



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 06:41 am GMT

PDB ID : 3H37  
Title : The structure of CCA-adding enzyme apo form I  
Authors : Toh, Y.; Tomita, K.  
Deposited on : 2009-04-16  
Resolution : 2.85 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  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
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) : recalc28949

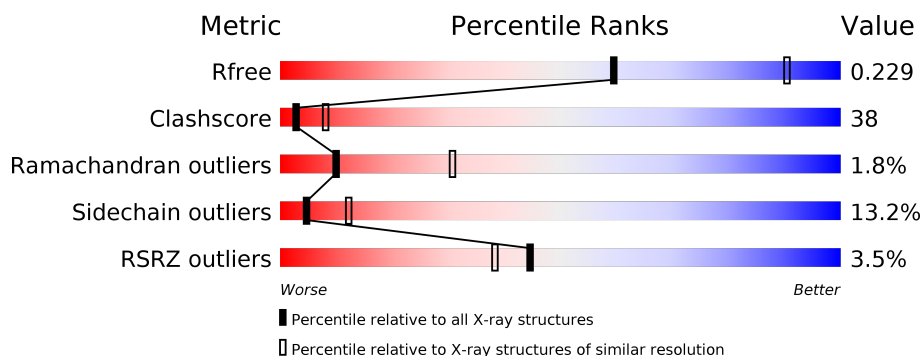
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.85 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))
$R_{free}$	100719	2469 (2.90-2.82)
Clashscore	112137	2749 (2.90-2.82)
Ramachandran outliers	110173	2687 (2.90-2.82)
Sidechain outliers	110143	2690 (2.90-2.82)
RSRZ outliers	101464	2487 (2.90-2.82)

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	441	<div> <div>2%</div> <div> <div></div> <div>43%</div> <div>44%</div> <div>7%</div> <div>6%</div> </div> </div>
1	B	441	<div> <div>5%</div> <div> <div></div> <div>42%</div> <div>45%</div> <div>8%</div> <div>5%</div> </div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6908 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 TRNA nucleotidyl transferase-related protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	415	Total	C	N	O	S	Se	0	0	0
			3413	2204	578	620	1	10			
1	B	421	Total	C	N	O	S	Se	0	0	0
			3459	2234	587	628	1	9			

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	-	EXPRESSION TAG	UNP Q9WZH4
A	429	LYS	-	EXPRESSION TAG	UNP Q9WZH4
A	430	LEU	-	EXPRESSION TAG	UNP Q9WZH4
A	431	ALA	-	EXPRESSION TAG	UNP Q9WZH4
A	432	ALA	-	EXPRESSION TAG	UNP Q9WZH4
A	433	ALA	-	EXPRESSION TAG	UNP Q9WZH4
A	434	LEU	-	EXPRESSION TAG	UNP Q9WZH4
A	435	GLU	-	EXPRESSION TAG	UNP Q9WZH4
A	436	HIS	-	EXPRESSION TAG	UNP Q9WZH4
A	437	HIS	-	EXPRESSION TAG	UNP Q9WZH4
A	438	HIS	-	EXPRESSION TAG	UNP Q9WZH4
A	439	HIS	-	EXPRESSION TAG	UNP Q9WZH4
A	440	HIS	-	EXPRESSION TAG	UNP Q9WZH4
A	441	HIS	-	EXPRESSION TAG	UNP Q9WZH4
B	1	MSE	-	EXPRESSION TAG	UNP Q9WZH4
B	429	LYS	-	EXPRESSION TAG	UNP Q9WZH4
B	430	LEU	-	EXPRESSION TAG	UNP Q9WZH4
B	431	ALA	-	EXPRESSION TAG	UNP Q9WZH4
B	432	ALA	-	EXPRESSION TAG	UNP Q9WZH4
B	433	ALA	-	EXPRESSION TAG	UNP Q9WZH4
B	434	LEU	-	EXPRESSION TAG	UNP Q9WZH4
B	435	GLU	-	EXPRESSION TAG	UNP Q9WZH4
B	436	HIS	-	EXPRESSION TAG	UNP Q9WZH4
B	437	HIS	-	EXPRESSION TAG	UNP Q9WZH4
B	438	HIS	-	EXPRESSION TAG	UNP Q9WZH4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	439	HIS	-	EXPRESSION TAG	UNP Q9WZH4
B	440	HIS	-	EXPRESSION TAG	UNP Q9WZH4
B	441	HIS	-	EXPRESSION TAG	UNP Q9WZH4

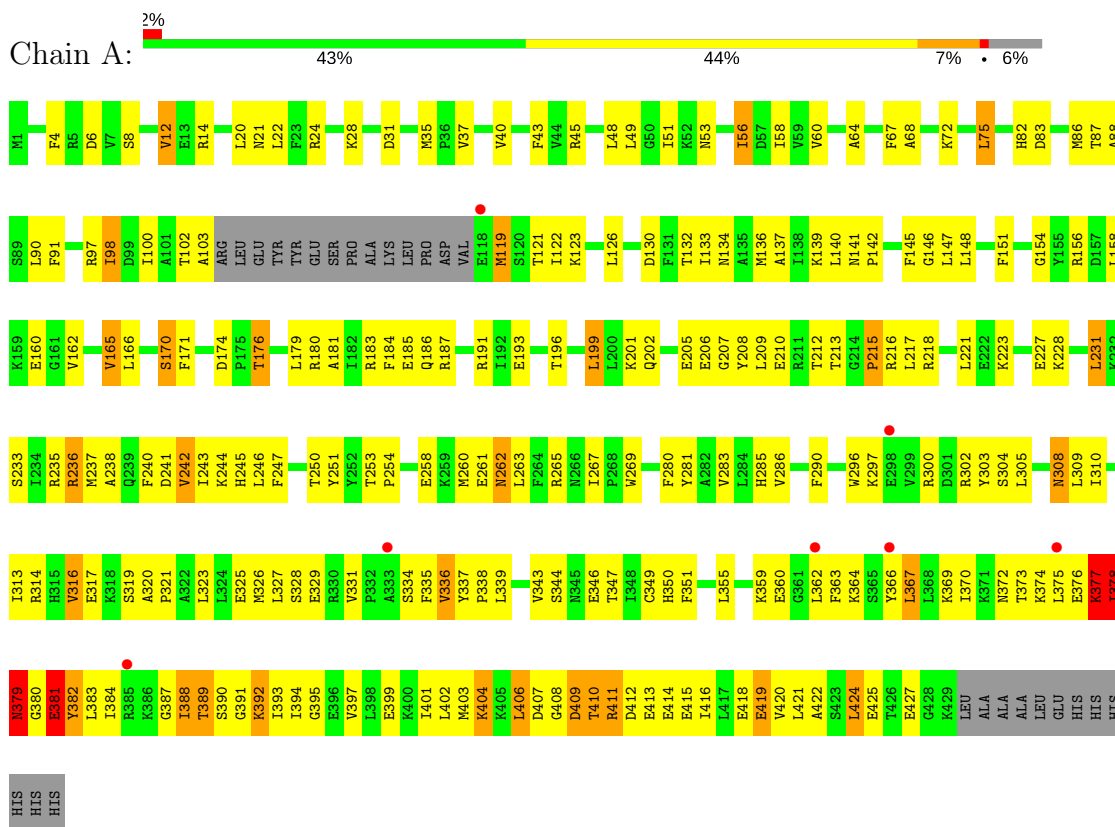
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	16	Total 16	O 16	0	0
2	B	20	Total 20	O 20	0	0

