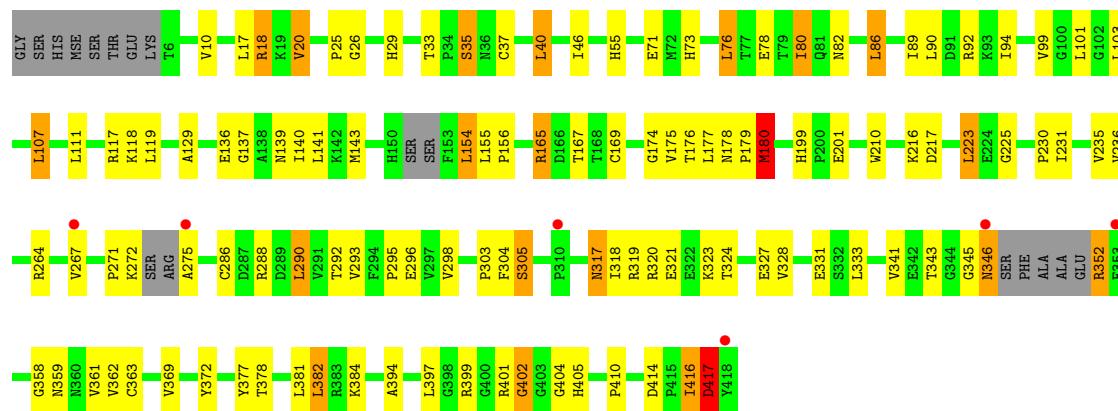
#### • Molecule 1: Arginine deiminase

Chain A: 



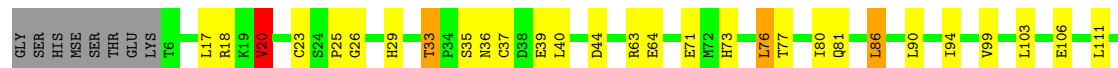
#### • Molecule 1: Arginine deiminase

Chain B: 



#### • Molecule 1: Arginine deiminase

Chain C: 





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	114.90Å 114.90Å 300.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.45 19.95 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-2.45) 99.9 (19.95-2.45)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.34 (at 2.44Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.198 , 0.264 0.200 , 0.264	Depositor DCC
$R_{free}$ test set	3802 reflections (5.09%)	DCC
Wilson B-factor (Å <sup>2</sup> )	42.8	Xtriage
Anisotropy	0.316	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 35.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	2 of 74675 reflections (0.003%)	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	13187	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	44.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.68% of the height of the origin peak. No significant pseudotranslation is detected.*

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



## 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	0.70	2/3242 (0.1%)	0.91	6/4379 (0.1%)
1	B	0.70	1/3216 (0.0%)	0.89	4/4342 (0.1%)
1	C	0.70	1/3273 (0.0%)	0.93	7/4422 (0.2%)
1	D	0.65	2/3192 (0.1%)	0.85	1/4313 (0.0%)
All	All	0.69	6/12923 (0.0%)	0.90	18/17456 (0.1%)

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

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

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	180	MSE	SE-CE	-7.41	1.51	1.95
1	D	363	CYS	CB-SG	-6.15	1.71	1.82
1	A	363	CYS	CB-SG	-6.08	1.72	1.82
1	A	169	CYS	CB-SG	-5.85	1.72	1.81
1	C	37	CYS	CB-SG	-5.61	1.72	1.81
1	D	37	CYS	CB-SG	-5.52	1.72	1.81

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	347	SER	N-CA-C	9.03	135.38	111.00
1	C	400	GLY	N-CA-C	-8.59	91.63	113.10
1	C	401	ARG	NE-CZ-NH2	-7.93	116.34	120.30
1	A	373	ASP	CB-CG-OD2	6.32	123.99	118.30
1	C	346	ASN	N-CA-C	6.18	127.68	111.00
1	A	180	MSE	CG-SE-CE	-5.91	85.90	98.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	GLY	N-CA-C	5.88	127.80	113.10
1	B	154	LEU	CA-CB-CG	5.71	128.42	115.30
1	C	177	LEU	N-CA-C	-5.54	96.05	111.00
1	B	382	LEU	CA-CB-CG	5.50	127.95	115.30
1	A	107	LEU	CA-CB-CG	5.33	127.55	115.30
1	D	177	LEU	N-CA-C	-5.25	96.82	111.00
1	A	294	PHE	N-CA-C	-5.22	96.89	111.00
1	C	20	VAL	CB-CA-C	-5.20	101.51	111.40
1	B	167	THR	N-CA-C	5.17	124.97	111.00
1	A	174	GLY	N-CA-C	-5.10	100.35	113.10
1	C	165	ARG	NE-CZ-NH2	-5.09	117.75	120.30
1	B	177	LEU	N-CA-C	-5.07	97.32	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	144	TYR	Sidechain
1	C	348	PHE	Sidechain

## 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3185	0	3161	121	0
1	B	3160	0	3139	114	0
1	C	3214	0	3186	99	0
1	D	3136	0	3119	106	0
2	A	113	0	0	15	0
2	B	147	0	0	16	0
2	C	144	0	0	20	0
2	D	88	0	0	13	0
All	All	13187	0	12605	432	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including

hydrogens) of the entry. The overall clashscore for this entry is 17.

