



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:28 PM GMT

PDB ID : 3TVI
Title : Crystal structure of Clostridium acetobutylicum aspartate kinase (CaAK): An important allosteric enzyme for industrial amino acids production
Authors : Manjasetty, B.A.; Chance, M.R.; Burley, S.K.; Almo, S.C.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2011-09-20
Resolution : 3.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

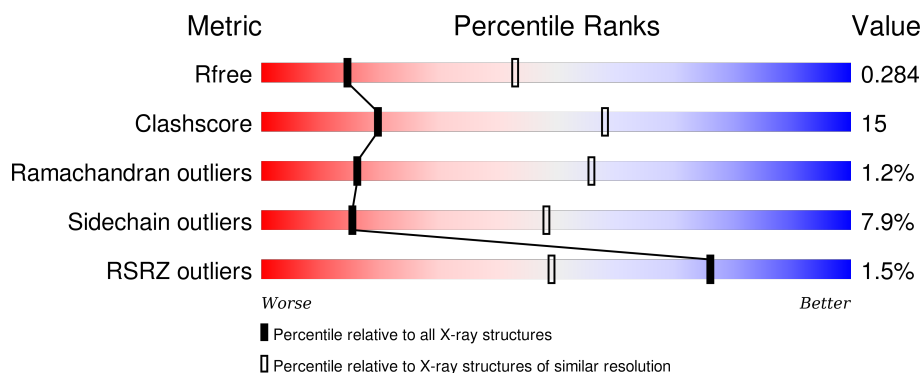
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	446	<div> <div>69%</div> <div>26%</div> <div>• •</div> </div>
1	B	446	<div> <div>72%</div> <div>23%</div> <div>• •</div> </div>
1	C	446	<div> <div>72%</div> <div>22%</div> <div>• •</div> </div>
1	D	446	<div> <div>70%</div> <div>25%</div> <div>• •</div> </div>
1	E	446	<div> <div>67%</div> <div>28%</div> <div>• •</div> </div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	446	
1	G	446	
1	H	446	
1	I	446	
1	J	446	
1	K	446	
1	L	446	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ASP	A	451	-	-	-	X
2	ASP	D	454	-	-	-	X
2	ASP	E	455	-	-	-	X
2	ASP	G	457	-	-	-	X
2	ASP	H	458	-	-	-	X
2	ASP	I	459	-	-	-	X
2	ASP	L	462	-	-	-	X
3	LYS	A	501	-	-	-	X
3	LYS	C	503	-	-	-	X
3	LYS	D	504	-	-	-	X
3	LYS	G	507	-	-	X	X
3	LYS	H	508	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 39043 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 Aspartokinase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	429	Total	C	N	O	S	Se	0	0	0
			3228	2045	530	638	7	8			
1	B	438	Total	C	N	O	S	Se	0	0	0
			3304	2104	538	647	7	8			
1	C	433	Total	C	N	O	S	Se	0	0	0
			3271	2078	536	643	7	7			
1	D	437	Total	C	N	O	S	Se	0	0	0
			3296	2093	539	649	7	8			
1	E	439	Total	C	N	O	S	Se	0	0	0
			3293	2091	539	648	7	8			
1	F	434	Total	C	N	O	S	Se	0	0	0
			3267	2073	533	647	7	7			
1	G	436	Total	C	N	O	S	Se	0	1	0
			3288	2089	537	648	7	7			
1	H	435	Total	C	N	O	S	Se	0	0	0
			3217	2041	524	638	6	8			
1	I	428	Total	C	N	O	S	Se	0	0	0
			3191	2024	521	633	6	7			
1	J	433	Total	C	N	O	S	Se	0	0	0
			3204	2032	525	633	6	8			
1	K	429	Total	C	N	O	S	Se	0	0	0
			3170	2005	518	633	6	8			
1	L	428	Total	C	N	O	S	Se	0	0	0
			3192	2021	522	636	6	7			

There are 120 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	SER	-	EXPRESSION TAG	UNP Q97MC0
A	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
A	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
A	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
A	440	HIS	-	EXPRESSION TAG	UNP Q97MC0

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
A	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
A	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
A	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
A	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
B	0	SER	-	EXPRESSION TAG	UNP Q97MC0
B	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
B	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
B	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
B	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
B	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
B	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
B	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
B	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
B	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
C	0	SER	-	EXPRESSION TAG	UNP Q97MC0
C	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
C	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
C	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
C	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
C	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
C	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
C	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
C	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
C	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
D	0	SER	-	EXPRESSION TAG	UNP Q97MC0
D	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
D	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
D	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
D	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
D	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
D	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
D	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
D	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
D	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
E	0	SER	-	EXPRESSION TAG	UNP Q97MC0
E	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
E	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
E	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
E	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
E	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
E	442	HIS	-	EXPRESSION TAG	UNP Q97MC0

Continued on next page...

Continued from previous page...

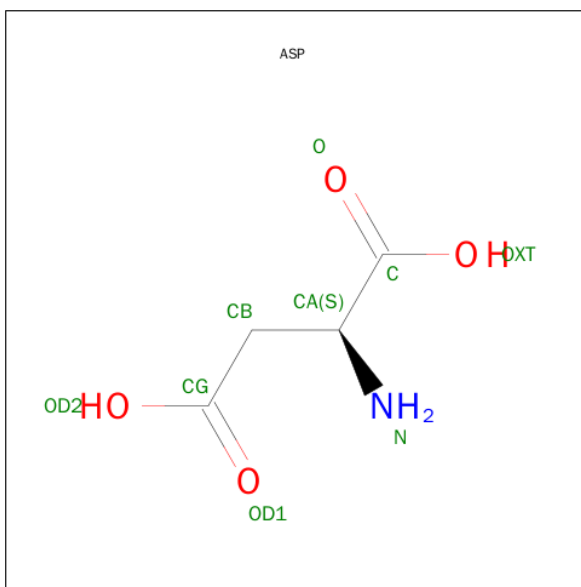
Chain	Residue	Modelled	Actual	Comment	Reference
E	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
E	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
E	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
F	0	SER	-	EXPRESSION TAG	UNP Q97MC0
F	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
F	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
F	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
F	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
F	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
F	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
F	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
F	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
F	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
G	0	SER	-	EXPRESSION TAG	UNP Q97MC0
G	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
G	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
G	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
G	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
G	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
G	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
G	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
G	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
G	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
H	0	SER	-	EXPRESSION TAG	UNP Q97MC0
H	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
H	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
H	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
H	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
H	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
H	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
H	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
H	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
H	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
I	0	SER	-	EXPRESSION TAG	UNP Q97MC0
I	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
I	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
I	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
I	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
I	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
I	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
I	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
I	444	HIS	-	EXPRESSION TAG	UNP Q97MC0

Continued on next page...

Continued from previous page...

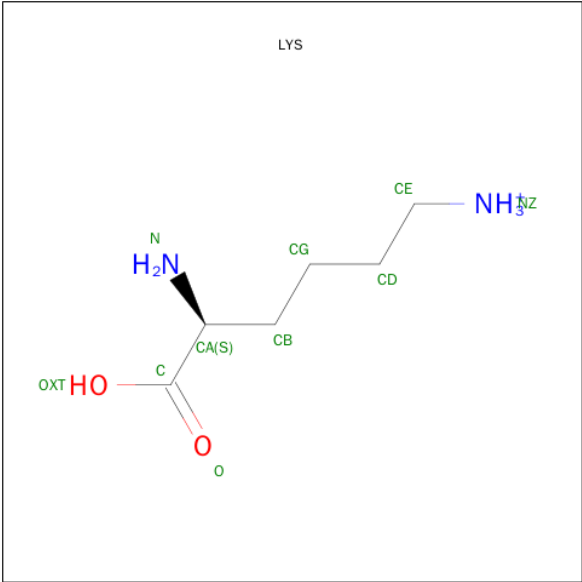
Chain	Residue	Modelled	Actual	Comment	Reference
I	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
J	0	SER	-	EXPRESSION TAG	UNP Q97MC0
J	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
J	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
J	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
J	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
J	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
J	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
J	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
J	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
J	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
K	0	SER	-	EXPRESSION TAG	UNP Q97MC0
K	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
K	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
K	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
K	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
K	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
K	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
K	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
K	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
K	445	HIS	-	EXPRESSION TAG	UNP Q97MC0
L	0	SER	-	EXPRESSION TAG	UNP Q97MC0
L	1	LEU	-	EXPRESSION TAG	UNP Q97MC0
L	438	GLU	-	EXPRESSION TAG	UNP Q97MC0
L	439	GLY	-	EXPRESSION TAG	UNP Q97MC0
L	440	HIS	-	EXPRESSION TAG	UNP Q97MC0
L	441	HIS	-	EXPRESSION TAG	UNP Q97MC0
L	442	HIS	-	EXPRESSION TAG	UNP Q97MC0
L	443	HIS	-	EXPRESSION TAG	UNP Q97MC0
L	444	HIS	-	EXPRESSION TAG	UNP Q97MC0
L	445	HIS	-	EXPRESSION TAG	UNP Q97MC0

- Molecule 2 is ASPARTIC ACID (three-letter code: ASP) (formula: C₄H₇NO₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			9	4	1	4		
2	D	1	Total	C	N	O	0	0
			9	4	1	4		
2	E	1	Total	C	N	O	0	0
			9	4	1	4		
2	G	1	Total	C	N	O	0	0
			9	4	1	4		
2	H	1	Total	C	N	O	0	0
			9	4	1	4		
2	I	1	Total	C	N	O	0	0
			8	4	1	3		
2	L	1	Total	C	N	O	0	0
			9	4	1	4		

- Molecule 3 is LYSINE (three-letter code: LYS) (formula: $C_6H_{15}N_2O_2$).