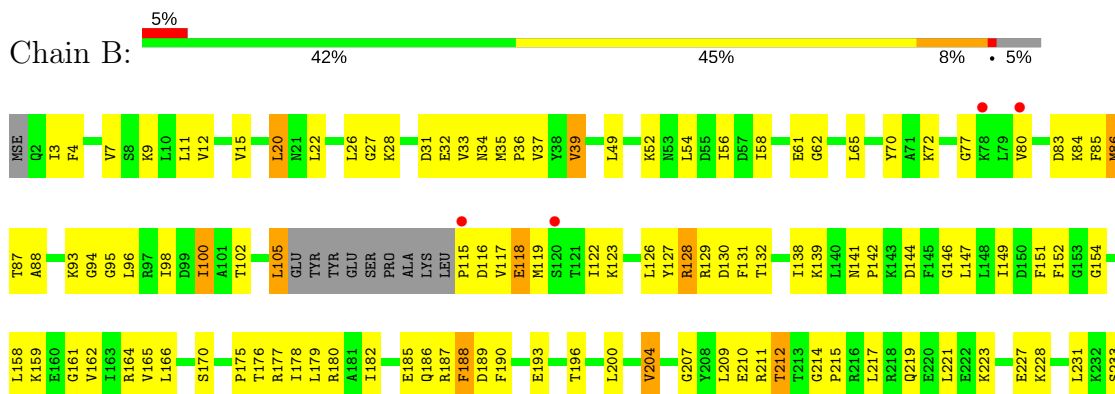
### 3 Residue-property plots

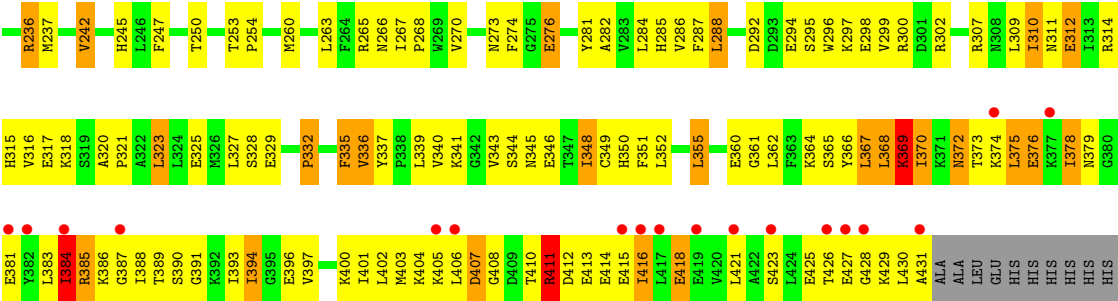
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: TRNA nucleotidyl transferase-related protein



#### • Molecule 1: TRNA nucleotidyl transferase-related protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	190.57Å 62.74Å 152.39Å 90.00° 103.96° 90.00°	Depositor
Resolution (Å)	48.64 – 2.85 48.64 – 2.85	Depositor EDS
% Data completeness (in resolution range)	94.7 (48.64-2.85) 97.8 (48.64-2.85)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.20 (at 2.86Å)	Xtriage
Refinement program	PHENIX (phenix.refine)	Depositor
R, $R_{free}$	0.230 , 0.267 0.228 , 0.229	Depositor DCC
$R_{free}$ test set	1980 reflections (4.90%)	DCC
Wilson B-factor (Å <sup>2</sup> )	81.0	Xtriage
Anisotropy	0.372	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 93.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	6908	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	104.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.69% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.39	0/3465	0.62	3/4639 (0.1%)
1	B	0.48	1/3512 (0.0%)	0.67	2/4704 (0.0%)
All	All	0.44	1/6977 (0.0%)	0.64	5/9343 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	370	ILE	CA-C	5.03	1.66	1.52

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	381	GLU	CB-CA-C	-7.94	94.51	110.40
1	A	381	GLU	N-CA-C	6.67	129.00	111.00
1	B	369	LYS	N-CA-C	-6.50	93.47	111.00
1	A	377	LYS	CB-CA-C	5.79	121.99	110.40
1	B	369	LYS	CB-CA-C	5.75	121.91	110.40

There are no chirality outliers.

There are no planarity outliers.

### 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	3413	0	3509	262	1
1	B	3459	0	3558	274	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	16	0	0	0	0
2	B	20	0	0	1	0
All	All	6908	0	7067	536	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 38.