All (432) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:352:ARG:HG3	1:B:352:ARG:HH11	1.13	1.11
1:A:343:THR:HG21	1:A:358:GLY:H	1.15	1.08
1:B:343:THR:HG21	1:B:358:GLY:H	1.21	1.04
1:D:343:THR:HG21	1:D:358:GLY:H	1.20	1.02
1:B:363:CYS:HB2	2:B:517:HOH:O	1.61	1.01
1:A:346:ASN:HB3	1:B:35:SER:HB3	1.45	0.98
1:A:352:ARG:HB3	2:A:436:HOH:O	1.60	0.98
1:A:306:LEU:HD13	1:A:318:ILE:HG12	1.49	0.94
1:C:399:ARG:HA	1:C:399:ARG:CZ	1.98	0.94
1:C:33:THR:HG22	1:C:36:ASN:H	1.37	0.90
1:B:361:VAL:HA	2:B:523:HOH:O	1.71	0.89
1:A:178:ASN:HB2	1:A:180:MSE:HE1	1.56	0.88
1:A:293:VAL:HG22	1:A:298:VAL:HG21	1.55	0.88
1:B:352:ARG:HG3	1:B:352:ARG:NH1	1.86	0.87
1:C:343:THR:HB	2:C:534:HOH:O	1.73	0.87
1:A:180:MSE:SE	2:A:515:HOH:O	2.43	0.86
1:C:398:GLY:HA2	2:C:551:HOH:O	1.74	0.85
1:C:130:ASP:HB2	2:C:545:HOH:O	1.78	0.82
1:B:352:ARG:N	2:B:516:HOH:O	2.13	0.81
1:B:343:THR:CG2	1:B:358:GLY:H	1.92	0.81
1:B:199:HIS:CD2	1:B:201:GLU:H	1.97	0.81
1:A:343:THR:HG21	1:A:358:GLY:N	1.96	0.81
1:D:343:THR:CG2	1:D:358:GLY:H	1.94	0.80
1:C:343:THR:HG21	1:C:358:GLY:H	1.45	0.80
1:A:343:THR:CG2	1:A:358:GLY:H	1.94	0.79
1:D:33:THR:HG22	1:D:36:ASN:H	1.47	0.79
1:D:199:HIS:CD2	1:D:201:GLU:H	2.01	0.79
1:A:271:PRO:O	1:A:272:LYS:HB3	1.82	0.78
1:B:199:HIS:HD2	1:B:201:GLU:H	1.28	0.78
1:A:307:ARG:HD2	2:A:514:HOH:O	1.84	0.77
1:C:348:PHE:O	1:C:349:ALA:HB2	1.83	0.77
1:A:376:THR:O	1:A:380:THR:HG23	1.85	0.77
1:D:46:ILE:HG22	1:D:399:ARG:HD2	1.66	0.77
1:B:17:LEU:HD11	1:B:20:VAL:HG13	1.65	0.76
1:A:240:MSE:HE2	1:A:246:ARG:CA	2.17	0.75
1:A:145:ARG:HD3	1:A:152:SER:HB3	1.70	0.73
1:B:343:THR:HG23	1:B:378:THR:OG1	1.87	0.73
1:A:17:LEU:HD11	1:A:20:VAL:CG1	2.19	0.73
1:C:402:GLY:HA3	2:C:551:HOH:O	1.87	0.73
1:A:352:ARG:HG2	1:A:377:TYR:CD1	2.24	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:352:ARG:HD3	1:A:353:GLU:H	1.54	0.72
1:C:240:MSE:HE2	1:C:246:ARG:HA	1.71	0.72
1:A:272:LYS:HZ1	1:A:275:ALA:N	1.86	0.72
1:D:267:VAL:HB	1:D:304:PHE:HB2	1.71	0.72
1:D:343:THR:HG21	1:D:358:GLY:N	2.01	0.72
1:B:17:LEU:HD21	1:B:20:VAL:HG11	1.71	0.72
1:A:324:THR:O	1:A:328:VAL:HG23	1.90	0.71
1:D:71:GLU:OE2	1:D:73:HIS:HB2	1.90	0.71
1:D:199:HIS:HD2	1:D:201:GLU:H	1.37	0.71
1:A:240:MSE:HE2	1:A:246:ARG:HA	1.73	0.70
1:A:352:ARG:HG2	1:A:377:TYR:CE1	2.26	0.70
1:B:55:HIS:HD2	2:B:521:HOH:O	1.72	0.70
1:D:103:LEU:HD13	1:D:154:LEU:CD1	2.22	0.70
1:C:33:THR:HG22	1:C:36:ASN:N	2.06	0.70
1:B:137:GLY:O	1:B:140:ILE:HG12	1.92	0.70
1:D:237:LEU:HD23	1:D:266:ILE:HB	1.73	0.69
1:A:343:THR:HG23	1:A:378:THR:OG1	1.92	0.69
1:B:103:LEU:CD1	1:B:141:LEU:HD11	2.22	0.69
1:A:345:GLY:HA3	1:A:348:PHE:CE2	2.28	0.69
1:D:49:ASN:HB3	2:D:477:HOH:O	1.91	0.68
1:B:343:THR:HG21	1:B:358:GLY:N	2.02	0.68
1:B:363:CYS:CB	2:B:517:HOH:O	2.29	0.68
1:B:352:ARG:HD3	2:B:519:HOH:O	1.94	0.68
1:D:358:GLY:HA3	1:D:378:THR:HG21	1.75	0.67
1:D:343:THR:HG23	1:D:378:THR:OG1	1.95	0.67
1:B:17:LEU:HD11	1:B:20:VAL:CG1	2.24	0.67
1:A:18:ARG:HG3	1:A:18:ARG:HH11	1.59	0.67
1:D:343:THR:HG22	1:D:344:GLY:H	1.60	0.66
1:D:288:ARG:HG2	1:D:416:ILE:HG21	1.76	0.66
1:B:165:ARG:O	1:B:225:GLY:HA3	1.94	0.66
1:A:178:ASN:HB3	1:A:223:LEU:O	1.96	0.66
1:A:331:GLU:HB2	2:A:512:HOH:O	1.96	0.66
1:B:317:ASN:HD21	1:B:319:ARG:HD3	1.58	0.66
1:C:358:GLY:HA3	1:C:378:THR:HG21	1.76	0.66
1:B:359:ASN:HB3	2:B:543:HOH:O	1.96	0.66
1:B:293:VAL:HG22	1:B:298:VAL:HG21	1.78	0.65
1:A:17:LEU:HD21	1:A:20:VAL:HG11	1.77	0.65
1:D:80:ILE:HD12	1:D:119:LEU:HD13	1.79	0.65
1:A:33:THR:HG22	1:A:36:ASN:H	1.62	0.65
1:D:324:THR:OG1	1:D:327:GLU:HG3	1.97	0.65
1:A:178:ASN:O	1:A:180:MSE:HE2	1.96	0.65
1:C:360:ASN:OD1	1:C:403:GLY:HA3	1.97	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:136:GLU:CD	1:D:137:GLY:H	2.00	0.64
1:C:106:GLU:HG2	2:C:541:HOH:O	1.96	0.64
1:D:30:GLN:NE2	2:D:490:HOH:O	2.27	0.64
1:D:77:THR:HG21	1:D:117:ARG:HD2	1.79	0.64