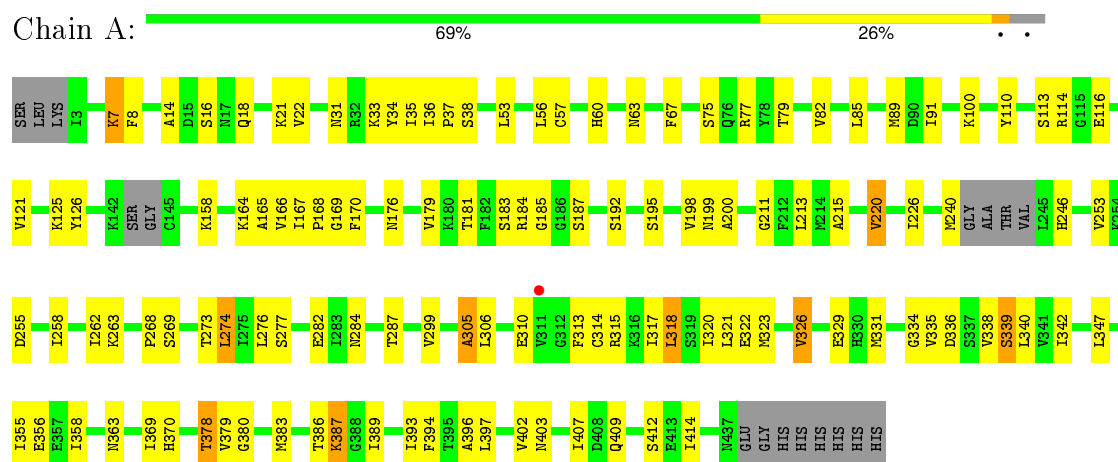


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			10	6	2	2		
3	B	1	Total	C	N	O	0	0
			10	6	2	2		
3	C	1	Total	C	N	O	0	0
			10	6	2	2		
3	D	1	Total	C	N	O	0	0
			10	6	2	2		
3	G	1	Total	C	N	O	0	0
			10	6	2	2		
3	H	1	Total	C	N	O	0	0
			10	6	2	2		

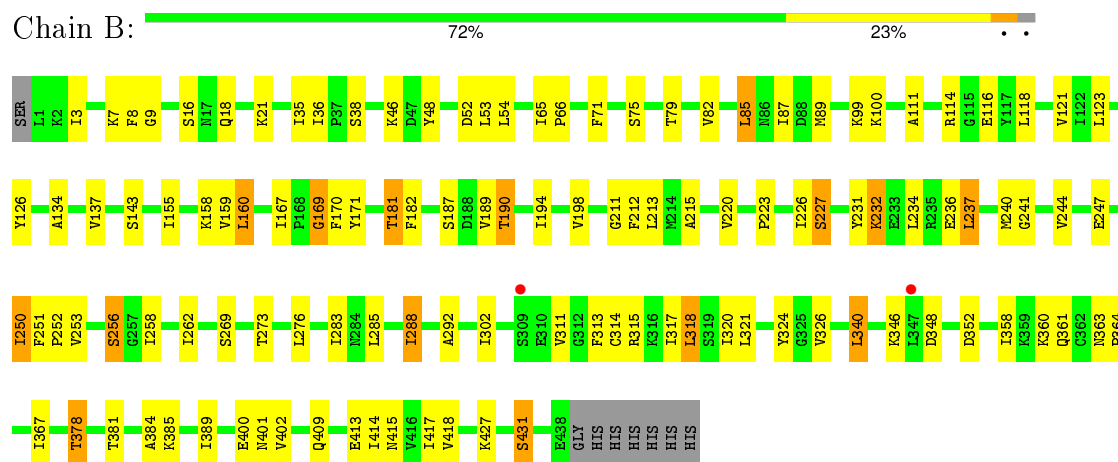
3 Residue-property plots

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.