All (536) 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:375:LEU:HD23	1:B:376:GLU:N	1.38	1.37
1:B:385:ARG:C	1:B:387:GLY:HA2	1.57	1.24
1:A:378:ILE:C	1:A:378:ILE:HD12	1.67	1.13
1:B:375:LEU:N	1:B:375:LEU:HD22	1.57	1.13
1:A:378:ILE:HD12	1:A:378:ILE:O	1.50	1.10
1:A:227:GLU:HG3	1:A:228:LYS:H	1.18	1.09
1:A:380:GLY:O	1:A:381:GLU:HG2	1.53	1.08
1:A:378:ILE:O	1:A:379:ASN:HB3	1.35	1.08
1:B:383:LEU:O	1:B:384:ILE:HB	1.23	1.03
1:B:179:LEU:HD22	1:B:237:MSE:HE3	1.36	1.03
1:B:179:LEU:HD22	1:B:237:MSE:CE	1.89	1.03
1:B:375:LEU:CD2	1:B:376:GLU:H	1.72	1.02
1:A:300:ARG:HA	1:A:305:LEU:HD23	1.43	1.01
1:A:373:THR:O	1:A:373:THR:HG22	1.61	0.99
1:A:392:LYS:HD2	1:A:392:LYS:H	1.24	0.99
1:A:35:MSE:HE1	1:A:67:PHE:HB2	1.41	0.98
1:B:383:LEU:O	1:B:384:ILE:CB	2.11	0.98
1:A:310:ILE:O	1:A:314:ARG:HG2	1.64	0.97
1:B:37:VAL:H	1:B:141:ASN:HD21	0.97	0.96
1:B:336:VAL:HG11	1:B:366:TYR:CD1	2.01	0.95
1:B:247:PHE:O	1:B:250:THR:HG22	1.66	0.95
1:B:386:LYS:N	1:B:387:GLY:HA2	1.81	0.94
1:B:375:LEU:CD2	1:B:375:LEU:N	2.30	0.94
1:B:375:LEU:HD23	1:B:376:GLU:H	0.78	0.94
1:A:326:MSE:HE3	1:A:335:PHE:HB3	1.51	0.93
1:A:375:LEU:HD12	1:A:377:LYS:HG2	1.48	0.92
1:B:179:LEU:CD2	1:B:237:MSE:CE	2.47	0.92
1:B:175:PRO:HB2	1:B:212:THR:HG21	1.49	0.92
1:A:165:VAL:H	1:A:196:THR:HG21	1.36	0.91
1:B:296:TRP:HE1	1:B:300:ARG:HD3	1.33	0.91
1:A:378:ILE:O	1:A:379:ASN:CB	2.18	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:426:THR:HG22	1:B:427:GLU:H	1.38	0.88
1:A:285:HIS:HE1	1:A:347:THR:HG22	1.36	0.88
1:B:328:SER:O	1:B:329:GLU:HB2	1.74	0.88
1:B:86:MSE:HE2	1:B:102:THR:HG21	1.55	0.87
1:A:387:GLY:O	1:A:388:ILE:HG22	1.75	0.87
1:A:37:VAL:H	1:A:141:ASN:HD21	1.15	0.87
1:A:171:PHE:HD2	1:A:199:LEU:HD12	1.38	0.87
1:B:429:LYS:HG2	1:B:430:LEU:H	1.37	0.86
1:A:380:GLY:O	1:A:381:GLU:CG	2.23	0.86
1:B:375:LEU:CD2	1:B:376:GLU:N	2.33	0.86
1:B:105:LEU:H	1:B:105:LEU:HD12	1.40	0.86
1:A:378:ILE:CD1	1:A:378:ILE:C	2.42	0.85
1:B:384:ILE:CD1	1:B:388:ILE:HD11	2.06	0.85
1:B:292:ASP:OD1	1:B:295:SER:HB2	1.77	0.85
1:B:296:TRP:CH2	1:B:310:ILE:N	2.46	0.84
1:B:323:LEU:HD12	1:B:351:PHE:HD2	1.41	0.83
1:B:375:LEU:H	1:B:375:LEU:HD22	1.41	0.83
1:A:237:MSE:HB3	1:A:242:VAL:HG22	1.60	0.82
1:B:179:LEU:CD2	1:B:237:MSE:HE3	2.08	0.82
1:A:260:MSE:HE1	1:A:283:VAL:HG13	1.60	0.82
1:A:247:PHE:O	1:A:250:THR:HG22	1.80	0.81
1:B:368:LEU:O	1:B:369:LYS:HB2	1.78	0.81
1:A:212:THR:HB	1:A:217:LEU:HD21	1.61	0.81
1:A:12:VAL:HA	1:A:20:LEU:HD11	1.61	0.80
1:A:387:GLY:O	1:A:388:ILE:CG2	2.29	0.80
1:B:369:LYS:HA	1:B:372:ASN:HB3	1.64	0.80
1:B:115:PRO:HB2	1:B:116:ASP:HA	1.64	0.80
1:B:37:VAL:N	1:B:141:ASN:HD21	1.79	0.80
1:A:373:THR:O	1:A:373:THR:CG2	2.30	0.80
1:B:321:PRO:O	1:B:325:GLU:HG3	1.83	0.79
1:A:254:PRO:O	1:A:258:GLU:HG2	1.82	0.79
1:B:296:TRP:HH2	1:B:310:ILE:N	1.80	0.79
1:B:379:ASN:O	1:B:383:LEU:HB3	1.83	0.79
1:A:387:GLY:O	1:A:388:ILE:CB	2.30	0.78
1:B:385:ARG:C	1:B:387:GLY:CA	2.48	0.78
1:A:316:VAL:HG21	1:A:350:HIS:CD2	2.18	0.77
1:B:323:LEU:HD12	1:B:351:PHE:CD2	2.20	0.77
1:B:378:ILE:HG22	1:B:412:ASP:HB3	1.67	0.77
1:A:384:ILE:O	1:A:389:THR:HG23	1.85	0.76
1:A:285:HIS:CE1	1:A:347:THR:HG22	2.20	0.76
1:A:388:ILE:O	1:A:388:ILE:HG12	1.86	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:352:LEU:HA	1:B:355:LEU:HD23	1.68	0.75
1:A:404:LYS:HB3	1:A:415:GLU:OE1	1.86	0.75
1:A:227:GLU:HG3	1:A:228:LYS:N	1.99	0.75
1:A:411:ARG:HD3	1:A:412:ASP:N	2.01	0.75
1:B:336:VAL:HG11	1:B:366:TYR:HD1	1.52	0.74
1:B:386:LYS:HG2	1:B:386:LYS:O	1.86	0.74
1:B:56:ILE:HD11	1:B:98:ILE:HD13	1.69	0.74
1:A:392:LYS:N	1:A:392:LYS:HD2	2.02	0.74
1:B:411:ARG:HD2	1:B:414:GLU:OE1	1.88	0.74
1:A:375:LEU:HD23	1:A:375:LEU:H	1.52	0.73
1:A:378:ILE:CD1	1:A:378:ILE:O	2.33	0.73
1:A:171:PHE:CD2	1:A:199:LEU:HD12	2.24	0.72
1:B:119:MSE:HA	1:B:122:ILE:HG22	1.71	0.72
1:B:385:ARG:O	1:B:387:GLY:HA2	1.88	0.72
1:A:375:LEU:HD12	1:A:377:LYS:CG	2.19	0.72
1:A:387:GLY:O	1:A:388:ILE:HB	1.88	0.72
1:A:328:SER:O	1:A:329:GLU:HB3	1.89	0.72
1:B:37:VAL:H	1:B:141:ASN:ND2	1.80	0.72
1:A:323:LEU:HD11	1:A:363:PHE:CD2	2.25	0.72
1:B:385:ARG:HG2	1:B:385:ARG:HH11	1.54	0.72
1:A:179:LEU:CD2	1:A:237:MSE:HE3	2.20	0.71
1:A:375:LEU:HG	1:A:377:LYS:HG3	1.72	0.71
1:A:87:THR:HG22	1:A:88:ALA:H	1.54	0.71
1:B:390:SER:HB3	1:B:393:ILE:HB	1.72	0.71
1:B:22:LEU:HD21	1:B:98:ILE:HD11	1.71	0.71
1:A:308:ASN:ND2	1:A:308:ASN:H	1.88	0.71
1:B:390:SER:O	1:B:394:ILE:HG22	1.91	0.70
1:B:335:PHE:HD1	1:B:335:PHE:H	1.39	0.70
1:B:165:VAL:H	1:B:196:THR:HG21	1.56	0.70
1:A:305:LEU:H	1:A:305:LEU:HD22	1.57	0.70
1:B:115:PRO:CB	1:B:116:ASP:HA	2.21	0.70
1:B:188:PHE:O	1:B:190:PHE:N	2.24	0.70
1:B:179:LEU:CD2	1:B:237:MSE:HE2	2.22	0.70
1:A:56:ILE:O	1:A:56:ILE:HG12	1.92	0.69
1:B:332:PRO:HB2	1:B:335:PHE:HE1	1.57	0.69