1:A:325:PHE:O	1:A:329:VAL:HG23	1.98	0.64
1:A:178:ASN:O	1:A:180:MSE:CE	2.47	0.63
1:D:376:THR:O	1:D:380:THR:HG23	1.97	0.63
1:D:48:VAL:HG12	1:D:52:LYS:HE2	1.79	0.63
1:A:145:ARG:HD3	1:A:152:SER:CB	2.28	0.63
1:B:103:LEU:HD11	1:B:141:LEU:HD11	1.81	0.63
1:A:165:ARG:O	1:A:225:GLY:HA3	1.98	0.63
1:B:416:ILE:HG22	1:B:417:ASP:N	2.14	0.62
1:C:295:PRO:O	1:C:299:LYS:HG2	2.00	0.62
1:A:53:ARG:HD3	1:C:64:GLU:OE1	2.00	0.61
1:A:20:VAL:HG12	1:A:410:PRO:HA	1.82	0.61
1:A:17:LEU:HD11	1:A:20:VAL:HG13	1.82	0.61
1:A:186:ARG:HG2	2:A:440:HOH:O	2.00	0.61
1:B:199:HIS:HD2	1:B:201:GLU:N	1.98	0.61
1:A:18:ARG:HE	1:A:414:ASP:CG	2.03	0.61
1:A:240:MSE:CE	1:A:246:ARG:HA	2.30	0.61
1:B:80:ILE:HD11	1:B:89:ILE:HD12	1.81	0.61
1:B:288:ARG:HH22	1:B:417:ASP:HB3	1.66	0.61
1:C:153:PHE:HB2	2:C:533:HOH:O	2.01	0.60
1:D:361:VAL:HB	1:D:369:VAL:HG13	1.83	0.60
1:C:286:CYS:HA	2:C:539:HOH:O	2.01	0.60
1:D:29:HIS:H	1:D:29:HIS:CD2	2.18	0.60
1:B:317:ASN:ND2	1:B:319:ARG:HD3	2.16	0.60
1:D:137:GLY:O	1:D:140:ILE:HG12	2.01	0.60
1:C:150:HIS:CE1	2:C:535:HOH:O	2.54	0.60
1:D:33:THR:HG23	1:D:35:SER:H	1.66	0.60
1:C:286:CYS:HB2	1:C:290:LEU:HD13	1.83	0.60
1:B:264:ARG:HD2	1:B:305:SER:OG	2.01	0.60
1:D:324:THR:O	1:D:328:VAL:HG23	2.01	0.60
1:A:84:GLU:HG2	1:A:198:PHE:CE1	2.36	0.60
1:C:363:CYS:SG	2:C:539:HOH:O	2.57	0.59
1:D:372:TYR:CG	1:D:394:ALA:HB2	2.36	0.59
1:A:35:SER:OG	1:B:346:ASN:HB2	2.01	0.59
1:A:80:ILE:HD12	1:A:119:LEU:HD13	1.85	0.59
1:D:272:LYS:HZ3	1:D:275:ALA:N	2.00	0.59
1:A:222:THR:O	1:A:244:SER:HA	2.03	0.58
1:A:240:MSE:HE2	1:A:246:ARG:CB	2.34	0.58
1:A:328:VAL:HA	1:A:331:GLU:HG2	1.85	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:165:ARG:O	1:C:225:GLY:HA3	2.03	0.58
1:B:119:LEU:O	1:B:119:LEU:HD22	2.03	0.58
1:C:145:ARG:HD3	1:C:152:SER:HB3	1.86	0.58
1:B:180:MSE:HA	1:B:180:MSE:HE2	1.84	0.58
1:B:156:PRO:HD2	2:B:440:HOH:O	2.03	0.58
1:C:363:CYS:HB2	2:C:539:HOH:O	2.03	0.58
1:D:106:GLU:HG2	2:D:451:HOH:O	2.04	0.58
1:A:240:MSE:HE2	1:A:246:ARG:HB3	1.85	0.57
1:A:55:HIS:HD2	2:A:433:HOH:O	1.87	0.57
1:C:33:THR:HG23	1:C:35:SER:H	1.69	0.57
1:D:59:VAL:HG13	1:D:69:VAL:HG11	1.86	0.57
1:B:323:LYS:HB3	1:B:327:GLU:OE1	2.04	0.57
1:B:352:ARG:NH1	2:B:520:HOH:O	2.38	0.57
1:D:107:LEU:HD11	1:D:155:LEU:HD22	1.87	0.57
1:A:84:GLU:HG2	1:A:198:PHE:HE1	1.69	0.56
1:C:193:THR:HG21	1:C:214:PRO:HG3	1.87	0.56
1:D:115:GLU:HG2	2:D:506:HOH:O	2.05	0.56
1:D:94:ILE:HD13	1:D:107:LEU:HD13	1.88	0.56
1:C:103:LEU:HD13	1:C:154:LEU:CD1	2.35	0.56
1:A:151:SER:HB2	2:A:510:HOH:O	2.04	0.56
1:B:178:ASN:HB2	1:B:180:MSE:HE1	1.86	0.56
1:A:118:LYS:HD3	2:A:495:HOH:O	2.06	0.55
1:A:77:THR:O	1:A:81:GLN:HG3	2.07	0.55
1:B:103:LEU:HD13	1:B:141:LEU:HD11	1.88	0.55
1:B:267:VAL:HB	1:B:304:PHE:HB2	1.88	0.55
1:A:345:GLY:HA3	1:A:348:PHE:HE2	1.69	0.55
1:D:55:HIS:O	1:D:58:PHE:HB3	2.06	0.55
1:A:18:ARG:HH11	1:A:18:ARG:CG	2.20	0.54
1:B:78:GLU:OE1	1:B:199:HIS:HE1	1.89	0.54
1:D:33:THR:HG22	1:D:36:ASN:N	2.19	0.54
1:C:178:ASN:HB3	1:C:223:LEU:O	2.07	0.54
1:B:303:PRO:HG2	1:B:321:GLU:HB2	1.88	0.54
1:A:153:PHE:N	2:A:472:HOH:O	2.34	0.54
1:D:33:THR:CG2	1:D:35:SER:H	2.20	0.54
1:B:404:GLY:HA3	2:B:523:HOH:O	2.06	0.54
1:D:372:TYR:CD2	1:D:394:ALA:HB2	2.43	0.54
1:D:118:LYS:HD3	2:D:506:HOH:O	2.07	0.54
1:C:33:THR:CG2	1:C:35:SER:H	2.20	0.54
1:C:343:THR:HG23	1:C:378:THR:OG1	2.07	0.54
1:D:145:ARG:HD3	1:D:152:SER:OG	2.08	0.54
1:A:99:VAL:HG22	1:A:154:LEU:HD12	1.90	0.54
1:B:286:CYS:HB2	1:B:290:LEU:HD13	1.90	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:169:CYS:HB2	1:B:176:THR:OG1	2.07	0.54
1:D:303:PRO:HB2	1:D:321:GLU:HB2	1.89	0.54
1:D:141:LEU:HD11	1:D:154:LEU:HD13	1.90	0.54
1:B:359:ASN:CB	2:B:543:HOH:O	2.55	0.54
1:C:293:VAL:HG13	1:C:298:VAL:HG21	1.90	0.54
1:D:367:GLY:O	1:D:387:VAL:HG13	2.07	0.54
1:B:174:GLY:HA3	1:B:210:TRP:CE2	2.43	0.53
1:C:26:GLY:H	1:C:29:HIS:CD2	2.27	0.53