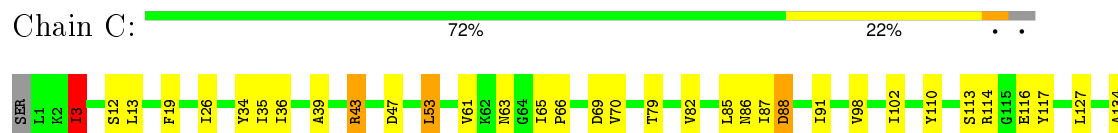
• Molecule 1: Aspartokinase

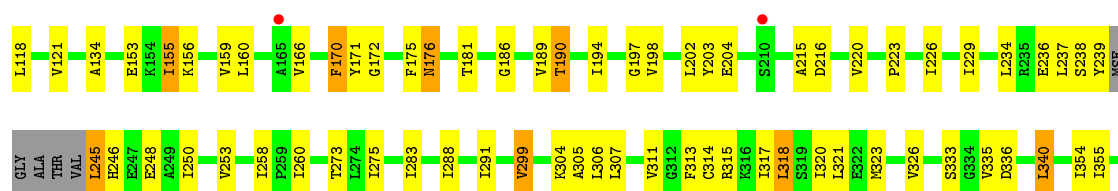


• Molecule 1: Aspartokinase



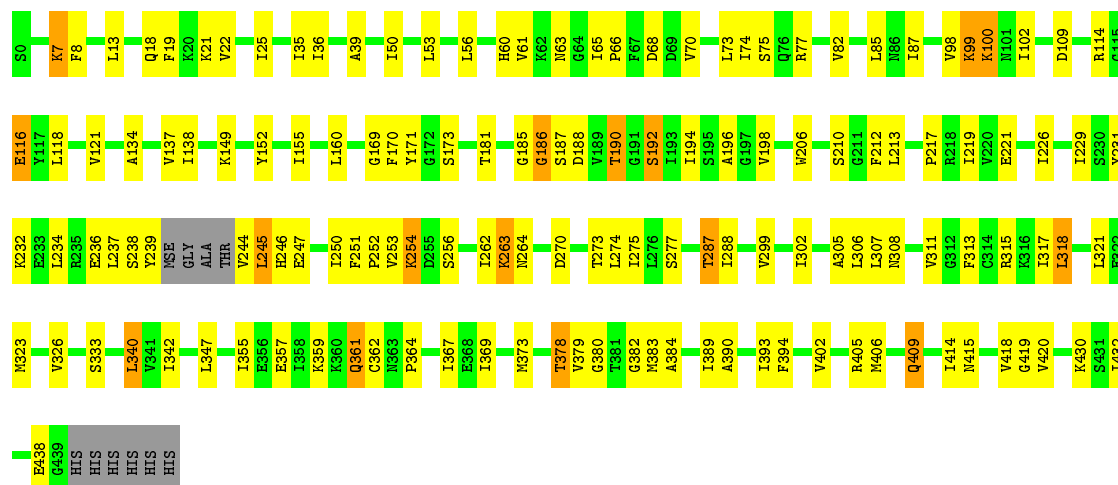
• Molecule 1: Aspartokinase





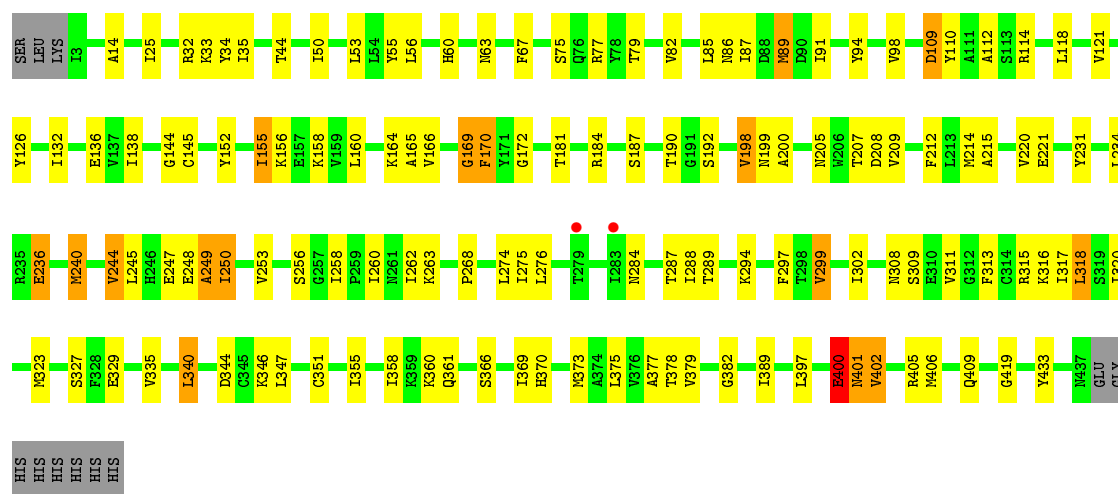
• Molecule 1: Aspartokinase

Chain G: 66% 28%



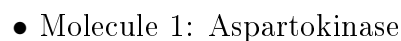
• Molecule 1: Aspartokinase

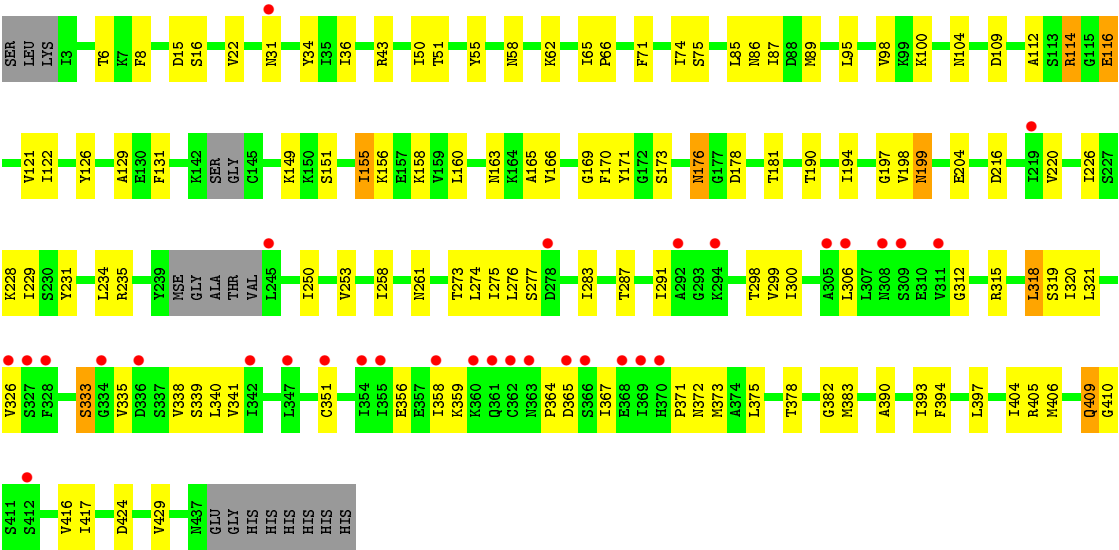
Chain H: 67% 26%



• Molecule 1: Aspartokinase

Chain I: 2% 68% 26%





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	109.04Å 274.22Å 114.04Å 90.00° 113.69° 90.00°	Depositor
Resolution (Å)	44.16 – 3.00 44.16 – 3.00	Depositor EDS
% Data completeness (in resolution range)	92.1 (44.16-3.00) 92.2 (44.16-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.92 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.6.0116	Depositor
R, R_{free}	0.206 , 0.273 0.209 , 0.284	Depositor DCC
R_{free} test set	924 reflections (0.83%)	DCC
Wilson B-factor (Å ²)	77.3	Xtriage
Anisotropy	0.086	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 41.4	EDS
Estimated twinning fraction	0.018 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 112573 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	39043	wwPDB-VP
Average B, all atoms (Å ²)	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.40	0/3270	0.58	0/4409
1	B	0.38	0/3349	0.57	0/4516
1	C	0.37	0/3317	0.55	0/4479
1	D	0.43	0/3341	0.58	0/4509
1	E	0.38	0/3339	0.56	0/4510
1	F	0.35	0/3311	0.51	0/4471
1	G	0.40	0/3338	0.58	0/4504
1	H	0.37	0/3260	0.57	1/4407 (0.0%)
1	I	0.34	0/3234	0.50	0/4371
1	J	0.35	0/3245	0.53	0/4383
1	K	0.36	0/3210	0.51	0/4336
1	L	0.35	0/3234	0.51	0/4369
All	All	0.37	0/39448	0.55	1/53264 (0.0%)

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	B	0	1
1	D	0	1
1	H	0	2
All	All	0	4

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	400	GLU	N-CA-C	5.09	124.74	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	169	GLY	Peptide
1	D	169	GLY	Peptide
1	H	169	GLY	Peptide
1	H	400	GLU	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3228	0	3156	81	0
1	B	3304	0	3281	88	0
1	C	3271	0	3214	107	0
1	D	3296	0	3257	95	0
1	E	3293	0	3224	112	0
1	F	3267	0	3209	93	0
1	G	3288	0	3244	118	0
1	H	3217	0	3103	103	0
1	I	3191	0	3092	105	0
1	J	3204	0	3116	103	0
1	K	3170	0	3042	109	0
1	L	3192	0	3093	110	0
2	A	9	0	3	2	0
2	D	9	0	3	0	0
2	E	9	0	3	1	0
2	G	9	0	3	1	0
2	H	9	0	3	1	0
2	I	8	0	3	0	0
2	L	9	0	3	0	0
3	A	10	0	12	0	0
3	B	10	0	12	0	0
3	C	10	0	12	3	0
3	D	10	0	12	0	0
3	G	10	0	12	7	0
3	H	10	0	12	1	0
All	All	39043	0	38124	1150	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 15.

All (1150) 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:K:169:GLY:O	1:K:190:THR:HG21	1.41	1.19
1:D:189:VAL:HA	1:D:249:ALA:CB	1.76	1.14
1:D:189:VAL:HA	1:D:249:ALA:HB3	1.30	1.08
1:G:288:ILE:HD13	1:G:383:MSE:HE2	1.35	1.08
1:L:160:LEU:HD13	1:L:198:VAL:HG13	1.37	1.06
1:C:226:ILE:O	1:C:273:THR:HG22	1.57	1.04
1:C:215:ALA:HB3	1:C:220:VAL:HG11	1.37	1.01
1:J:137:VAL:HG13	1:J:155:ILE:HG22	1.42	0.98
1:I:155:ILE:HG23	1:I:159:VAL:HG21	1.45	0.97
1:D:383:MSE:HE1	1:D:416:VAL:HG23	1.45	0.95
1:I:318:LEU:HD11	1:J:318:LEU:HD11	1.43	0.95
1:A:355:ILE:HD11	1:A:369:ILE:HD11	1.44	0.95
1:G:308[B]:ASN:CG	3:G:507:LYS:HG3	1.90	0.93
1:D:169:GLY:O	1:D:190:THR:HG21	1.69	0.93
1:F:155:ILE:HG23	1:F:198:VAL:HG23	1.51	0.92
1:H:320:ILE:HD13	1:H:358:ILE:HG22	1.51	0.92
1:C:383:MSE:HB2	1:C:389:ILE:HG21	1.52	0.92
1:G:288:ILE:CD1	1:G:383:MSE:HE2	2.01	0.90
1:F:253:VAL:HG13	1:F:258:ILE:HB	1.53	0.90
1:G:364:PRO:HG2	1:G:367:ILE:HD11	1.53	0.90
1:G:308[B]:ASN:OD1	3:G:507:LYS:HG3	1.72	0.89
1:C:397:LEU:HD22	1:C:402:VAL:HG21	1.54	0.88
1:E:189:VAL:O	1:E:193:ILE:HD12	1.75	0.86
1:I:155:ILE:HG23	1:I:159:VAL:CG2	2.06	0.85
1:C:85:LEU:HD23	1:C:87:ILE:HD11	1.57	0.85
1:G:212:PHE:H	1:G:273:THR:CG2	1.90	0.84
1:K:341:VAL:HG11	1:K:375:LEU:HD11	1.60	0.83
1:J:215:ALA:HB3	1:J:220:VAL:HG11	1.60	0.83
1:H:373:MSE:HE3	1:H:405:ARG:HB2	1.59	0.83
1:H:355:ILE:HD13	1:H:369:ILE:HD11	1.59	0.83
1:F:288:ILE:HD12	1:F:383:MSE:HE2	1.59	0.83
1:G:373:MSE:HE1	1:G:406:MSE:HB2	1.58	0.83
1:E:50:ILE:HD11	1:E:77:ARG:HG3	1.60	0.83
1:I:226:ILE:O	1:I:273:THR:HG22	1.79	0.82
1:D:383:MSE:CE	1:D:416:VAL:HG23	2.08	0.82
1:D:320:ILE:HD13	1:D:358:ILE:HG22	1.61	0.82
1:L:155:ILE:HG23	1:L:198:VAL:HG23	1.60	0.81
1:K:320:ILE:HG23	1:K:323:MSE:HE2	1.60	0.81