1:B:164:ARG:HA	1:B:196:THR:HG21	1.73	0.69
1:A:387:GLY:C	1:A:388:ILE:HG22	2.12	0.69
1:B:295:SER:HA	1:B:298:GLU:HG3	1.74	0.69
1:B:396:GLU:O	1:B:400:LYS:HG2	1.91	0.69
1:B:368:LEU:O	1:B:369:LYS:CB	2.41	0.69
1:B:340:VAL:O	1:B:343:VAL:HG22	1.93	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:122:ILE:O	1:A:126:LEU:HG	1.94	0.68
1:A:370:ILE:O	1:A:374:LYS:HD2	1.93	0.68
1:B:296:TRP:C	1:B:296:TRP:CD1	2.67	0.68
1:A:260:MSE:CE	1:A:283:VAL:HG13	2.24	0.68
1:B:375:LEU:HD21	1:B:405:LYS:HG2	1.76	0.68
1:B:182:ILE:HD12	1:B:236:ARG:HG2	1.75	0.68
1:A:320:ALA:HB3	1:A:321:PRO:HD3	1.76	0.68
1:A:410:THR:HG22	1:A:411:ARG:H	1.60	0.67
1:A:247:PHE:CE2	1:A:303:TYR:CE1	2.83	0.67
1:B:276:GLU:HA	1:B:276:GLU:OE1	1.93	0.67
1:B:410:THR:C	1:B:411:ARG:HG2	2.13	0.67
1:A:241:ASP:OD1	1:A:244:LYS:HD3	1.93	0.67
1:A:375:LEU:HD23	1:A:375:LEU:N	2.10	0.67
1:B:115:PRO:HB2	1:B:116:ASP:CA	2.25	0.66
1:B:369:LYS:HE2	1:B:406:LEU:O	1.95	0.66
1:A:375:LEU:CD1	1:A:377:LYS:CG	2.73	0.66
1:B:49:LEU:HD21	1:B:158:LEU:HD22	1.77	0.66
1:A:212:THR:HB	1:A:217:LEU:CD2	2.26	0.66
1:B:413:GLU:O	1:B:416:ILE:HG22	1.95	0.66
1:A:375:LEU:CD2	1:A:375:LEU:H	2.09	0.65
1:B:369:LYS:O	1:B:372:ASN:N	2.30	0.65
1:A:375:LEU:CD1	1:A:377:LYS:HG2	2.26	0.65
1:B:390:SER:O	1:B:394:ILE:CG2	2.45	0.65
1:B:52:LYS:HE3	1:B:54:LEU:HD13	1.79	0.65
1:B:369:LYS:CA	1:B:372:ASN:HB3	2.26	0.65
1:A:247:PHE:HE2	1:A:303:TYR:CE1	2.14	0.65
1:A:415:GLU:O	1:A:419:GLU:HB2	1.96	0.65
1:B:296:TRP:CZ3	1:B:310:ILE:HA	2.31	0.65
1:A:91:PHE:CE1	1:A:97:ARG:HG3	2.32	0.64
1:A:37:VAL:H	1:A:141:ASN:ND2	1.94	0.64
1:B:178:ILE:HD12	1:B:209:LEU:CD2	2.28	0.64
1:B:332:PRO:HB2	1:B:335:PHE:CE1	2.32	0.64
1:A:346:GLU:H	1:A:346:GLU:CD	2.01	0.64
1:A:380:GLY:C	1:A:381:GLU:HG2	2.16	0.64
1:B:11:LEU:O	1:B:15:VAL:HG23	1.98	0.64
1:A:72:LYS:HE2	1:A:75:LEU:O	1.98	0.64
1:A:379:ASN:CG	1:A:379:ASN:O	2.35	0.63
1:B:381:GLU:HG3	1:B:394:ILE:HD11	1.79	0.63
1:A:300:ARG:HA	1:A:305:LEU:CD2	2.26	0.63
1:B:296:TRP:HE1	1:B:300:ARG:CD	2.10	0.63
1:B:312:GLU:O	1:B:316:VAL:HG23	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:MSE:HB3	1:A:242:VAL:CG2	2.28	0.63
1:A:326:MSE:HE1	1:A:336:VAL:HA	1.80	0.63
1:A:378:ILE:HD12	1:A:379:ASN:N	2.12	0.63
1:A:35:MSE:CE	1:A:67:PHE:HB2	2.24	0.63
1:B:65:LEU:HD21	1:B:86:MSE:HA	1.79	0.63
1:A:344:SER:OG	1:A:347:THR:HG23	1.99	0.63
1:B:179:LEU:HD21	1:B:237:MSE:HE2	1.79	0.63
1:B:385:ARG:O	1:B:387:GLY:CA	2.47	0.63
1:B:285:HIS:ND1	1:B:350:HIS:CD2	2.67	0.63
1:B:430:LEU:N	1:B:430:LEU:HD12	2.14	0.63
1:B:310:ILE:O	1:B:314:ARG:HG3	1.99	0.63
1:A:326:MSE:HE2	1:A:336:VAL:HG13	1.80	0.62
1:B:175:PRO:HB2	1:B:212:THR:CG2	2.25	0.62
1:B:285:HIS:ND1	1:B:350:HIS:HB2	2.14	0.62
1:A:262:ASN:ND2	1:A:265:ARG:HH11	1.98	0.62
1:A:210:GLU:OE1	1:A:245:HIS:ND1	2.32	0.62
1:A:8:SER:HB3	1:A:146:GLY:HA3	1.81	0.62
1:B:407:ASP:OD1	1:B:407:ASP:N	2.30	0.62
1:A:337:TYR:HB3	1:A:403:MSE:HE1	1.82	0.61
1:A:227:GLU:CG	1:A:228:LYS:H	2.02	0.61
1:B:385:ARG:CG	1:B:385:ARG:HH11	2.11	0.61
1:A:4:PHE:HB3	1:A:147:LEU:HD11	1.82	0.61
1:B:105:LEU:N	1:B:105:LEU:HD12	2.15	0.61
1:B:384:ILE:HG21	1:B:394:ILE:HD13	1.81	0.61
1:B:332:PRO:O	1:B:335:PHE:CD1	2.55	0.60
1:B:335:PHE:CD1	1:B:335:PHE:N	2.69	0.60
1:A:378:ILE:HD12	1:A:379:ASN:CB	2.32	0.60
1:A:308:ASN:HD22	1:A:308:ASN:H	1.49	0.60
1:B:375:LEU:O	1:B:376:GLU:C	2.35	0.60
1:A:45:ARG:HD3	1:A:134:ASN:OD1	2.01	0.60
1:A:202:GLN:O	1:A:206:GLU:HG2	2.02	0.60
1:A:309:LEU:O	1:A:313:ILE:HG13	2.02	0.59
1:A:334:SER:HA	1:A:406:LEU:HD11	1.84	0.59
1:B:123:LYS:HB2	1:B:151:PHE:CE2	2.36	0.59
1:B:72:LYS:HD3	1:B:72:LYS:O	2.02	0.59
1:A:132:THR:HA	1:A:166:LEU:HD21	1.84	0.59
1:A:336:VAL:HG21	1:A:366:TYR:HD1	1.67	0.59
1:B:178:ILE:HD12	1:B:209:LEU:HD21	1.83	0.59
1:B:193:GLU:OE2	1:B:196:THR:HG23	2.01	0.59
1:A:260:MSE:SE	1:A:263:LEU:HD23	2.53	0.59
1:A:6:ASP:OD1	1:A:6:ASP:O	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:410:THR:O	1:B:411:ARG:CB	2.50	0.59
1:B:285:HIS:ND1	1:B:350:HIS:HD2	2.00	0.59
1:B:426:THR:HG22	1:B:427:GLU:N	2.13	0.58
1:B:296:TRP:CD1	1:B:297:LYS:N	2.71	0.58
1:B:369:LYS:HA	1:B:373:THR:H	1.68	0.58
1:B:187:ARG:HD3	1:B:188:PHE:CZ	2.38	0.58
1:A:375:LEU:O	1:A:376:GLU:HB3	2.03	0.58
1:A:359:LYS:H	1:A:359:LYS:HD2	1.68	0.58
1:B:376:GLU:OE2	1:B:401:ILE:HG13	2.03	0.57
1:A:233:SER:O	1:A:237:MSE:HG3	2.05	0.57
1:B:207:GLY:O	1:B:210:GLU:HG2	2.03	0.57
1:B:376:GLU:OE1	1:B:376:GLU:HA	2.04	0.57
1:B:384:ILE:HD13	1:B:388:ILE:HD11	1.82	0.57
1:A:401:ILE:HD11	1:A:416:ILE:HA	1.86	0.57
1:B:263:LEU:HD11	1:B:282:ALA:HB1	1.87	0.57
1:B:410:THR:O	1:B:411:ARG:HB2	2.04	0.57
1:A:247:PHE:CE2	1:A:303:TYR:HE1	2.22	0.57
1:B:162:VAL:HG13	1:B:193:GLU:HB3	1.87	0.57
1:A:269:TRP:CG	1:A:364:LYS:HE3	2.39	0.56