1:B:296:GLU:HB2	2:B:546:HOH:O	2.08	0.53
1:C:71:GLU:OE2	1:C:73:HIS:HB2	2.08	0.53
1:A:267:VAL:HB	1:A:304:PHE:HB2	1.90	0.53
1:C:103:LEU:CD1	1:C:141:LEU:HD11	2.38	0.53
1:D:165:ARG:O	1:D:225:GLY:HA3	2.08	0.53
1:C:376:THR:O	1:C:380:THR:HG23	2.09	0.53
1:C:361:VAL:HG21	1:C:369:VAL:HG21	1.91	0.53
1:A:12:SER:O	1:A:413:ARG:HD2	2.09	0.53
1:C:363:CYS:CB	2:C:539:HOH:O	2.55	0.53
1:D:29:HIS:CD2	1:D:29:HIS:N	2.77	0.53
1:D:231:ILE:HD12	1:D:333:LEU:HD21	1.91	0.53
1:D:398:GLY:C	1:D:400:GLY:H	2.11	0.52
1:A:174:GLY:HA3	1:A:210:TRP:NE1	2.23	0.52
1:B:17:LEU:HD21	1:B:20:VAL:CG1	2.39	0.52
1:A:398:GLY:C	1:A:400:GLY:H	2.12	0.52
1:A:272:LYS:HE2	1:A:275:ALA:O	2.09	0.52
1:B:293:VAL:O	1:B:295:PRO:HD3	2.09	0.52
1:B:46:ILE:HG22	1:B:399:ARG:HD2	1.92	0.52
1:B:352:ARG:HD3	1:B:352:ARG:N	2.25	0.52
1:D:343:THR:HG22	1:D:344:GLY:N	2.24	0.52
1:A:26:GLY:H	1:A:29:HIS:CD2	2.27	0.52
1:C:399:ARG:NE	1:C:399:ARG:HA	2.24	0.52
1:C:343:THR:HG22	1:C:344:GLY:N	2.24	0.52
1:C:18:ARG:NE	1:C:414:ASP:OD2	2.43	0.51
1:D:278:HIS:O	1:D:281:THR:HB	2.10	0.51
1:B:94:ILE:HD13	1:B:107:LEU:HD13	1.92	0.51
1:D:165:ARG:CZ	1:D:405:HIS:CE1	2.93	0.51
1:C:166:ASP:HB3	1:C:180:MSE:HE1	1.91	0.51
1:A:240:MSE:CE	1:A:246:ARG:HB3	2.40	0.51
1:C:63:ARG:NH1	2:C:554:HOH:O	2.42	0.51
1:B:352:ARG:CD	1:B:352:ARG:N	2.74	0.51
1:A:33:THR:CG2	1:A:35:SER:H	2.23	0.51
1:C:26:GLY:H	1:C:29:HIS:HD2	1.59	0.51
1:A:199:HIS:CD2	1:A:201:GLU:H	2.29	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:103:LEU:HD13	1:D:154:LEU:HD11	1.92	0.50
1:A:345:GLY:HA3	1:A:348:PHE:CD2	2.45	0.50
1:A:119:LEU:O	1:A:123:LEU:HG	2.11	0.50
1:A:374:ARG:NE	2:A:429:HOH:O	2.30	0.50
1:B:272:LYS:HZ1	1:B:275:ALA:N	2.09	0.50
1:C:293:VAL:O	1:C:295:PRO:HD3	2.11	0.50
1:B:178:ASN:HB3	1:B:223:LEU:O	2.11	0.50
1:D:398:GLY:C	1:D:400:GLY:N	2.63	0.50
1:C:278:HIS:O	1:C:281:THR:HB	2.11	0.50
1:B:372:TYR:CG	1:B:394:ALA:HB2	2.46	0.50
1:D:165:ARG:NH2	2:D:465:HOH:O	2.42	0.50
1:A:174:GLY:HA3	1:A:210:TRP:CE2	2.47	0.50
1:B:352:ARG:HB3	2:B:527:HOH:O	2.10	0.49
1:A:235:VAL:HG12	1:A:236:VAL:N	2.27	0.49
1:B:71:GLU:OE1	1:B:73:HIS:N	2.45	0.49
1:A:114:LEU:HD22	1:A:118:LYS:HE3	1.94	0.49
1:D:93:LYS:HD2	2:D:444:HOH:O	2.12	0.49
1:C:163:PHE:CE1	1:C:402:GLY:HA2	2.48	0.49
1:D:105:SER:HB3	2:D:493:HOH:O	2.11	0.49
1:D:298:VAL:HA	1:D:301:ILE:HD12	1.95	0.49
1:C:398:GLY:O	1:C:399:ARG:C	2.51	0.48
1:C:359:ASN:ND2	2:C:534:HOH:O	2.46	0.48
1:C:293:VAL:HG13	1:C:298:VAL:CG2	2.43	0.48
1:C:235:VAL:HG12	1:C:236:VAL:N	2.27	0.48
1:D:288:ARG:NH1	1:D:366:PRO:HB3	2.28	0.48
1:D:401:ARG:O	1:D:402:GLY:O	2.32	0.48
1:B:286:CYS:HA	2:B:517:HOH:O	2.12	0.48
1:C:169:CYS:SG	1:C:225:GLY:HA2	2.53	0.48
1:C:235:VAL:HG11	1:C:266:ILE:HD12	1.96	0.48
1:B:352:ARG:CB	2:B:527:HOH:O	2.61	0.48
1:A:151:SER:CB	2:A:510:HOH:O	2.60	0.48
1:A:26:GLY:H	1:A:29:HIS:HD2	1.60	0.48
1:A:281:THR:HG22	1:A:282:VAL:HG13	1.95	0.48
1:B:231:ILE:HD12	1:B:333:LEU:HD21	1.96	0.48
1:C:343:THR:CG2	1:C:378:THR:OG1	2.62	0.48
1:A:288:ARG:HG3	1:A:416:ILE:HG21	1.96	0.48
1:D:298:VAL:HA	1:D:301:ILE:CD1	2.44	0.48
1:D:414:ASP:HB3	1:D:415:PRO:HD2	1.95	0.48
1:A:288:ARG:NH1	1:A:416:ILE:HG23	2.29	0.48
1:C:23:CYS:HB3	1:C:161:THR:O	2.14	0.48
1:B:292:THR:HA	1:B:341:VAL:O	2.14	0.48
1:C:285:PHE:HA	1:C:291:VAL:HG12	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:324:THR:O	1:C:328:VAL:HG23	2.13	0.47
1:A:137:GLY:O	1:A:140:ILE:HG12	2.15	0.47
1:B:18:ARG:HE	1:B:414:ASP:CG	2.17	0.47
1:C:343:THR:O	2:C:534:HOH:O	2.20	0.47
1:B:94:ILE:HD11	1:B:111:LEU:HD12	1.96	0.47
1:A:80:ILE:HD12	1:A:119:LEU:CD1	2.44	0.47
1:D:94:ILE:CD1	1:D:107:LEU:HD13	2.45	0.47
1:D:13:GLU:OE1	1:D:229:MSE:HG2	2.15	0.47
1:C:394:ALA:HB1	1:C:398:GLY:HA3	1.97	0.47
1:C:399:ARG:NH1	1:C:399:ARG:HA	2.29	0.47
1:B:416:ILE:CG2	1:B:417:ASP:N	2.77	0.47
1:D:307:ARG:HB3	1:D:308:PRO:HD2	1.97	0.47
1:A:178:ASN:HA	1:A:179:PRO:HD3	1.74	0.47