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:ASN:O	1:A:287:THR:HG22	1.81	0.81
1:E:335:VAL:HG13	1:F:239:TYR:CD1	2.15	0.81
1:L:253:VAL:HG11	1:L:258:ILE:O	1.81	0.80
1:A:274:LEU:HD22	1:A:276:LEU:HD11	1.62	0.80
1:K:211:GLY:HA3	1:K:273:THR:HG23	1.63	0.80
1:J:155:ILE:CD1	1:J:198:VAL:HG13	2.11	0.80
1:J:127:LEU:O	1:J:129:ALA:N	2.15	0.80
1:D:189:VAL:HG23	1:D:249:ALA:HB2	1.63	0.80
1:L:98:VAL:HG13	1:L:114:ARG:HG2	1.62	0.79
1:B:16:SER:HB2	1:B:85:LEU:HD13	1.62	0.79
1:D:189:VAL:HA	1:D:249:ALA:HB2	1.61	0.79
1:J:157:GLU:O	1:J:161:SER:OG	2.01	0.78
1:K:226:ILE:O	1:K:273:THR:HG22	1.83	0.78
1:F:186:GLY:O	1:F:189:VAL:HG12	1.83	0.78
1:C:308:ASN:HD21	3:C:503:LYS:HE2	1.47	0.78
1:K:155:ILE:HG23	1:K:159:VAL:CG1	2.14	0.78
1:A:14:ALA:O	1:A:77:ARG:NH2	2.16	0.78
1:G:50:ILE:HD11	1:G:77:ARG:HG2	1.66	0.78
1:F:82:VAL:HG21	1:F:89:MSE:HE2	1.65	0.78
1:K:238:SER:OG	1:L:335:VAL:CG1	2.32	0.78
1:J:253:VAL:HG13	1:J:258:ILE:HB	1.65	0.78
1:L:320:ILE:HD13	1:L:358:ILE:HG22	1.64	0.78
1:C:87:ILE:HG22	1:C:88:ASP:H	1.48	0.78
1:D:189:VAL:CB	1:D:249:ALA:HB2	2.15	0.77
1:B:288:ILE:HD11	1:B:378:THR:OG1	1.84	0.77
1:G:379:VAL:C	1:G:383:MSE:HE3	2.05	0.77
1:G:134:ALA:HB3	1:G:171:TYR:CE1	2.20	0.77
1:A:318:LEU:HD11	1:B:318:LEU:HD11	1.65	0.77
1:I:245:LEU:HD23	1:I:245:LEU:N	2.00	0.77
1:C:320:ILE:HD11	1:C:358:ILE:HG23	1.67	0.77
1:K:406:MSE:HE2	1:K:408:ASP:HB2	1.66	0.76
1:J:261:ASN:HD22	1:J:274:LEU:HD13	1.50	0.76
1:L:87:ILE:HG21	1:L:89:MSE:HE3	1.67	0.75
1:L:155:ILE:HD11	1:L:194:ILE:HD13	1.69	0.75
1:E:406:MSE:HE2	1:E:408:ASP:HB2	1.67	0.75
1:F:155:ILE:HD12	1:F:198:VAL:HG23	1.67	0.75
1:J:397:LEU:O	1:J:402:VAL:HG12	1.87	0.74
1:G:373:MSE:HE3	1:G:405:ARG:CB	2.18	0.74
1:F:63:ASN:HD22	1:G:53:LEU:HD12	1.52	0.74
1:E:397:LEU:HD22	1:E:402:VAL:HG11	1.70	0.74
1:D:189:VAL:CA	1:D:249:ALA:CB	2.64	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:GLY:O	1:A:187:SER:HA	1.88	0.73
1:H:313:PHE:CE2	1:H:317:ILE:HD11	2.23	0.73
1:I:253:VAL:HG13	1:I:258:ILE:HB	1.70	0.73
1:H:373:MSE:HE2	1:H:419:GLY:HA3	1.70	0.73
1:B:215:ALA:HB3	1:B:220:VAL:HG11	1.69	0.73
1:G:238:SER:HB3	1:G:244:VAL:HG11	1.71	0.73
1:G:355:ILE:CD1	1:G:369:ILE:HD11	2.19	0.73
1:E:423:VAL:HG13	1:E:424:ASP:OD1	1.89	0.73
1:G:288:ILE:CD1	1:G:383:MSE:CE	2.67	0.73
1:G:373:MSE:HE3	1:G:405:ARG:HB3	1.70	0.73
1:J:237:LEU:HD12	1:J:241:GLY:HA3	1.70	0.73
1:G:212:PHE:H	1:G:273:THR:HG23	1.52	0.72
1:F:170:PHE:CG	1:F:170:PHE:O	2.43	0.72
1:D:155:ILE:HG23	1:D:159:VAL:CG1	2.19	0.72
1:C:155:ILE:HD11	1:C:194:ILE:HD13	1.72	0.72
1:K:355:ILE:HD11	1:K:369:ILE:HD11	1.72	0.71
1:F:245:LEU:HD22	1:F:246:HIS:H	1.54	0.71
1:B:75:SER:O	1:B:79:THR:HG23	1.90	0.71
1:B:116:GLU:HG3	1:B:170:PHE:HB3	1.73	0.70
1:D:355:ILE:HD11	1:D:369:ILE:HD11	1.72	0.70
1:I:239:TYR:HB2	1:I:292:ALA:HB1	1.73	0.70
1:H:82:VAL:HG21	1:H:89:MSE:CE	2.20	0.70
1:K:238:SER:OG	1:L:335:VAL:HG11	1.91	0.70
1:H:85:LEU:HD23	1:H:126:TYR:CZ	2.26	0.70
1:H:284:ASN:HB2	1:H:287:THR:HG21	1.74	0.70
1:E:373:MSE:HE3	1:E:405:ARG:CB	2.22	0.70
1:E:373:MSE:HE1	1:E:406:MSE:CB	2.21	0.69
1:G:39:ALA:HB3	2:G:457:ASP:OD2	1.91	0.69
1:F:291:ILE:HG21	1:F:429:VAL:HG13	1.74	0.69
1:G:355:ILE:HD11	1:G:369:ILE:HD11	1.74	0.69
1:E:323:MSE:HE1	1:E:361:GLN:HE22	1.57	0.69
1:D:189:VAL:CA	1:D:249:ALA:HB2	2.21	0.69
1:G:118:LEU:O	1:G:121:VAL:HG22	1.93	0.69
1:E:323:MSE:HE2	1:G:315:ARG:NH2	2.07	0.69
1:F:299:VAL:HG12	1:F:370:HIS:HB2	1.74	0.69
1:C:39:ALA:HB2	1:C:116:GLU:OE1	1.91	0.69
1:F:155:ILE:HD13	1:F:159:VAL:HG21	1.73	0.69
1:D:189:VAL:CG2	1:D:249:ALA:HB2	2.21	0.69
1:C:3:ILE:HD11	1:C:200:ALA:HA	1.74	0.69
1:H:82:VAL:HG21	1:H:89:MSE:HE2	1.74	0.69
1:H:274:LEU:HD23	1:H:276:LEU:HD11	1.74	0.68

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:318:LEU:HD12	1:L:319:SER:N	2.07	0.68
1:E:52:ASP:HB3	1:H:63:ASN:HD21	1.58	0.68
1:C:220:VAL:HG13	1:C:220:VAL:O	1.93	0.68
1:K:318:LEU:CD2	1:L:318:LEU:HD21	2.23	0.68
1:E:299:VAL:HG13	1:E:370:HIS:HB2	1.76	0.68
1:H:215:ALA:HB3	1:H:220:VAL:HG11	1.75	0.68
1:E:35:ILE:C	1:E:36:ILE:HD12	2.14	0.68
1:G:409:GLN:HE21	1:G:409:GLN:C	1.96	0.68
1:I:155:ILE:CG2	1:I:159:VAL:HG21	2.23	0.67
1:A:274:LEU:CD2	1:A:276:LEU:HD11	2.25	0.67
1:K:109:ASP:OD2	1:K:181:THR:HG22	1.94	0.67
1:D:234:LEU:HD22	1:D:275:ILE:HD13	1.77	0.67
1:C:320:ILE:CD1	1:C:358:ILE:HG23	2.25	0.67
1:K:194:ILE:HG22	1:K:195:SER:N	2.10	0.66
1:H:187:SER:OG	2:H:458:ASP:OD2	2.08	0.66
1:L:34:TYR:CD1	1:L:165:ALA:HB3	2.31	0.66
1:D:155:ILE:HG23	1:D:159:VAL:HG13	1.78	0.66
1:F:56:LEU:O	1:F:59:ALA:HB3	1.95	0.66
1:H:323:MSE:HE1	1:H:361:GLN:NE2	2.11	0.66
1:E:373:MSE:HE3	1:E:405:ARG:HB2	1.76	0.66
1:E:36:ILE:N	1:E:36:ILE:HD12	2.10	0.66
1:B:415:ASN:HD21	1:B:417:ILE:HD11	1.61	0.66
1:L:375:LEU:HD22	1:L:417:ILE:HG22	1.78	0.65
1:H:160:LEU:HD13	1:H:198:VAL:HG13	1.77	0.65
1:D:320:ILE:HG21	1:D:358:ILE:CG2	2.26	0.65
1:L:341:VAL:HG11	1:L:406:MSE:HE1	1.77	0.65
1:C:284:ASN:O	1:C:287:THR:HG22	1.97	0.65
1:F:355:ILE:CD1	1:F:369:ILE:HD11	2.27	0.65
1:A:320:ILE:HD13	1:A:358:ILE:HG22	1.79	0.65
1:J:39:ALA:N	1:J:116:GLU:OE2	2.29	0.65
1:E:373:MSE:HE1	1:E:406:MSE:HB3	1.79	0.65
1:D:18:GLN:HE22	1:D:21:LYS:NZ	1.95	0.65
1:L:378:THR:HG21	1:L:393:ILE:HD13	1.79	0.65
1:I:14:ALA:O	1:I:77:ARG:NH2	2.30	0.64
1:C:318:LEU:HD11	1:D:318:LEU:HD11	1.80	0.64
1:K:213:LEU:H	1:K:213:LEU:HD12	1.63	0.64
1:H:253:VAL:HG13	1:H:258:ILE:HB	1.79	0.64
1:E:60:HIS:ND1	1:H:56:LEU:HD21	2.12	0.64
1:F:1:LEU:H1	1:F:1:LEU:HD13	1.63	0.64
1:K:238:SER:OG	1:L:335:VAL:HG13	1.96	0.64
1:K:326:VAL:HG11	1:K:347:LEU:HD12	1.80	0.64