1:B:219:GLN:HE21	1:B:223:LYS:NZ	2.03	0.56
1:B:298:GLU:O	1:B:302:ARG:HB3	2.05	0.56
1:A:328:SER:O	1:A:329:GLU:CB	2.52	0.56
1:A:377:LYS:CB	1:A:377:LYS:NZ	2.67	0.56
1:B:296:TRP:CH2	1:B:310:ILE:CA	2.88	0.56
1:B:187:ARG:HG3	1:B:227:GLU:OE1	2.06	0.56
1:B:361:GLY:O	1:B:364:LYS:HB2	2.06	0.56
1:A:237:MSE:HE2	1:A:242:VAL:CG2	2.36	0.56
1:B:3:ILE:HD12	1:B:151:PHE:HD1	1.70	0.56
1:A:325:GLU:O	1:A:329:GLU:HB3	2.05	0.56
1:A:336:VAL:HG21	1:A:366:TYR:CD1	2.41	0.56
1:B:247:PHE:HB2	1:B:250:THR:CG2	2.35	0.56
1:B:85:PHE:O	1:B:87:THR:HG23	2.06	0.56
1:A:126:LEU:HD11	1:A:137:ALA:HB2	1.87	0.56
1:A:376:GLU:C	1:A:377:LYS:O	2.39	0.56
1:A:372:ASN:O	1:A:373:THR:C	2.45	0.56
1:B:296:TRP:HD1	1:B:297:LYS:N	2.03	0.56
1:A:209:LEU:HD21	1:A:246:LEU:HG	1.87	0.55
1:A:297:LYS:HE2	1:A:300:ARG:HH22	1.70	0.55
1:B:128:ARG:HB3	1:B:128:ARG:HH21	1.71	0.55
1:B:56:ILE:CD1	1:B:98:ILE:HD13	2.35	0.55
1:A:247:PHE:HB2	1:A:250:THR:CG2	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:370:ILE:HD13	1:A:406:LEU:HD22	1.87	0.55
1:A:421:LEU:HA	1:A:424:LEU:HB3	1.87	0.55
1:A:235:ARG:O	1:A:238:ALA:HB3	2.06	0.55
1:A:343:VAL:HB	1:A:347:THR:OG1	2.06	0.55
1:A:406:LEU:HD12	1:A:407:ASP:OD1	2.07	0.55
1:B:386:LYS:N	1:B:387:GLY:CA	2.62	0.55
1:B:36:PRO:HG2	1:B:61:GLU:OE2	2.07	0.55
1:A:265:ARG:NH2	1:A:360:GLU:OE1	2.41	0.54
1:B:185:GLU:OE1	1:B:236:ARG:HD3	2.07	0.54
1:B:129:ARG:O	1:B:166:LEU:HD12	2.08	0.54
1:A:302:ARG:HH21	1:A:302:ARG:HG2	1.72	0.54
1:B:165:VAL:N	1:B:196:THR:HG21	2.21	0.54
1:B:352:LEU:HA	1:B:355:LEU:CD2	2.35	0.54
1:A:366:TYR:O	1:A:370:ILE:HG12	2.08	0.54
1:A:401:ILE:HG23	1:A:415:GLU:HG2	1.88	0.54
1:B:348:ILE:HG23	1:B:367:LEU:CD2	2.37	0.54
1:A:180:ARG:HG2	1:A:183:ARG:NH2	2.23	0.54
1:B:378:ILE:CG2	1:B:412:ASP:HB3	2.37	0.54
1:B:385:ARG:CG	1:B:385:ARG:NH1	2.68	0.54
1:B:404:LYS:HB2	1:B:415:GLU:OE1	2.08	0.54
1:A:174:ASP:OD1	1:A:176:THR:HG22	2.08	0.54
1:B:7:VAL:HG22	1:B:146:GLY:O	2.08	0.53
1:A:87:THR:HG22	1:A:88:ALA:N	2.21	0.53
1:B:3:ILE:HD12	1:B:151:PHE:CD1	2.43	0.53
1:B:88:ALA:O	1:B:100:ILE:HD12	2.09	0.53
1:A:102:THR:HG22	1:A:103:ALA:N	2.24	0.53
1:A:160:GLU:O	1:A:162:VAL:HG23	2.08	0.53
1:A:376:GLU:O	1:A:377:LYS:C	2.44	0.53
1:B:161:GLY:HA2	1:B:190:PHE:CE2	2.44	0.53
1:A:35:MSE:HE3	1:A:60:VAL:HB	1.91	0.52
1:B:84:LYS:O	1:B:85:PHE:CD1	2.62	0.52
1:A:397:VAL:O	1:A:401:ILE:HG12	2.08	0.52
1:B:369:LYS:N	1:B:372:ASN:HB2	2.25	0.52
1:A:231:LEU:HD22	1:A:235:ARG:NE	2.25	0.52
1:B:386:LYS:CG	1:B:386:LYS:O	2.56	0.52
1:A:409:ASP:OD1	1:A:415:GLU:OE2	2.27	0.52
1:A:326:MSE:HE3	1:A:331:VAL:HG21	1.90	0.52
1:B:72:LYS:HD3	1:B:72:LYS:C	2.30	0.52
1:A:237:MSE:HE2	1:A:242:VAL:HG23	1.92	0.51
1:A:377:LYS:HZ2	1:A:377:LYS:HB3	1.75	0.51
1:A:413:GLU:HA	1:A:416:ILE:HG22	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:376:GLU:OE2	1:B:402:LEU:N	2.43	0.51
1:B:253:THR:HB	1:B:254:PRO:HD2	1.92	0.51
1:B:4:PHE:HE2	1:B:149:ILE:HG12	1.76	0.51
1:A:179:LEU:HD21	1:A:237:MSE:HE3	1.91	0.51
1:A:308:ASN:N	1:A:308:ASN:ND2	2.57	0.51
1:A:346:GLU:N	1:A:346:GLU:CD	2.64	0.51
1:B:384:ILE:HD11	1:B:397:VAL:HG11	1.93	0.51
1:A:49:LEU:HD23	1:A:158:LEU:HD11	1.92	0.51
1:A:326:MSE:HE1	1:A:336:VAL:CA	2.40	0.51
1:A:165:VAL:HG13	1:A:170:SER:OG	2.10	0.51
1:A:285:HIS:ND1	1:A:350:HIS:CD2	2.79	0.51
1:A:31:ASP:OD2	1:A:142:PRO:HD2	2.11	0.51
1:B:186:GLN:HG3	1:B:233:SER:OG	2.11	0.51
1:A:326:MSE:HE1	1:A:335:PHE:C	2.31	0.51
1:A:377:LYS:NZ	1:A:377:LYS:HB3	2.26	0.51
1:B:430:LEU:O	1:B:431:ALA:HB2	2.09	0.51
1:A:130:ASP:N	1:A:130:ASP:OD1	2.34	0.51
1:A:316:VAL:HG23	1:A:317:GLU:H	1.76	0.51
1:B:116:ASP:HB3	1:B:118:GLU:CG	2.41	0.51
1:B:379:ASN:HA	1:B:383:LEU:HD13	1.92	0.51
1:A:316:VAL:HG12	1:A:351:PHE:CE1	2.46	0.50
1:B:429:LYS:HG2	1:B:430:LEU:N	2.16	0.50
1:B:65:LEU:HD22	1:B:65:LEU:H	1.77	0.50
1:B:314:ARG:HA	1:B:317:GLU:HB3	1.93	0.50
1:B:323:LEU:HD22	1:B:327:LEU:HD11	1.92	0.50
1:B:3:ILE:CD1	1:B:151:PHE:HA	2.41	0.50
1:A:310:ILE:O	1:A:314:ARG:CG	2.50	0.50
1:B:178:ILE:HG23	1:B:200:LEU:HD21	1.93	0.50
1:B:316:VAL:HG13	1:B:351:PHE:CD1	2.46	0.50
1:A:49:LEU:CD2	1:A:158:LEU:HD11	2.42	0.50
1:A:56:ILE:HD13	1:A:98:ILE:HG22	1.93	0.50
1:B:369:LYS:CE	1:B:406:LEU:O	2.59	0.50
1:A:296:TRP:CD2	1:A:310:ILE:HB	2.47	0.50
1:A:165:VAL:CG1	1:A:170:SER:OG	2.60	0.50
1:B:12:VAL:HG12	1:B:20:LEU:HD11	1.92	0.50
1:B:34:ASN:OD1	1:B:34:ASN:O	2.30	0.50
1:A:379:ASN:OD1	1:A:379:ASN:O	2.29	0.49
1:A:411:ARG:C	1:A:411:ARG:HD3	2.31	0.49
1:B:296:TRP:CZ3	1:B:310:ILE:CA	2.94	0.49
1:B:410:THR:HG22	1:B:411:ARG:H	1.77	0.49
1:B:378:ILE:HG23	1:B:379:ASN:N	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:HIS:HB3	1:A:350:HIS:CD2	2.48	0.49
1:A:35:MSE:HE1	1:A:67:PHE:CB	2.28	0.49
1:A:269:TRP:CD2	1:A:364:LYS:HE3	2.47	0.49