1:B:20:VAL:HG12	1:B:410:PRO:HA	1.96	0.47
1:A:76:LEU:O	1:A:80:ILE:HG12	2.14	0.47
1:D:305:SER:OG	1:D:321:GLU:OE2	2.27	0.47
1:D:169:CYS:SG	1:D:225:GLY:HA2	2.55	0.47
1:A:240:MSE:CE	1:A:246:ARG:CB	2.93	0.46
1:A:18:ARG:NH1	1:A:18:ARG:CG	2.78	0.46
1:C:17:LEU:HD11	1:C:20:VAL:HG13	1.97	0.46
1:B:26:GLY:H	1:B:29:HIS:HD2	1.63	0.46
1:C:99:VAL:HG12	1:C:103:LEU:HB2	1.96	0.46
1:A:307:ARG:HG2	1:A:307:ARG:HH11	1.79	0.46
1:D:14:ALA:HB3	1:D:416:ILE:HD11	1.96	0.46
1:B:216:LYS:CG	1:B:217:ASP:N	2.78	0.46
1:B:324:THR:O	1:B:328:VAL:HG23	2.15	0.46
1:C:165:ARG:NH2	2:C:478:HOH:O	2.48	0.46
1:C:76:LEU:O	1:C:80:ILE:HG12	2.15	0.46
1:B:352:ARG:HH11	1:B:352:ARG:CG	2.01	0.46
1:D:288:ARG:NH1	2:D:494:HOH:O	2.48	0.46
1:B:80:ILE:CD1	1:B:89:ILE:HD12	2.45	0.46
1:C:361:VAL:CG2	1:C:369:VAL:HG21	2.46	0.46
1:A:346:ASN:HA	1:B:33:THR:HB	1.97	0.46
1:B:103:LEU:HD13	1:B:154:LEU:CD1	2.46	0.46
1:B:86:LEU:HD22	1:B:90:LEU:HG	1.98	0.46
1:D:9:GLY:O	1:D:412:VAL:HA	2.16	0.46
1:B:76:LEU:HD22	1:B:80:ILE:HD13	1.97	0.45
1:C:356:ASP:HB2	1:C:375:ASN:OD1	2.16	0.45
1:D:61:LYS:HD3	1:D:390:ILE:CG2	2.46	0.45
1:A:90:LEU:HD22	1:A:94:ILE:HD12	1.98	0.45
1:D:290:LEU:HD23	1:D:339:ARG:HB2	1.99	0.45
1:B:235:VAL:HG12	1:B:236:VAL:N	2.31	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:352:ARG:HG2	1:A:377:TYR:CZ	2.51	0.45
1:D:77:THR:O	1:D:81:GLN:HG3	2.16	0.45
1:D:107:LEU:HD23	1:D:132:LEU:HD21	1.99	0.45
1:A:163:PHE:CE1	1:A:402:GLY:HA2	2.51	0.45
1:A:352:ARG:HG2	1:A:377:TYR:CG	2.51	0.45
1:C:348:PHE:O	1:C:349:ALA:CB	2.51	0.45
1:D:344:GLY:C	2:D:474:HOH:O	2.55	0.45
1:A:30:GLN:NE2	2:A:489:HOH:O	2.48	0.45
1:D:33:THR:CG2	1:D:35:SER:N	2.80	0.45
1:C:222:THR:O	1:C:244:SER:HA	2.17	0.45
1:C:90:LEU:HD22	1:C:94:ILE:HD12	1.99	0.45
1:B:363:CYS:SG	2:B:517:HOH:O	2.61	0.44
1:D:163:PHE:CE1	1:D:402:GLY:HA2	2.53	0.44
1:C:103:LEU:HD11	1:C:141:LEU:HD11	1.99	0.44
1:D:401:ARG:O	1:D:401:ARG:HD2	2.16	0.44
1:C:86:LEU:HD22	1:C:90:LEU:CD1	2.47	0.44
1:C:270:LEU:HD23	1:C:301:ILE:HG12	1.99	0.44
1:D:29:HIS:CE1	1:D:162:GLN:HE21	2.34	0.44
1:B:320:ARG:HH11	1:B:320:ARG:HG2	1.82	0.44
1:C:343:THR:C	2:C:534:HOH:O	2.55	0.44
1:C:231:ILE:HD13	1:C:237:LEU:HD21	1.99	0.44
1:B:82:ASN:C	1:B:82:ASN:OD1	2.56	0.44
1:B:140:ILE:O	1:B:143:MSE:HB2	2.17	0.44
1:A:36:ASN:O	1:A:39:GLU:HG2	2.18	0.44
1:D:318:ILE:HG23	1:D:318:ILE:O	2.17	0.44
1:C:145:ARG:HD3	1:C:152:SER:CB	2.47	0.44
1:D:290:LEU:HD22	1:D:291:VAL:N	2.32	0.44
1:B:40:LEU:HD12	1:B:40:LEU:HA	1.83	0.44
1:D:29:HIS:HA	1:D:32:LEU:HG	1.99	0.44
1:B:169:CYS:O	1:B:175:VAL:HA	2.16	0.44
1:D:392:ILE:HB	2:D:438:HOH:O	2.18	0.44
1:C:86:LEU:HD22	1:C:90:LEU:HG	1.99	0.43
1:C:160:ASN:HB3	1:C:185:ARG:NH2	2.33	0.43
1:B:117:ARG:HH11	1:B:117:ARG:HG3	1.83	0.43
1:C:36:ASN:O	1:C:39:GLU:HG2	2.19	0.43
1:D:235:VAL:HG21	1:D:332:SER:HB2	1.99	0.43
1:A:231:ILE:HG21	1:A:237:LEU:CD1	2.48	0.43
1:C:372:TYR:CG	1:C:394:ALA:HB2	2.53	0.43
1:A:33:THR:HG23	1:B:346:ASN:CA	2.49	0.43
1:A:33:THR:HG23	1:B:346:ASN:HA	1.99	0.43
1:C:153:PHE:CB	2:C:533:HOH:O	2.65	0.43
1:D:290:LEU:HD23	1:D:339:ARG:CB	2.49	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:383:ARG:HH11	1:D:383:ARG:HD2	1.69	0.43
1:B:180:MSE:CA	1:B:180:MSE:HE2	2.48	0.43
1:A:55:HIS:HE1	2:A:425:HOH:O	2.02	0.43
1:A:306:LEU:CD1	1:A:318:ILE:HG12	2.34	0.43
1:D:140:ILE:HA	1:D:143:MSE:HE2	1.99	0.43
1:D:331:GLU:C	1:D:333:LEU:N	2.71	0.43
1:C:77:THR:O	1:C:81:GLN:HG3	2.19	0.43
1:C:235:VAL:CG1	1:C:266:ILE:HD12	2.49	0.43
1:D:370:VAL:HG22	1:D:390:ILE:HB	2.01	0.43
1:D:82:ASN:HA	1:D:83:PRO:HD3	1.87	0.43
1:D:394:ALA:O	1:D:395:SER:C	2.57	0.43
1:C:140:ILE:O	1:C:140:ILE:HG13	2.15	0.43
1:A:145:ARG:HD3	1:A:152:SER:OG	2.19	0.43
1:D:288:ARG:HG2	1:D:416:ILE:CG2	2.44	0.43
1:D:107:LEU:HD11	1:D:155:LEU:CD2	2.48	0.43
1:B:94:ILE:CD1	1:B:107:LEU:HD13	2.48	0.43
1:D:82:ASN:OD1	1:D:82:ASN:C	2.55	0.43