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:155:ILE:C	1:J:155:ILE:HD12	2.18	0.64
1:E:60:HIS:CE1	1:H:56:LEU:HD21	2.33	0.64
1:E:246:HIS:HB3	1:E:248:GLU:HG2	1.80	0.64
1:K:169:GLY:C	1:K:190:THR:HG21	2.17	0.64
1:E:323:MSE:HG2	1:G:311:VAL:HG11	1.79	0.64
1:F:321:LEU:HD23	1:F:326:VAL:HG21	1.80	0.64
1:E:85:LEU:HD11	1:E:126:TYR:CZ	2.33	0.64
1:B:169:GLY:O	1:B:190:THR:HG21	1.98	0.64
1:H:308:ASN:HA	3:H:508:LYS:HA	1.80	0.64
1:D:320:ILE:HG21	1:D:358:ILE:HG22	1.80	0.63
1:L:198:VAL:HG12	1:L:198:VAL:O	1.98	0.63
1:I:409:GLN:CB	1:I:416:VAL:HG22	2.29	0.63
1:G:137:VAL:HG12	1:G:138:ILE:HG13	1.80	0.63
1:C:215:ALA:CB	1:C:220:VAL:HG11	2.22	0.63
1:A:378:THR:O	1:A:383:MSE:HE1	1.99	0.63
1:C:216:ASP:O	1:C:220:VAL:HG12	1.99	0.63
1:H:355:ILE:CD1	1:H:369:ILE:HD11	2.28	0.63
1:J:320:ILE:CD1	1:J:358:ILE:HG22	2.29	0.63
1:A:89:MSE:HE1	1:A:121:VAL:HG23	1.81	0.62
1:J:137:VAL:CG1	1:J:155:ILE:HG22	2.25	0.62
1:D:253:VAL:HG21	1:D:260:ILE:HD11	1.81	0.62
1:C:79:THR:HG22	1:C:91:ILE:HG21	1.80	0.62
1:G:379:VAL:CA	1:G:383:MSE:HE3	2.29	0.62
1:H:82:VAL:CG2	1:H:89:MSE:HE2	2.28	0.62
1:E:253:VAL:HG21	1:E:260:ILE:HD11	1.81	0.62
2:E:455:ASP:N	2:E:455:ASP:OD1	2.31	0.62
1:J:151:SER:O	1:J:155:ILE:HG23	2.00	0.62
1:A:215:ALA:HB3	1:A:220:VAL:HG11	1.81	0.62
1:B:53:LEU:HD21	1:C:65:ILE:HD11	1.81	0.62
1:H:313:PHE:HE2	1:H:317:ILE:HD11	1.63	0.62
1:K:318:LEU:HD21	1:L:318:LEU:HD21	1.82	0.62
1:B:237:LEU:HD12	1:B:292:ALA:CB	2.29	0.62
1:G:380:GLY:N	1:G:383:MSE:HE3	2.14	0.61
1:H:317:ILE:CG2	1:H:340:LEU:HD21	2.30	0.61
1:C:299:VAL:HG13	1:C:370:HIS:HB2	1.82	0.61
1:J:320:ILE:HD13	1:J:358:ILE:HG22	1.80	0.61
1:H:109:ASP:OD2	1:H:181:THR:HG22	2.01	0.61
1:K:169:GLY:O	1:K:190:THR:CG2	2.34	0.61
1:D:98:VAL:HG22	1:D:114:ARG:HD2	1.82	0.61
1:F:220:VAL:HG21	1:F:433:TYR:CD1	2.35	0.61
1:J:215:ALA:CB	1:J:220:VAL:HG11	2.30	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:330:HIS:NE2	1:J:417:ILE:HD13	2.15	0.61
1:G:373:MSE:HE2	1:G:419:GLY:HA3	1.83	0.61
1:E:330:HIS:CG	1:E:406:MSE:HE1	2.35	0.61
1:D:212:PHE:CD1	1:D:244:VAL:HG12	2.36	0.61
1:L:85:LEU:HD23	1:L:126:TYR:CE1	2.36	0.61
1:F:155:ILE:HD11	1:F:194:ILE:CD1	2.31	0.61
1:I:320:ILE:HD12	1:I:358:ILE:HG22	1.83	0.61
1:I:291:ILE:HG21	1:I:429:VAL:HG13	1.83	0.61
1:F:321:LEU:HD23	1:F:326:VAL:CG2	2.30	0.60
1:J:155:ILE:HD11	1:J:198:VAL:HG13	1.84	0.60
1:B:35:ILE:C	1:B:36:ILE:HD12	2.21	0.60
1:C:261:ASN:HD22	1:C:274:LEU:HD13	1.66	0.60
1:I:159:VAL:HG23	1:I:160:LEU:H	1.67	0.60
1:L:359:LYS:HE3	1:L:367:ILE:HD12	1.83	0.60
1:J:194:ILE:O	1:J:198:VAL:HG22	2.02	0.60
1:E:313:PHE:HE2	1:E:317:ILE:HD11	1.67	0.60
1:J:283:ILE:HG23	1:J:283:ILE:O	2.01	0.60
1:A:63:ASN:HD22	1:D:56:LEU:HD22	1.66	0.60
1:A:110:TYR:HD2	1:A:179:VAL:HG21	1.67	0.60
1:C:231:TYR:CE2	1:C:277:SER:HA	2.36	0.60
1:D:114:ARG:HA	1:D:114:ARG:HH11	1.67	0.60
1:H:138:ILE:HD11	1:H:190:THR:HG23	1.84	0.60
1:K:35:ILE:N	1:K:35:ILE:HD12	2.16	0.60
1:H:323:MSE:HE1	1:H:361:GLN:HE22	1.67	0.60
1:E:313:PHE:CE2	1:E:317:ILE:HD11	2.36	0.60
1:G:155:ILE:CD1	1:G:194:ILE:HD13	2.32	0.59
1:D:321:LEU:HG	1:D:326:VAL:HG23	1.84	0.59
1:E:65:ILE:HD13	1:E:66:PRO:O	2.02	0.59
1:K:5:VAL:HG22	1:K:34:TYR:HB2	1.83	0.59
1:G:226:ILE:O	1:G:273:THR:HG22	2.03	0.59
1:I:53:LEU:HG	1:L:65:ILE:HD11	1.84	0.59
1:D:245:LEU:HD23	1:D:250:ILE:HD11	1.83	0.59
1:I:155:ILE:HG22	1:I:156:LYS:N	2.16	0.59
1:D:320:ILE:CD1	1:D:358:ILE:HG22	2.32	0.59
1:F:299:VAL:HA	1:F:340:LEU:O	2.03	0.59
1:I:284:ASN:O	1:I:287:THR:HG22	2.02	0.59
1:L:116:GLU:HG3	1:L:170:PHE:CB	2.32	0.59
1:L:287:THR:HG22	1:L:382:GLY:HA3	1.84	0.59
1:H:89:MSE:HE1	1:H:91:ILE:HD13	1.83	0.59
1:C:36:ILE:HG12	1:C:190:THR:HG22	1.85	0.59
1:C:335:VAL:HG11	1:D:236:GLU:HA	1.84	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:CYS:HA	1:A:317:ILE:HD12	1.84	0.59
1:C:261:ASN:ND2	1:C:274:LEU:HD13	2.17	0.59
1:L:65:ILE:HG22	1:L:66:PRO:O	2.03	0.59
1:J:26:ILE:HD12	1:J:35:ILE:HD11	1.84	0.59
1:A:342:ILE:HG21	1:A:347:LEU:HD13	1.84	0.59
1:H:274:LEU:CD2	1:H:276:LEU:HD11	2.32	0.59
1:I:318:LEU:HD21	1:J:318:LEU:CD2	2.33	0.58
1:L:98:VAL:CG1	1:L:114:ARG:HG2	2.31	0.58
1:D:212:PHE:CE1	1:D:244:VAL:HG12	2.37	0.58
1:B:52:ASP:HB3	1:C:63:ASN:HD21	1.68	0.58
1:I:291:ILE:HD11	1:I:432:ILE:HG22	1.84	0.58
1:E:54:LEU:HD23	1:E:74:ILE:HD13	1.85	0.58
1:J:341:VAL:HG21	1:J:406:MSE:SE	2.53	0.58
1:F:237:LEU:HD11	1:F:379:VAL:HB	1.84	0.58
1:C:207:THR:OG1	1:C:208:ASP:N	2.36	0.58
1:C:373:MSE:HE3	1:C:375:LEU:HD21	1.86	0.58
1:A:263:LYS:NZ	1:A:268:PRO:O	2.37	0.58
1:L:6:THR:HG22	1:L:204:GLU:HB2	1.84	0.58
1:E:251:PHE:CG	1:E:252:PRO:HD3	2.38	0.58