1:A:56:ILE:HD13	1:A:98:ILE:CG2	2.42	0.49
1:B:247:PHE:HB2	1:B:250:THR:HG21	1.93	0.49
1:B:336:VAL:HG11	1:B:366:TYR:CE1	2.47	0.49
1:A:427:GLU:HA	1:A:427:GLU:OE1	2.13	0.49
1:A:154:GLY:O	1:A:158:LEU:HB2	2.13	0.49
1:B:3:ILE:HD13	1:B:151:PHE:HA	1.94	0.49
1:B:430:LEU:CD1	1:B:430:LEU:N	2.75	0.49
1:A:296:TRP:CE2	1:A:310:ILE:HB	2.47	0.49
1:B:185:GLU:O	1:B:188:PHE:O	2.30	0.49
1:A:21:ASN:ND2	1:A:24:ARG:HH11	2.11	0.49
1:B:378:ILE:CG2	1:B:379:ASN:N	2.75	0.49
1:B:384:ILE:HD12	1:B:388:ILE:HD11	1.92	0.49
1:B:39:VAL:HG23	1:B:138:ILE:HB	1.95	0.49
1:A:290:PHE:CD2	1:A:317:GLU:OE1	2.66	0.49
1:B:369:LYS:CA	1:B:372:ASN:CB	2.90	0.49
1:A:375:LEU:O	1:A:376:GLU:C	2.49	0.48
1:B:27:GLY:O	1:B:142:PRO:HD3	2.13	0.48
1:A:359:LYS:N	1:A:359:LYS:HD2	2.28	0.48
1:B:72:LYS:HE3	1:B:77:GLY:O	2.13	0.48
1:A:206:GLU:HB2	1:A:208:TYR:CD2	2.48	0.48
1:A:411:ARG:HD3	1:A:412:ASP:H	1.77	0.48
1:A:213:THR:OG1	1:A:216:ARG:HD3	2.13	0.48
1:A:8:SER:O	1:A:12:VAL:HG12	2.12	0.48
1:B:116:ASP:HB3	1:B:118:GLU:HG3	1.96	0.48
1:B:426:THR:CG2	1:B:427:GLU:H	2.07	0.48
1:A:187:ARG:HD3	1:A:227:GLU:OE1	2.14	0.48
1:A:374:LYS:HA	1:A:402:LEU:HD11	1.94	0.48
1:B:411:ARG:HB3	1:B:414:GLU:HG2	1.96	0.48
1:A:392:LYS:CD	1:A:392:LYS:H	2.10	0.48
1:B:369:LYS:C	1:B:372:ASN:H	2.16	0.48
1:B:404:LYS:O	1:B:408:GLY:N	2.47	0.48
1:B:237:MSE:HB3	1:B:242:VAL:HG22	1.96	0.48
1:A:399:GLU:O	1:A:403:MSE:HG2	2.14	0.47
1:B:139:LYS:HD3	1:B:144:ASP:HB2	1.96	0.47
1:B:320:ALA:HB3	1:B:321:PRO:HD3	1.96	0.47
1:A:209:LEU:HD21	1:A:246:LEU:CD2	2.44	0.47
1:A:391:GLY:O	1:A:394:ILE:HG23	2.13	0.47
1:A:326:MSE:CE	1:A:335:PHE:HB3	2.33	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:ARG:HG3	1:A:240:PHE:CE2	2.49	0.47
1:A:247:PHE:HB2	1:A:250:THR:HG22	1.96	0.47
1:B:323:LEU:O	1:B:327:LEU:HG	2.15	0.47
1:B:369:LYS:O	1:B:373:THR:N	2.47	0.47
1:A:123:LYS:HG3	1:A:151:PHE:CD2	2.50	0.47
1:A:165:VAL:HB	1:A:196:THR:HG22	1.96	0.47
1:A:250:THR:HG23	1:A:250:THR:O	2.15	0.47
1:B:390:SER:OG	1:B:391:GLY:N	2.47	0.47
1:A:165:VAL:H	1:A:196:THR:CG2	2.15	0.47
1:B:297:LYS:O	1:B:298:GLU:C	2.51	0.47
1:B:204:VAL:O	1:B:245:HIS:CE1	2.68	0.47
1:A:241:ASP:O	1:A:245:HIS:HD2	1.97	0.47
1:A:323:LEU:HD11	1:A:363:PHE:HD2	1.75	0.47
1:B:312:GLU:H	1:B:312:GLU:HG2	1.54	0.47
1:B:316:VAL:HG13	1:B:351:PHE:CE1	2.50	0.47
1:A:132:THR:HG22	1:A:166:LEU:CD2	2.44	0.47
1:B:214:GLY:N	1:B:215:PRO:HD2	2.29	0.47
1:B:281:TYR:HB3	1:B:346:GLU:HG3	1.97	0.47
1:B:28:LYS:HD2	1:B:32:GLU:OE1	2.14	0.47
1:A:139:LYS:O	1:A:145:PHE:O	2.33	0.47
1:A:262:ASN:N	1:A:262:ASN:ND2	2.61	0.47
1:B:127:TYR:HD2	1:B:152:PHE:CZ	2.33	0.47
1:B:161:GLY:HA2	1:B:190:PHE:CZ	2.49	0.47
1:A:381:GLU:HG3	1:A:382:TYR:N	2.30	0.46
1:B:310:ILE:HD13	1:B:311:ASN:ND2	2.29	0.46
1:B:379:ASN:HD22	1:B:416:ILE:HG21	1.80	0.46
1:A:37:VAL:N	1:A:141:ASN:HD21	1.97	0.46
1:B:4:PHE:CE2	1:B:149:ILE:HG12	2.50	0.46
1:B:295:SER:HA	1:B:298:GLU:CG	2.45	0.46
1:A:326:MSE:HE1	1:A:336:VAL:N	2.30	0.46
1:A:45:ARG:HD2	1:A:133:ILE:HD12	1.96	0.46
1:B:31:ASP:CG	1:B:142:PRO:HD2	2.36	0.46
1:A:162:VAL:HG13	1:A:193:GLU:HB3	1.97	0.46
1:A:285:HIS:ND1	1:A:350:HIS:HB2	2.30	0.46
1:B:267:ILE:HG12	1:B:349:CYS:SG	2.56	0.46
1:B:323:LEU:HD22	1:B:327:LEU:CD1	2.46	0.46
1:B:383:LEU:HD23	1:B:384:ILE:N	2.30	0.46
1:B:93:LYS:O	1:B:95:GLY:N	2.49	0.46
1:B:315:HIS:NE2	1:B:339:LEU:O	2.39	0.46
1:A:327:LEU:HD11	1:A:363:PHE:HB2	1.96	0.46
1:A:40:VAL:HG12	1:A:137:ALA:CB	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:GLU:O	1:A:349:CYS:HB2	2.16	0.46
1:B:86:MSE:HG2	1:B:102:THR:OG1	2.16	0.46
1:B:296:TRP:CH2	1:B:309:LEU:HB3	2.51	0.46
1:B:346:GLU:CD	1:B:346:GLU:H	2.19	0.46
1:A:411:ARG:HH11	1:A:412:ASP:H	1.64	0.45
1:A:98:ILE:O	1:A:98:ILE:HG12	2.17	0.45
1:B:266:ASN:O	1:B:270:VAL:HG23	2.17	0.45
1:A:263:LEU:HD22	1:A:286:VAL:HG21	1.99	0.45
1:A:247:PHE:CD2	1:A:303:TYR:HE1	2.34	0.45
1:A:48:LEU:HD12	1:A:136:MSE:HE1	1.98	0.45
1:B:175:PRO:HG2	1:B:212:THR:HG22	1.99	0.45
1:B:284:LEU:O	1:B:288:LEU:HB2	2.16	0.45
1:A:251:TYR:O	1:A:253:THR:HG23	2.17	0.45
1:B:132:THR:HB	1:B:154:GLY:HA2	1.99	0.45
1:B:247:PHE:N	1:B:247:PHE:CD1	2.84	0.45
1:B:348:ILE:HG23	1:B:367:LEU:HD22	1.98	0.45
1:B:410:THR:O	1:B:411:ARG:CG	2.64	0.45
1:A:410:THR:HG21	1:A:414:GLU:CD	2.37	0.45
1:B:186:GLN:CG	1:B:233:SER:OG	2.65	0.45
1:A:263:LEU:O	1:A:267:ILE:HG13	2.17	0.45
1:A:404:LYS:HA	1:A:404:LYS:HD2	1.59	0.45
1:B:178:ILE:HD12	1:B:209:LEU:HD23	1.98	0.45
1:B:187:ARG:O	1:B:228:LYS:HE2	2.16	0.45
1:B:362:LEU:HA	1:B:362:LEU:HD23	1.78	0.45
1:B:4:PHE:CZ	1:B:119:MSE:SE	3.20	0.45
1:A:363:PHE:CE1	1:A:367:LEU:HD22	2.52	0.44
1:A:375:LEU:CG	1:A:377:LYS:HG3	2.43	0.44
1:B:273:ASN:C	1:B:274:PHE:CD2	2.91	0.44
1:A:218:ARG:HG3	1:A:280:PHE:CE2	2.52	0.44
1:B:35:MSE:O	1:B:37:VAL:HG23	2.17	0.44