1:C:333:LEU:HD22	1:C:418:TYR:CE2	2.53	0.43
1:B:343:THR:CG2	1:B:378:THR:OG1	2.62	0.43
1:A:86:LEU:HD22	1:A:90:LEU:HG	2.01	0.43
1:A:180:MSE:HE3	1:A:189:THR:OG1	2.19	0.42
1:D:141:LEU:HD11	1:D:154:LEU:CD1	2.50	0.42
1:D:237:LEU:CD2	1:D:266:ILE:HB	2.46	0.42
1:B:377:TYR:CZ	1:B:381:LEU:HD11	2.54	0.42
1:A:417:ASP:OD2	1:A:417:ASP:C	2.57	0.42
1:C:213:ASP:HA	1:C:214:PRO:HD2	1.89	0.42
1:A:86:LEU:HA	1:A:86:LEU:HD23	1.93	0.42
1:B:101:LEU:HA	1:B:101:LEU:HD23	1.77	0.42
1:B:129:ALA:HA	1:B:154:LEU:HD21	2.01	0.42
1:D:26:GLY:H	1:D:29:HIS:CD2	2.37	0.42
1:D:238:ILE:HG21	1:D:249:ILE:HG12	2.01	0.42
1:C:373:ASP:HB3	2:C:549:HOH:O	2.19	0.42
1:A:242:GLU:HG2	2:A:454:HOH:O	2.18	0.42
1:D:303:PRO:HG3	1:D:325:PHE:HA	2.01	0.42
1:C:29:HIS:CD2	1:C:29:HIS:H	2.36	0.42
1:A:374:ARG:NH2	2:A:429:HOH:O	2.48	0.42
1:B:358:GLY:HA3	1:B:378:THR:HG21	2.01	0.42
1:C:398:GLY:O	1:C:400:GLY:N	2.52	0.42
1:B:372:TYR:CD2	1:B:394:ALA:HB2	2.55	0.42
1:C:111:LEU:HD22	1:C:119:LEU:CD2	2.50	0.42
1:D:78:GLU:OE1	1:D:199:HIS:HE1	2.02	0.42
1:A:372:TYR:CG	1:A:394:ALA:HB2	2.55	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:288:ARG:HD3	2:D:494:HOH:O	2.19	0.42
1:B:71:GLU:OE1	1:B:73:HIS:HB2	2.20	0.42
1:C:175:VAL:HG22	1:C:176:THR:N	2.35	0.42
1:A:328:VAL:O	1:A:331:GLU:HG3	2.20	0.42
1:A:232:GLY:O	1:A:233:ASN:HB3	2.20	0.42
1:C:29:HIS:CD2	1:C:29:HIS:N	2.88	0.42
1:A:33:THR:HG22	1:A:35:SER:N	2.34	0.41
1:C:103:LEU:HD13	1:C:141:LEU:HD11	2.02	0.41
1:B:92:ARG:HG3	1:B:92:ARG:HH11	1.85	0.41
1:B:345:GLY:O	1:B:346:ASN:C	2.58	0.41
1:B:90:LEU:HD22	1:B:94:ILE:HD12	2.02	0.41
1:B:18:ARG:NE	1:B:414:ASP:OD2	2.54	0.41
1:B:26:GLY:H	1:B:29:HIS:CD2	2.38	0.41
1:C:350:ALA:CB	2:C:540:HOH:O	2.68	0.41
1:B:136:GLU:O	1:B:139:ASN:HB2	2.20	0.41
1:D:361:VAL:HG22	2:D:429:HOH:O	2.20	0.41
1:B:272:LYS:HE3	1:B:275:ALA:HB3	2.02	0.41
1:A:352:ARG:HD3	1:A:353:GLU:N	2.30	0.41
1:A:17:LEU:HD21	1:A:20:VAL:CG1	2.49	0.41
1:A:85:ALA:HB2	1:A:198:PHE:CG	2.56	0.41
1:A:140:ILE:HG12	1:A:140:ILE:H	1.73	0.41
1:D:379:ASN:O	1:D:383:ARG:HG3	2.20	0.41
1:B:401:ARG:O	1:B:402:GLY:O	2.39	0.41
1:A:34:PRO:HD2	1:B:346:ASN:HB3	2.01	0.41
1:B:178:ASN:HA	1:B:179:PRO:HD2	1.82	0.41
1:D:178:ASN:HB3	1:D:223:LEU:O	2.20	0.41
1:C:343:THR:CG2	1:C:358:GLY:H	2.23	0.41
1:D:33:THR:HG22	1:D:35:SER:N	2.36	0.41
1:A:271:PRO:O	1:A:272:LYS:CB	2.60	0.41
1:B:165:ARG:HD2	1:B:405:HIS:O	2.21	0.41
1:A:33:THR:HG23	1:B:346:ASN:CB	2.50	0.41
1:A:169:CYS:SG	1:A:225:GLY:HA2	2.61	0.41
1:C:235:VAL:CG1	1:C:236:VAL:N	2.84	0.41
1:C:119:LEU:O	1:C:123:LEU:HG	2.21	0.41
1:B:362:VAL:HG13	1:B:362:VAL:O	2.21	0.41
1:C:383:ARG:HA	1:C:387:VAL:O	2.21	0.41
1:A:323:LYS:HB3	1:A:327:GLU:OE1	2.20	0.41
1:B:10:VAL:HG12	1:B:230:PRO:HG2	2.03	0.41
1:A:46:ILE:HG22	1:A:399:ARG:HD2	2.02	0.41
1:B:174:GLY:HA3	1:B:210:TRP:NE1	2.35	0.40
1:C:416:ILE:HD11	1:C:418:TYR:CZ	2.56	0.40
1:A:397:LEU:HG	1:A:407:MSE:SE	2.71	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:271:PRO:O	1:B:272:LYS:HB2	2.21	0.40
1:C:279:LEU:HD12	1:C:279:LEU:HA	1.86	0.40
1:B:318:ILE:O	1:B:319:ARG:HD2	2.21	0.40
1:A:302:VAL:HA	1:A:303:PRO:HD3	1.95	0.40
1:D:199:HIS:HD2	1:D:201:GLU:N	2.11	0.40
1:A:331:GLU:HG3	1:A:332:SER:N	2.36	0.40
1:B:99:VAL:HG12	1:B:103:LEU:HB2	2.03	0.40
1:B:288:ARG:NH2	1:B:417:ASP:HB3	2.34	0.40
1:C:64:GLU:HG2	2:C:468:HOH:O	2.20	0.40
1:A:235:VAL:CG1	1:A:236:VAL:N	2.85	0.40
1:C:119:LEU:HA	1:C:119:LEU:HD23	1.90	0.40
1:D:343:THR:CG2	1:D:378:THR:OG1	2.66	0.40
1:A:199:HIS:HD2	1:A:201:GLU:H	1.69	0.40
1:A:401:ARG:O	1:A:402:GLY:O	2.39	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	402/421 (96%)	381 (95%)	18 (4%)	3 (1%)	30	47
1	B	396/421 (94%)	373 (94%)	21 (5%)	2 (0%)	38	57
1	C	408/421 (97%)	385 (94%)	18 (4%)	5 (1%)	19	30
1	D	396/421 (94%)	371 (94%)	23 (6%)	2 (0%)	38	57
All	All	1602/1684 (95%)	1510 (94%)	80 (5%)	12 (1%)	30	47