1:D:212:PHE:CZ	1:D:262:ILE:HD13	2.38	0.58
1:K:421:GLU:HG3	1:K:423:VAL:HG12	1.86	0.58
1:C:391:ASN:OD1	1:D:391:ASN:OD1	2.22	0.58
1:C:236:GLU:HG2	1:C:415:ASN:HB2	1.86	0.58
1:F:36:ILE:HG21	1:F:190:THR:HG22	1.86	0.58
1:H:373:MSE:CE	1:H:405:ARG:HB2	2.32	0.58
1:K:202:LEU:HD12	1:K:259:PRO:O	2.03	0.58
1:H:35:ILE:HB	1:H:166:VAL:HG22	1.86	0.58
1:K:163:ASN:O	1:K:164:LYS:C	2.43	0.58
1:K:110:TYR:CZ	1:K:114:ARG:HD2	2.39	0.58
1:I:355:ILE:HD11	1:I:369:ILE:HD11	1.86	0.57
1:G:239:TYR:CD2	1:H:335:VAL:HG22	2.38	0.57
1:B:232:LYS:HG3	1:B:414:ILE:HD11	1.86	0.57
1:G:287:THR:HG22	1:G:382:GLY:HA3	1.84	0.57
1:A:274:LEU:CD2	1:A:276:LEU:CD1	2.82	0.57
1:B:169:GLY:C	1:B:190:THR:HG21	2.25	0.57
1:D:5:VAL:HG21	1:D:195:SER:HA	1.86	0.57
1:I:301:ALA:HB3	1:I:368:GLU:HB2	1.86	0.57
1:A:213:LEU:O	1:A:240:MSE:CE	2.53	0.57
1:C:253:VAL:HG13	1:C:258:ILE:HB	1.86	0.57
1:E:137:VAL:HG13	1:E:155:ILE:HG13	1.85	0.57
1:G:357:GLU:OE2	1:G:361:GLN:NE2	2.38	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:321:LEU:HG	1:K:326:VAL:HG23	1.86	0.57
1:C:395:THR:HA	1:D:391:ASN:HD21	1.68	0.57
1:C:219:ILE:HD11	1:C:429:VAL:CG1	2.35	0.57
1:H:256:SER:HB3	1:H:258:ILE:HD12	1.87	0.57
1:I:4:VAL:HG13	1:I:202:LEU:HD23	1.87	0.57
1:I:134:ALA:HB3	1:I:171:TYR:CE2	2.40	0.57
1:A:18:GLN:O	1:A:22:VAL:HG23	2.05	0.57
1:I:390:ALA:HB1	1:I:394:PHE:CE2	2.40	0.57
1:C:315:ARG:HB2	1:D:318:LEU:HD13	1.87	0.57
1:J:214:MSE:HE2	1:J:433:TYR:CE2	2.39	0.57
1:G:302:ILE:HD12	1:G:317:ILE:HD13	1.86	0.57
1:G:212:PHE:H	1:G:273:THR:HG21	1.70	0.57
1:K:332:PRO:HG3	1:K:406:MSE:HE3	1.87	0.57
1:A:331:MSE:HE2	1:A:340:LEU:HD11	1.86	0.57
1:E:307:LEU:HD22	1:E:313:PHE:CD2	2.40	0.56
1:F:85:LEU:HD23	1:F:87:ILE:HD11	1.87	0.56
1:H:110:TYR:CZ	1:H:114:ARG:HD2	2.38	0.56
1:B:240:MSE:N	1:B:241:GLY:HA2	2.20	0.56
1:A:393:ILE:O	1:A:396:ALA:HB3	2.05	0.56
1:F:155:ILE:HG22	1:F:156:LYS:N	2.21	0.56
1:E:54:LEU:HD13	1:E:111:ALA:O	2.04	0.56
1:K:160:LEU:HG	1:K:198:VAL:HG13	1.87	0.56
1:D:18:GLN:HE22	1:D:21:LYS:HZ3	1.53	0.56
1:F:220:VAL:HG13	1:F:223:PRO:HG3	1.87	0.56
1:A:187:SER:OG	2:A:451:ASP:OD2	2.22	0.56
1:B:36:ILE:HD12	1:B:36:ILE:N	2.20	0.56
1:L:226:ILE:O	1:L:273:THR:HG22	2.05	0.56
1:L:359:LYS:CE	1:L:367:ILE:HD12	2.36	0.56
1:H:132:ILE:HD13	1:H:158:LYS:O	2.06	0.56
1:I:137:VAL:HG12	1:I:138:ILE:HG13	1.87	0.56
1:D:75:SER:O	1:D:79:THR:HG23	2.05	0.56
1:L:409:GLN:HE21	1:L:410:GLY:N	2.04	0.56
1:I:5:VAL:HG22	1:I:34:TYR:HB2	1.88	0.56
1:I:137:VAL:HG13	1:I:155:ILE:HG13	1.86	0.56
1:C:318:LEU:HD23	1:C:331:MSE:HE1	1.88	0.56
1:H:287:THR:HG22	1:H:382:GLY:HA3	1.87	0.56
1:E:202:LEU:HD12	1:E:203:TYR:N	2.21	0.56
1:D:284:ASN:O	1:D:287:THR:HG22	2.06	0.56
1:G:305:ALA:C	1:G:306:LEU:HD22	2.26	0.55
1:E:239:TYR:CG	1:F:335:VAL:HG13	2.41	0.55
1:E:54:LEU:CD2	1:E:74:ILE:HD13	2.36	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:383:MSE:HB2	1:G:389:ILE:HG21	1.88	0.55
1:C:226:ILE:O	1:C:273:THR:CG2	2.44	0.55
1:C:219:ILE:HD11	1:C:429:VAL:HG11	1.87	0.55
1:G:7:LYS:HZ1	1:G:188:ASP:CG	2.09	0.55
1:G:373:MSE:HE3	1:G:405:ARG:HB2	1.87	0.55
1:A:18:GLN:HE22	1:A:21:LYS:HE3	1.71	0.55
1:E:239:TYR:CD2	1:F:335:VAL:HG13	2.42	0.55
1:L:231:TYR:CE2	1:L:277:SER:HA	2.41	0.55
1:F:234:LEU:HD22	1:F:275:ILE:HD13	1.88	0.55
1:L:87:ILE:HG21	1:L:89:MSE:CE	2.36	0.55
1:E:4:VAL:HG22	1:E:202:LEU:HB3	1.87	0.55
1:G:213:LEU:HD13	1:G:217:PRO:HG3	1.89	0.55
1:D:78:TYR:O	1:D:82:VAL:HG12	2.07	0.55
1:K:155:ILE:HG23	1:K:159:VAL:HG13	1.88	0.55
1:L:116:GLU:HG3	1:L:170:PHE:HB3	1.88	0.55
1:B:65:ILE:CG2	1:B:66:PRO:HD2	2.36	0.55
1:H:302:ILE:HD11	1:H:358:ILE:HD12	1.87	0.55
1:A:38:SER:HB3	2:A:451:ASP:OD2	2.07	0.55
1:C:335:VAL:HG12	1:D:239:TYR:CD2	2.42	0.55
1:F:109:ASP:CG	1:F:181:THR:HG22	2.26	0.55
1:D:263:LYS:NZ	1:D:270:ASP:O	2.39	0.55
1:L:34:TYR:HD1	1:L:165:ALA:HB3	1.70	0.55
1:J:137:VAL:HG13	1:J:155:ILE:CG2	2.28	0.55
1:C:397:LEU:HD22	1:C:402:VAL:CG2	2.33	0.55
1:G:160:LEU:HD13	1:G:198:VAL:HG13	1.89	0.55
1:I:37:PRO:HB3	1:I:123:LEU:HD12	1.89	0.55
1:H:198:VAL:O	1:H:200:ALA:N	2.40	0.55
1:B:326:VAL:HG12	1:B:346:LYS:O	2.07	0.55
1:H:247:GLU:HA	1:H:249:ALA:N	2.22	0.55
1:B:9:GLY:HA2	1:B:38:SER:OG	2.07	0.55
1:I:288:ILE:HG22	1:I:289:THR:N	2.23	0.54
1:C:43:ARG:H	1:C:43:ARG:CD	2.19	0.54
1:E:326:VAL:HG12	1:E:346:LYS:O	2.06	0.54
1:K:54:LEU:HD13	1:K:111:ALA:O	2.07	0.54
1:L:390:ALA:HB1	1:L:394:PHE:CE2	2.42	0.54
1:K:402:VAL:HG23	1:K:424:ASP:HB3	1.89	0.54
1:B:65:ILE:HD11	1:C:53:LEU:HD11	1.89	0.54
1:E:315:ARG:HA	1:E:318:LEU:HD12	1.89	0.54
1:L:8:PHE:CZ	1:L:22:VAL:HG13	2.43	0.54
1:I:39:ALA:N	1:I:116:GLU:OE2	2.39	0.54
1:A:397:LEU:HB3	1:A:402:VAL:HG13	1.88	0.54