1:B:401:ILE:HG21	1:B:416:ILE:HB	1.98	0.44
1:A:304:SER:O	1:A:305:LEU:C	2.54	0.44
1:B:285:HIS:HB3	1:B:350:HIS:CD2	2.53	0.44
1:A:392:LYS:CD	1:A:392:LYS:N	2.75	0.44
1:B:296:TRP:HH2	1:B:309:LEU:HB3	1.83	0.44
1:A:186:GLN:HG3	1:A:233:SER:OG	2.18	0.44
1:B:138:ILE:HA	1:B:147:LEU:O	2.17	0.44
1:B:369:LYS:NZ	1:B:406:LEU:O	2.48	0.44
1:A:218:ARG:HG3	1:A:280:PHE:CZ	2.53	0.44
1:B:425:GLU:CG	1:B:426:THR:N	2.81	0.44
1:B:423:SER:O	1:B:425:GLU:O	2.36	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:GLU:O	1:A:328:SER:O	2.35	0.44
1:A:64:ALA:HB3	1:A:86:MSE:O	2.18	0.44
1:B:402:LEU:O	1:B:405:LYS:HB3	2.18	0.44
1:A:183:ARG:HD2	1:A:223:LYS:HB3	1.99	0.43
1:A:285:HIS:ND1	1:A:350:HIS:HD2	2.16	0.43
1:A:379:ASN:C	1:A:379:ASN:OD1	2.54	0.43
1:B:130:ASP:OD1	1:B:131:PHE:N	2.44	0.43
1:A:21:ASN:HD22	1:A:24:ARG:HH11	1.65	0.43
1:A:313:ILE:O	1:A:317:GLU:HB2	2.18	0.43
1:B:425:GLU:CD	1:B:426:THR:H	2.22	0.43
1:B:93:LYS:C	1:B:95:GLY:H	2.21	0.43
1:A:388:ILE:O	1:A:388:ILE:CG1	2.59	0.43
1:A:418:GLU:O	1:A:422:ALA:HB2	2.19	0.43
1:A:215:PRO:O	1:A:216:ARG:C	2.56	0.43
1:A:313:ILE:O	1:A:316:VAL:HG23	2.18	0.43
1:B:406:LEU:HA	1:B:406:LEU:HD23	1.83	0.43
1:B:385:ARG:HA	1:B:385:ARG:HD2	1.32	0.43
1:A:140:LEU:HD23	1:A:140:LEU:HA	1.81	0.43
1:B:345:ASN:HA	1:B:348:ILE:HG13	2.00	0.43
1:A:316:VAL:HG23	1:A:317:GLU:N	2.34	0.43
1:B:26:LEU:HD23	1:B:26:LEU:HA	1.82	0.43
1:A:49:LEU:HD21	1:A:158:LEU:HD21	2.00	0.43
1:A:316:VAL:HG12	1:A:351:PHE:CZ	2.54	0.43
1:B:310:ILE:HG23	1:B:311:ASN:HD22	1.84	0.43
1:B:429:LYS:CG	1:B:430:LEU:H	2.16	0.43
1:B:84:LYS:HE2	1:B:85:PHE:CE2	2.54	0.43
1:A:184:PHE:HA	1:A:187:ARG:HB3	2.00	0.42
1:B:128:ARG:HB3	1:B:128:ARG:NH2	2.34	0.42
1:B:32:GLU:OE2	1:B:70:TYR:OH	2.29	0.42
1:B:348:ILE:HG12	1:B:348:ILE:H	1.45	0.42
1:B:370:ILE:O	1:B:374:LYS:HB3	2.19	0.42
1:B:93:LYS:C	1:B:95:GLY:N	2.73	0.42
1:A:180:ARG:O	1:A:181:ALA:C	2.58	0.42
1:B:9:LYS:O	1:B:12:VAL:HG22	2.19	0.42
1:A:49:LEU:HD21	1:A:158:LEU:CD2	2.50	0.42
1:B:361:GLY:O	1:B:364:LYS:N	2.52	0.42
1:A:119:MSE:SE	1:A:139:LYS:NZ	3.03	0.42
1:B:314:ARG:HB3	1:B:318:LYS:HE3	2.01	0.42
1:A:201:LYS:O	1:A:205:GLU:HG2	2.20	0.42
1:A:302:ARG:NH2	1:A:302:ARG:HG2	2.33	0.42
1:B:425:GLU:HG3	1:B:426:THR:N	2.34	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:GLU:HB2	1:A:208:TYR:HD2	1.84	0.42
1:A:56:ILE:HG13	1:A:58:ILE:CD1	2.50	0.42
1:B:177:ARG:HA	1:B:180:ARG:HB2	2.00	0.42
1:B:56:ILE:HG13	1:B:98:ILE:HA	2.02	0.42
1:A:367:LEU:HA	1:A:367:LEU:HD12	1.86	0.42
1:A:82:HIS:HD2	1:A:87:THR:HB	1.85	0.42
1:B:115:PRO:CB	1:B:116:ASP:CA	2.91	0.42
1:A:369:LYS:O	1:A:373:THR:HB	2.20	0.42
1:A:424:LEU:HD23	1:A:425:GLU:N	2.35	0.42
1:A:375:LEU:HD11	1:A:377:LYS:HD2	2.01	0.41
1:B:105:LEU:HD23	2:B:445:HOH:O	2.18	0.41
1:B:219:GLN:HE21	1:B:223:LYS:HZ2	1.67	0.41
1:A:43:PHE:HA	1:A:53:ASN:ND2	2.35	0.41
1:B:117:VAL:O	1:B:119:MSE:N	2.53	0.41
1:B:165:VAL:HG22	1:B:196:THR:CG2	2.50	0.41
1:B:22:LEU:CD2	1:B:98:ILE:HD11	2.48	0.41
1:A:319:SER:HB3	1:A:339:LEU:HD23	2.01	0.41
1:A:370:ILE:CD1	1:A:406:LEU:HD22	2.49	0.41
1:B:260:MSE:HE3	1:B:287:PHE:CE2	2.55	0.41
1:B:369:LYS:HG3	1:B:373:THR:OG1	2.19	0.41
1:A:394:ILE:HG13	1:A:395:GLY:N	2.34	0.41
1:A:326:MSE:C	1:A:328:SER:O	2.59	0.41
1:A:380:GLY:C	1:A:381:GLU:CG	2.85	0.41
1:A:51:ILE:HA	1:A:51:ILE:HD13	1.78	0.41
1:B:300:ARG:C	1:B:302:ARG:H	2.24	0.41
1:B:383:LEU:HD23	1:B:384:ILE:H	1.86	0.41
1:A:68:ALA:HB2	1:A:100:ILE:HD12	2.02	0.41
1:A:185:GLU:OE2	1:A:236:ARG:HD3	2.20	0.41
1:A:323:LEU:HD11	1:A:363:PHE:CE2	2.55	0.41
1:A:156:ARG:O	1:A:160:GLU:HG2	2.20	0.41
1:A:205:GLU:C	1:A:207:GLY:H	2.24	0.41
1:B:189:ASP:O	1:B:190:PHE:HD2	2.04	0.41
1:B:410:THR:C	1:B:411:ARG:CG	2.81	0.41
1:A:121:THR:C	1:A:123:LYS:N	2.74	0.41
1:B:34:ASN:OD1	1:B:34:ASN:C	2.58	0.41
1:A:337:TYR:N	1:A:338:PRO:HD2	2.35	0.41
1:A:401:ILE:CD1	1:A:416:ILE:HA	2.51	0.41
1:B:267:ILE:N	1:B:268:PRO:CD	2.84	0.41
1:B:337:TYR:CD2	1:B:337:TYR:C	2.94	0.41
1:A:141:ASN:HA	1:A:142:PRO:HD3	1.90	0.40
1:A:290:PHE:N	1:A:290:PHE:CD2	2.88	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:393:ILE:O	1:A:397:VAL:HG13	2.21	0.40
1:A:419:GLU:OE1	1:A:419:GLU:O	2.40	0.40
1:B:273:ASN:O	1:B:274:PHE:CD2	2.74	0.40
1:B:375:LEU:HD21	1:B:405:LYS:CG	2.48	0.40
1:B:418:GLU:O	1:B:421:LEU:HB3	2.21	0.40
1:A:378:ILE:HD12	1:A:379:ASN:HB3	2.02	0.40
1:A:420:VAL:HG23	1:A:421:LEU:N	2.36	0.40
1:A:372:ASN:C	1:A:374:LYS:N	2.72	0.40
1:B:316:VAL:HG13	1:B:351:PHE:CG	2.56	0.40
1:B:286:VAL:O	1:B:287:PHE:C	2.59	0.40
1:B:372:ASN:HB3	1:B:373:THR:H	1.78	0.40
1:B:375:LEU:O	1:B:376:GLU:O	2.39	0.40
1:B:430:LEU:HB3	1:B:431:ALA:H	1.79	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:281:TYR:OH	1:A:382:TYR:OH[4_546]	1.44	0.76