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	402	GLY
1	C	347	SER
1	C	402	GLY
1	D	152	SER

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Mol	Chain	Res	Type
1	A	402	GLY
1	C	350	ALA
1	C	399	ARG
1	D	402	GLY
1	B	417	ASP
1	A	353	GLU
1	C	349	ALA
1	A	399	ARG

### 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	347/346 (100%)	318 (92%)	29 (8%)	16	26
1	B	343/346 (99%)	316 (92%)	27 (8%)	18	30
1	C	349/346 (101%)	328 (94%)	21 (6%)	27	45
1	D	342/346 (99%)	318 (93%)	24 (7%)	21	36
All	All	1381/1384 (100%)	1280 (93%)	101 (7%)	20	34

All (101) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	THR
1	A	18	ARG
1	A	33	THR
1	A	37	CYS
1	A	40	LEU
1	A	76	LEU
1	A	86	LEU
1	A	99	VAL
1	A	107	LEU
1	A	119	LEU
1	A	140	ILE
1	A	150	HIS
1	A	152	SER
1	A	154	LEU

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Mol	Chain	Res	Type
1	A	155	LEU
1	A	223	LEU
1	A	281	THR
1	A	290	LEU
1	A	293	VAL
1	A	317	ASN
1	A	319	ARG
1	A	343	THR
1	A	351	GLU
1	A	352	ARG
1	A	354	GLN
1	A	369	VAL
1	A	382	LEU
1	A	397	LEU
1	A	417	ASP
1	B	18	ARG
1	B	20	VAL
1	B	25	PRO
1	B	35	SER
1	B	37	CYS
1	B	40	LEU
1	B	76	LEU
1	B	80	ILE
1	B	86	LEU
1	B	107	LEU
1	B	118	LYS
1	B	155	LEU
1	B	165	ARG
1	B	180	MSE
1	B	223	LEU
1	B	290	LEU
1	B	305	SER
1	B	317	ASN
1	B	331	GLU
1	B	346	ASN
1	B	352	ARG
1	B	369	VAL
1	B	382	LEU
1	B	384	LYS
1	B	397	LEU
1	B	416	ILE
1	B	417	ASP