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:170:PHE:O	1:D:170:PHE:CG	2.61	0.54
1:B:3:ILE:HD12	1:B:3:ILE:N	2.22	0.54
1:A:226:ILE:O	1:A:273:THR:HG22	2.06	0.54
1:L:253:VAL:O	1:L:253:VAL:HG12	2.07	0.54
1:C:256:SER:O	1:C:258:ILE:N	2.41	0.54
1:F:314:CYS:O	1:F:318:LEU:HD12	2.08	0.54
1:B:384:ALA:HB2	1:B:413:GLU:O	2.07	0.54
1:A:18:GLN:NE2	1:A:21:LYS:HE3	2.22	0.54
1:I:155:ILE:O	1:I:159:VAL:HG22	2.08	0.54
1:H:320:ILE:HA	1:H:323:MSE:HE3	1.90	0.54
1:F:155:ILE:HD11	1:F:194:ILE:HD13	1.88	0.54
1:K:318:LEU:HD21	1:L:318:LEU:CG	2.38	0.54
1:L:364:PRO:HG3	1:L:367:ILE:HD11	1.89	0.54
1:B:253:VAL:HG13	1:B:258:ILE:HB	1.90	0.54
1:K:393:ILE:HG22	1:K:397:LEU:HD12	1.89	0.54
1:D:231:TYR:CE1	1:D:250:ILE:HG23	2.43	0.54
1:E:202:LEU:HD12	1:E:203:TYR:H	1.73	0.54
1:H:247:GLU:HA	1:H:248:GLU:C	2.28	0.54
1:J:321:LEU:CD2	1:J:326:VAL:HG23	2.38	0.54
1:C:155:ILE:O	1:C:159:VAL:HG12	2.08	0.53
1:L:169:GLY:O	1:L:190:THR:OG1	2.14	0.53
1:H:86:ASN:HD22	1:H:86:ASN:N	2.04	0.53
1:A:274:LEU:HD22	1:A:276:LEU:CD1	2.36	0.53
1:H:87:ILE:HG22	1:H:89:MSE:HG2	1.90	0.53
1:L:75:SER:CB	1:L:95:LEU:HD13	2.38	0.53
1:G:378:THR:C	1:G:383:MSE:HE1	2.28	0.53
1:F:379:VAL:C	1:F:383:MSE:HE3	2.29	0.53
1:B:237:LEU:HD12	1:B:292:ALA:HB3	1.90	0.53
1:I:106:ALA:HB1	1:I:110:TYR:CD1	2.43	0.53
1:E:288:ILE:HG22	1:E:289:THR:N	2.23	0.53
1:I:404:ILE:HG21	1:I:407:ILE:HD11	1.89	0.53
1:K:25:ILE:HG21	1:K:206:TRP:CZ2	2.44	0.53
1:C:155:ILE:HG22	1:C:156:LYS:N	2.24	0.53
1:A:63:ASN:ND2	1:D:56:LEU:HD22	2.23	0.53
1:K:114:ARG:HA	1:K:114:ARG:NE	2.24	0.53
1:E:226:ILE:HG22	1:E:228:LYS:O	2.09	0.53
1:C:315:ARG:HA	1:C:318:LEU:HD11	1.91	0.53
1:A:379:VAL:HA	1:A:383:MSE:CE	2.38	0.53
1:K:421:GLU:CG	1:K:423:VAL:HG12	2.39	0.53
1:C:235:ARG:NH1	1:C:236:GLU:OE2	2.41	0.53
1:B:212:PHE:H	1:B:273:THR:CG2	2.21	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:321:LEU:HD12	1:L:340:LEU:HD23	1.89	0.53
1:L:34:TYR:CE2	1:L:198:VAL:HG11	2.43	0.53
1:J:87:ILE:HG21	1:J:89:MSE:CE	2.39	0.53
1:J:351:CYS:SG	1:J:352:ASP:N	2.81	0.53
1:H:212:PHE:CZ	1:H:244:VAL:HA	2.43	0.53
1:C:212:PHE:H	1:C:273:THR:HG23	1.73	0.53
1:B:65:ILE:HD11	1:C:53:LEU:CD1	2.38	0.53
1:B:212:PHE:H	1:B:273:THR:HG21	1.73	0.53
1:F:35:ILE:HD12	1:F:35:ILE:N	2.24	0.53
1:F:155:ILE:HD13	1:F:159:VAL:CG2	2.39	0.53
1:H:247:GLU:HB3	1:H:250:ILE:HD13	1.91	0.53
1:C:110:TYR:CZ	1:C:114:ARG:HD2	2.44	0.53
1:H:34:TYR:CD1	1:H:165:ALA:HB3	2.44	0.53
1:A:125:LYS:O	1:A:126:TYR:C	2.47	0.53
1:J:134:ALA:HB3	1:J:171:TYR:CE1	2.43	0.53
1:C:320:ILE:CD1	1:C:358:ILE:CG2	2.86	0.53
1:J:237:LEU:HD13	1:J:292:ALA:HB2	1.91	0.53
1:J:22:VAL:HA	1:J:25:ILE:HD12	1.91	0.53
1:K:300:ILE:HG22	1:K:302:ILE:HG13	1.91	0.53
1:C:238:SER:HB2	1:D:335:VAL:HG11	1.91	0.53
1:H:34:TYR:HD1	1:H:165:ALA:HB3	1.73	0.53
1:D:306:LEU:O	1:D:308:ASN:N	2.42	0.53
1:H:320:ILE:CD1	1:H:358:ILE:HG22	2.33	0.52
1:H:87:ILE:HD11	1:H:126:TYR:HB2	1.91	0.52
1:G:155:ILE:CD1	1:G:194:ILE:CD1	2.87	0.52
1:F:354:ILE:O	1:F:358:ILE:HG22	2.08	0.52
1:J:333:SER:HB3	1:J:338:VAL:HG23	1.90	0.52
1:J:364:PRO:HG3	1:J:367:ILE:HD11	1.90	0.52
1:F:317:ILE:HA	1:F:320:ILE:HD12	1.90	0.52
1:H:170:PHE:O	1:H:170:PHE:CG	2.60	0.52
1:I:155:ILE:CG2	1:I:159:VAL:CG2	2.84	0.52
1:I:159:VAL:HG12	1:I:167:ILE:HD11	1.90	0.52
1:I:318:LEU:HD21	1:J:318:LEU:HG	1.92	0.52
1:G:53:LEU:HB3	1:G:74:ILE:HD11	1.91	0.52
1:I:170:PHE:CZ	1:I:181:THR:HG21	2.44	0.52
1:C:79:THR:HA	1:C:82:VAL:HG12	1.91	0.52
1:D:58:ASN:HD21	1:D:62:LYS:HE3	1.74	0.52
1:L:383:MSE:HE1	1:L:416:VAL:HG23	1.90	0.52
1:G:288:ILE:HD13	1:G:383:MSE:CE	2.21	0.52
1:A:318:LEU:HD11	1:B:318:LEU:CD1	2.38	0.52
1:E:373:MSE:HE2	1:E:419:GLY:HA3	1.91	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:ALA:HB3	1:B:220:VAL:CG1	2.39	0.52
1:L:320:ILE:HG21	1:L:358:ILE:CG2	2.39	0.52
1:K:332:PRO:CG	1:K:406:MSE:HE3	2.39	0.52
1:K:318:LEU:HD21	1:L:318:LEU:CD2	2.39	0.52
1:L:375:LEU:HD21	1:L:406:MSE:HE3	1.91	0.52
1:K:383:MSE:CE	1:K:416:VAL:HG23	2.39	0.52
1:I:159:VAL:HG23	1:I:160:LEU:N	2.24	0.52
1:F:82:VAL:HG21	1:F:89:MSE:CE	2.38	0.52
1:I:390:ALA:HB1	1:I:394:PHE:HE2	1.74	0.52
1:G:302:ILE:CD1	1:G:317:ILE:HD13	2.39	0.52
1:J:213:LEU:HD12	1:J:213:LEU:N	2.25	0.52
1:J:241:GLY:CA	1:J:292:ALA:HB1	2.40	0.52
1:J:321:LEU:HD23	1:J:326:VAL:HG23	1.92	0.52
1:B:82:VAL:HG23	1:B:87:ILE:HB	1.90	0.52
1:J:117:TYR:O	1:J:121:VAL:HG13	2.09	0.52
1:E:143:SER:O	1:E:145:CYS:N	2.42	0.52
1:D:320:ILE:HD13	1:D:358:ILE:HA	1.92	0.52
1:D:352:ASP:HA	1:D:355:ILE:HD12	1.91	0.52
1:J:35:ILE:HD12	1:J:35:ILE:N	2.25	0.52
1:I:85:LEU:O	1:I:86:ASN:C	2.48	0.52
1:L:129:ALA:HB3	1:L:166:VAL:HG23	1.92	0.52
1:F:226:ILE:CG2	1:F:229:ILE:HB	2.40	0.52
1:G:232:LYS:HG2	1:G:414:ILE:HD11	1.91	0.52
1:L:155:ILE:HG21	1:L:197:GLY:HA3	1.92	0.52
1:C:320:ILE:HD12	1:C:357:GLU:HB3	1.92	0.52
1:K:318:LEU:HD12	1:K:319:SER:N	2.24	0.52
1:B:53:LEU:HD11	1:C:65:ILE:HD11	1.91	0.52
1:B:326:VAL:HG23	1:B:326:VAL:O	2.10	0.52
1:J:318:LEU:HD21	1:J:318:LEU:HD21	1.90	0.51
1:B:187:SER:O	1:B:190:THR:HG23	2.10	0.51
1:B:211:GLY:HA2	1:B:262:ILE:HG22	1.92	0.51
1:K:114:ARG:N	1:K:114:ARG:HE	2.07	0.51
1:I:326:VAL:HG12	1:I:346:LYS:O	2.11	0.51
1:G:238:SER:CB	1:G:244:VAL:HG11	2.39	0.51
1:G:245:LEU:HD12	1:G:246:HIS:N	2.25	0.51
1:F:355:ILE:HD11	1:F:369:ILE:HD11	1.92	0.51
1:K:326:VAL:HG11	1:K:347:LEU:CD1	2.40	0.51
1:I:409:GLN:HG2	1:J:407:ILE:HD12	1.92	0.51
1:G:155:ILE:HD12	1:G:194:ILE:HD13	1.93	0.51
1:H:50:ILE:HD11	1:H:77:ARG:HD3	1.91	0.51
1:L:216:ASP:O	1:L:220:VAL:HG12	2.10	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:236:GLU:HB3	1:H:379:VAL:HG21	1.91	0.51
1:C:320:ILE:HD13	1:C:358:ILE:CG2	2.40	0.51
1:J:34:TYR:C	1:J:35:ILE:HD12	2.31	0.51
1:B:313:PHE:CE2	1:B:317:ILE:HD11	2.45	0.51
1:J:262:ILE:CD1	1:J:275:ILE:HD11	2.40	0.51
1:C:79:THR:HG22	1:C:91:ILE:CG2	2.41	0.51
1:L:364:PRO:CG	1:L:367:ILE:HD11	2.40	0.51
1:I:198:VAL:O	1:I:199:ASN:C	2.48	0.51
1:K:58:ASN:HD21	1:K:62:LYS:HE3	1.76	0.51
1:A:57:CYS:HG	1:A:67:PHE:HD1	1.58	0.51
1:I:250:ILE:O	1:I:250:ILE:HG22	2.11	0.51
1:H:85:LEU:HD23	1:H:126:TYR:CE1	2.45	0.51
1:C:43:ARG:H	1:C:43:ARG:HD3	1.75	0.51
1:I:137:VAL:HG22	1:I:155:ILE:HA	1.93	0.51
1:A:315:ARG:HA	1:B:318:LEU:HD13	1.93	0.51
1:A:35:ILE:HB	1:A:166:VAL:HG22	1.93	0.51