## 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	411/441 (93%)	375 (91%)	30 (7%)	6 (2%)	12	35
1	B	417/441 (95%)	366 (88%)	42 (10%)	9 (2%)	8	25
All	All	828/882 (94%)	741 (90%)	72 (9%)	15 (2%)	10	31

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	378	ILE
1	A	379	ASN
1	A	388	ILE
1	B	118	GLU
1	B	332	PRO
1	B	341	LYS
1	B	369	LYS
1	B	384	ILE
1	B	411	ARG
1	B	428	GLY
1	A	381	GLU
1	A	408	GLY
1	A	215	PRO
1	B	94	GLY
1	B	62	GLY

### 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	373/385 (97%)	329 (88%)	44 (12%)	6	16
1	B	378/385 (98%)	323 (85%)	55 (15%)	3	10
All	All	751/770 (98%)	652 (87%)	99 (13%)	5	12

All (99) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	VAL
1	A	14	ARG
1	A	22	LEU
1	A	28	LYS
1	A	56	ILE
1	A	75	LEU
1	A	83	ASP
1	A	90	LEU
1	A	98	ILE

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Mol	Chain	Res	Type
1	A	119	MSE
1	A	148	LEU
1	A	165	VAL
1	A	170	SER
1	A	176	THR
1	A	191	ARG
1	A	199	LEU
1	A	221	LEU
1	A	231	LEU
1	A	236	ARG
1	A	242	VAL
1	A	243	ILE
1	A	261	GLU
1	A	262	ASN
1	A	308	ASN
1	A	316	VAL
1	A	336	VAL
1	A	355	LEU
1	A	362	LEU
1	A	367	LEU
1	A	377	LYS
1	A	378	ILE
1	A	379	ASN
1	A	382	TYR
1	A	383	LEU
1	A	389	THR
1	A	390	SER
1	A	392	LYS
1	A	404	LYS
1	A	406	LEU
1	A	409	ASP
1	A	410	THR
1	A	411	ARG
1	A	419	GLU
1	A	424	LEU
1	B	20	LEU
1	B	33	VAL
1	B	39	VAL
1	B	58	ILE
1	B	80	VAL
1	B	83	ASP
1	B	86	MSE

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Mol	Chain	Res	Type
1	B	96	LEU
1	B	100	ILE
1	B	105	LEU
1	B	126	LEU
1	B	128	ARG
1	B	159	LYS
1	B	170	SER
1	B	176	THR
1	B	188	PHE
1	B	204	VAL
1	B	211	ARG
1	B	212	THR
1	B	217	LEU
1	B	221	LEU
1	B	231	LEU
1	B	236	ARG
1	B	242	VAL
1	B	265	ARG
1	B	276	GLU
1	B	288	LEU
1	B	294	GLU
1	B	299	VAL
1	B	307	ARG
1	B	310	ILE
1	B	312	GLU
1	B	323	LEU
1	B	335	PHE
1	B	336	VAL
1	B	344	SER
1	B	348	ILE
1	B	355	LEU
1	B	360	GLU
1	B	365	SER
1	B	367	LEU
1	B	368	LEU
1	B	372	ASN
1	B	375	LEU
1	B	376	GLU
1	B	378	ILE
1	B	384	ILE
1	B	385	ARG
1	B	389	THR

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Mol	Chain	Res	Type
1	B	394	ILE
1	B	403	MSE
1	B	407	ASP
1	B	411	ARG
1	B	416	ILE
1	B	418	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (16) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	2	GLN
1	A	21	ASN
1	A	34	ASN
1	A	82	HIS
1	A	141	ASN
1	A	219	GLN
1	A	262	ASN
1	A	308	ASN
1	A	350	HIS
1	B	141	ASN
1	B	219	GLN
1	B	245	HIS
1	B	311	ASN
1	B	345	ASN
1	B	350	HIS
1	B	372	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

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	405/441 (91%)	0.06	7 (1%) 70 68	60, 107, 146, 186	0
1	B	412/441 (93%)	0.25	22 (5%) 27 22	51, 88, 186, 300	0
All	All	817/882 (92%)	0.15	29 (3%) 44 38	51, 99, 163, 300	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	427	GLU	9.7
1	B	419	GLU	8.6
1	B	417	LEU	6.8
1	B	428	GLY	4.1
1	B	381	GLU	3.9
1	B	416	ILE	3.4
1	A	385	ARG	3.2
1	B	431	ALA	3.2
1	B	115	PRO	3.0
1	A	118	GLU	3.0
1	B	405	LYS	2.8
1	B	382	TYR	2.7
1	B	415	GLU	2.7
1	B	387	GLY	2.7
1	B	406	LEU	2.6
1	B	377	LYS	2.6
1	A	362	LEU	2.6
1	B	374	LYS	2.5
1	B	80	VAL	2.4
1	A	298	GLU	2.3
1	B	78	LYS	2.2
1	A	333	ALA	2.1
1	B	120	SER	2.1
1	B	421	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	426	THR	2.1
1	A	375	LEU	2.1
1	B	423	SER	2.1
1	B	384	ILE	2.1
1	A	366	TYR	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.