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Mol	Chain	Res	Type
1	C	20	VAL
1	C	25	PRO
1	C	33	THR
1	C	40	LEU
1	C	44	ASP
1	C	76	LEU
1	C	86	LEU
1	C	119	LEU
1	C	140	ILE
1	C	150	HIS
1	C	155	LEU
1	C	162	GLN
1	C	223	LEU
1	C	259	LYS
1	C	281	THR
1	C	290	LEU
1	C	319	ARG
1	C	347	SER
1	C	369	VAL
1	C	397	LEU
1	C	399	ARG
1	D	33	THR
1	D	37	CYS
1	D	40	LEU
1	D	76	LEU
1	D	86	LEU
1	D	105	SER
1	D	107	LEU
1	D	117	ARG
1	D	119	LEU
1	D	136	GLU
1	D	155	LEU
1	D	161	THR
1	D	162	GLN
1	D	200	PRO
1	D	223	LEU
1	D	290	LEU
1	D	305	SER
1	D	337	LYS
1	D	343	THR
1	D	360	ASN
1	D	363	CYS

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Mol	Chain	Res	Type
1	D	382	LEU
1	D	397	LEU
1	D	401	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	29	HIS
1	A	55	HIS
1	A	150	HIS
1	A	162	GLN
1	A	199	HIS
1	B	29	HIS
1	B	55	HIS
1	B	199	HIS
1	B	317	ASN
1	C	29	HIS
1	C	160	ASN
1	C	162	GLN
1	D	29	HIS
1	D	55	HIS
1	D	81	GLN
1	D	160	ASN
1	D	162	GLN
1	D	199	HIS

### 5.3.3 RNA ⓘ

There are no RNA chains in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

There are no ligands in this entry.

## 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 ⓘ

### 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	408/421 (96%)	-0.35	7 (1%) 67 68	26, 41, 69, 91	0
1	B	404/421 (95%)	-0.45	6 (1%) 70 71	22, 37, 65, 97	0
1	C	412/421 (97%)	-0.35	8 (1%) 64 65	23, 39, 69, 99	0
1	D	402/421 (95%)	-0.31	2 (0%) 88 90	31, 46, 73, 89	0
All	All	1626/1684 (96%)	-0.36	23 (1%) 72 73	22, 42, 71, 99	0

All (23) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	351	GLU	6.4
1	B	418	TYR	5.7
1	C	347	SER	5.2
1	C	348	PHE	5.2
1	C	350	ALA	4.8
1	C	399	ARG	4.7
1	A	6	THR	3.6
1	A	352	ARG	3.6
1	C	274	ARG	3.5
1	C	152	SER	3.4
1	D	6	THR	3.3
1	A	416	ILE	2.9
1	A	417	ASP	2.9
1	A	346	ASN	2.8
1	D	311	SER	2.7
1	C	275	ALA	2.3
1	B	346	ASN	2.3
1	A	311	SER	2.3
1	A	348	PHE	2.3
1	B	275	ALA	2.2
1	B	310	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	267	VAL	2.1
1	B	353	GLU	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 ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.