1:K:18:GLN:HE22	1:K:21:LYS:HZ2	1.59	0.51
1:E:65:ILE:HG12	1:E:66:PRO:HD2	1.93	0.51
1:J:87:ILE:HG21	1:J:89:MSE:HE3	1.93	0.51
1:G:19:PHE:HB3	1:G:85:LEU:HD21	1.93	0.51
1:E:323:MSE:HE2	1:G:315:ARG:HH22	1.74	0.51
1:G:318:LEU:HD11	1:H:318:LEU:HD11	1.93	0.51
1:K:305:ALA:C	1:K:306:LEU:HD12	2.32	0.51
1:K:394:PHE:O	1:K:398:SER:N	2.44	0.50
1:J:188:ASP:HB3	1:J:249:ALA:HB1	1.92	0.50
1:I:138:ILE:HD13	1:I:190:THR:HG22	1.93	0.50
1:B:237:LEU:HD12	1:B:292:ALA:HB2	1.92	0.50
1:B:314:CYS:HA	1:B:317:ILE:HD12	1.93	0.50
1:I:305:ALA:HB1	1:I:306:LEU:HD12	1.93	0.50
1:D:16:SER:HB2	1:D:85:LEU:HD12	1.93	0.50
1:B:160:LEU:O	1:B:160:LEU:HD12	2.12	0.50
1:E:373:MSE:HE1	1:E:406:MSE:HB2	1.94	0.50
1:I:305:ALA:CB	1:I:306:LEU:HD12	2.42	0.50
1:H:152:TYR:HA	1:H:155:ILE:HD12	1.93	0.50
1:K:36:ILE:N	1:K:36:ILE:HD12	2.26	0.50
1:G:169:GLY:C	1:G:190:THR:HG21	2.32	0.50
1:E:250:ILE:CG2	1:E:250:ILE:O	2.60	0.50
1:L:283:ILE:O	1:L:283:ILE:HG23	2.11	0.50
1:G:379:VAL:CA	1:G:383:MSE:CE	2.90	0.50
1:C:383:MSE:CB	1:C:389:ILE:HG21	2.34	0.50
1:C:3:ILE:HD12	1:C:3:ILE:O	2.11	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:213:LEU:HD23	1:K:223:PRO:O	2.11	0.50
1:G:18:GLN:HE22	1:G:21:LYS:HZ2	1.60	0.50
1:L:100:LYS:O	1:L:104:ASN:ND2	2.44	0.50
1:J:48:TYR:CD1	1:J:53:LEU:HD22	2.47	0.50
1:L:320:ILE:CD1	1:L:358:ILE:HG22	2.38	0.50
1:I:320:ILE:CD1	1:I:358:ILE:HG22	2.41	0.50
1:H:98:VAL:HG22	1:H:114:ARG:HD3	1.93	0.50
1:E:321:LEU:HD11	1:E:342:ILE:HD11	1.92	0.50
1:I:16:SER:HB3	1:I:85:LEU:HD13	1.94	0.50
1:H:118:LEU:O	1:H:121:VAL:HG22	2.12	0.50
1:A:226:ILE:O	1:A:273:THR:CG2	2.59	0.50
1:G:263:LYS:NZ	1:G:270:ASP:O	2.34	0.50
1:G:313:PHE:N	3:G:507:LYS:O	2.45	0.50
1:J:402:VAL:HG23	1:J:424:ASP:HB3	1.92	0.50
1:B:226:ILE:O	1:B:273:THR:HG22	2.11	0.50
1:J:212:PHE:N	1:J:273:THR:OG1	2.39	0.50
1:K:147:ASP:OD2	1:K:148:GLU:N	2.44	0.50
1:F:159:VAL:HB	1:F:198:VAL:HG21	1.93	0.49
1:K:318:LEU:HD23	1:L:318:LEU:HD21	1.93	0.49
1:B:240:MSE:N	1:B:241:GLY:CA	2.75	0.49
1:C:61:VAL:HG21	1:C:102:ILE:O	2.12	0.49
1:A:56:LEU:HD22	1:D:63:ASN:ND2	2.26	0.49
1:I:23:LYS:O	1:I:27:ASP:OD1	2.30	0.49
1:E:18:GLN:HE22	1:E:21:LYS:NZ	2.10	0.49
1:L:34:TYR:HE2	1:L:198:VAL:HG11	1.77	0.49
1:K:235:ARG:O	1:K:238:SER:HB3	2.12	0.49
1:E:373:MSE:HE2	1:E:419:GLY:C	2.32	0.49
1:E:132:ILE:HD11	1:E:162:CYS:SG	2.52	0.49
1:H:60:HIS:CG	1:H:67:PHE:HB3	2.47	0.49
1:A:318:LEU:HD13	1:B:315:ARG:HA	1.95	0.49
1:E:155:ILE:HG23	1:E:159:VAL:CG1	2.42	0.49
1:J:288:ILE:HD13	1:J:383:MSE:SE	2.62	0.49
1:L:320:ILE:HG21	1:L:358:ILE:HG22	1.95	0.49
1:I:253:VAL:CG1	1:I:258:ILE:O	2.60	0.49
1:B:317:ILE:O	1:B:321:LEU:HD13	2.13	0.49
1:J:110:TYR:CZ	1:J:114:ARG:HD2	2.47	0.49
1:L:160:LEU:HB2	1:L:198:VAL:HG22	1.93	0.49
1:E:373:MSE:HE3	1:E:405:ARG:HB3	1.92	0.49
1:L:75:SER:HB3	1:L:95:LEU:HD13	1.93	0.49
1:H:400:GLU:H	1:H:401:ASN:HA	1.77	0.49
1:E:7:LYS:NZ	1:E:188:ASP:OD1	2.46	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:78:TYR:CE1	1:F:118:LEU:HD12	2.48	0.49
1:I:169:GLY:O	1:I:190:THR:CG2	2.60	0.49
1:A:379:VAL:HA	1:A:383:MSE:HE2	1.93	0.49
1:I:213:LEU:HD12	1:I:217:PRO:HD3	1.94	0.49
1:I:213:LEU:HD13	1:I:223:PRO:HG2	1.94	0.49
1:L:397:LEU:HD12	1:L:404:ILE:HD11	1.95	0.49
1:H:207:THR:HG23	1:H:209:VAL:H	1.77	0.49
1:G:379:VAL:C	1:G:383:MSE:CE	2.77	0.49
1:G:198:VAL:CG1	1:G:198:VAL:O	2.60	0.49
1:F:155:ILE:HD12	1:F:198:VAL:CG2	2.40	0.49
1:C:65:ILE:HG22	1:C:66:PRO:O	2.12	0.49
1:A:167:ILE:N	1:A:167:ILE:HD12	2.28	0.49
1:F:198:VAL:O	1:F:198:VAL:HG12	2.13	0.49
1:K:369:ILE:HG22	1:K:371:PRO:HD3	1.95	0.49
1:I:409:GLN:HB3	1:I:416:VAL:HG22	1.94	0.49
1:L:155:ILE:HG22	1:L:156:LYS:N	2.28	0.48
1:H:373:MSE:HE2	1:H:419:GLY:CA	2.42	0.48
1:F:291:ILE:CG2	1:F:429:VAL:HG13	2.42	0.48
1:H:14:ALA:O	1:H:77:ARG:NH2	2.43	0.48
1:B:320:ILE:HD11	1:B:361:GLN:HE21	1.78	0.48
1:J:198:VAL:O	1:J:199:ASN:C	2.50	0.48
1:F:75:SER:HB2	1:F:95:LEU:HD13	1.94	0.48
1:G:35:ILE:HD12	1:G:35:ILE:N	2.28	0.48
1:A:7:LYS:HD2	1:A:8:PHE:N	2.28	0.48
1:B:194:ILE:O	1:B:198:VAL:HG12	2.13	0.48
1:I:262:ILE:O	1:I:272:GLY:HA3	2.14	0.48
1:G:308[B]:ASN:OD1	3:G:507:LYS:CG	2.54	0.48
1:D:182:PHE:CE2	1:D:190:THR:HG22	2.48	0.48
1:H:155:ILE:CG2	1:H:198:VAL:HG23	2.43	0.48
1:E:54:LEU:HD23	1:E:74:ILE:CD1	2.43	0.48
1:L:169:GLY:HA2	1:L:190:THR:HG21	1.95	0.48
1:A:79:THR:HG22	1:A:91:ILE:CG2	2.44	0.48
1:A:387:LYS:HD2	1:B:401:ASN:HD22	1.79	0.48
1:J:287:THR:HG22	1:J:382:GLY:HA3	1.95	0.48
1:A:320:ILE:CD1	1:A:358:ILE:HG22	2.41	0.48
1:I:130:GLU:CB	1:I:162:CYS:SG	3.02	0.48
1:K:85:LEU:HD22	1:K:87:ILE:HD11	1.96	0.48
1:H:262:ILE:HD11	1:H:275:ILE:HD11	1.96	0.48
1:D:320:ILE:HG21	1:D:358:ILE:HG23	1.96	0.48
1:D:19:PHE:HB3	1:D:85:LEU:HD21	1.95	0.48
1:A:253:VAL:CG1	1:A:258:ILE:O	2.61	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:205:ASN:ND2	1:H:245:LEU:HD22	2.28	0.48
1:C:87:ILE:HG22	1:C:88:ASP:N	2.24	0.48
1:C:335:VAL:HG23	1:C:336:ASP:N	2.28	0.48
1:I:170:PHE:CZ	1:I:181:THR:CG2	2.97	0.48
1:A:305:ALA:HB1	1:A:306:LEU:HD12	1.94	0.48
1:E:383:MSE:CE	1:E:416:VAL:HG23	2.44	0.48
1:L:228:LYS:HE2	1:L:276:LEU:HD21	1.94	0.48
1:J:402:VAL:HG23	1:J:424:ASP:CB	2.44	0.48
1:H:169:GLY:HA2	1:H:190:THR:HG21	1.95	0.48
1:I:288:ILE:HD11	1:I:436:PHE:CZ	2.48	0.48
1:I:216:ASP:HB3	1:I:219:ILE:HD13	1.95	0.48
1:A:363:ASN:O	1:A:363:ASN:ND2	2.47	0.48
1:K:238:SER:O	1:K:239:TYR:C	2.53	0.48
1:I:198:VAL:O	1:I:198:VAL:HG12	2.14	0.48
1:I:198:VAL:O	1:I:200:ALA:N	2.46	0.48
1:B:364:PRO:CG	1:B:367:ILE:HD11	2.43	0.48
1:B:364:PRO:HG3	1:B:367:ILE:HD11	1.96	0.48
1:H:288:ILE:CG2	1:H:289:THR:N	2.76	0.48
1:G:390:ALA:HB1	1:G:394:PHE:CE2	2.49	0.48
1:H:55:TYR:CZ	1:H:112:ALA:HB2	2.49	0.48
1:A:274:LEU:HD23	1:A:276:LEU:CD1	2.44	0.48
1:K:347:LEU:HD11	1:K:354:ILE:CD1	2.44	0.48
1:G:18:GLN:HE22	1:G:21:LYS:NZ	2.11	0.48
1:E:169:GLY:C	1:E:190:THR:HG21	2.34	0.48
1:D:186:GLY:O	1:D:189:VAL:HG12	2.13	0.47
1:I:318:LEU:HD21	1:J:318:LEU:CG	2.44	0.47
1:A:383:MSE:HE3	1:A:414:ILE:C	2.34	0.47
1:L:85:LEU:HD23	1:L:126:TYR:CD1	2.49	0.47
1:I:53:LEU:CG	1:L:65:ILE:HD11	2.44	0.47
1:K:114:ARG:CA	1:K:114:ARG:NE	2.77	0.47
1:A:192:SER:HB3	1:A:253:VAL:HG23	1.96	0.47
1:H:299:VAL:HG13	1:H:370:HIS:HB2	1.96	0.47
1:I:36:ILE:N	1:I:36:ILE:HD12	2.28	0.47
1:B:302:ILE:HD13	1:B:358:ILE:HD11	1.96	0.47
1:L:89:MSE:HE1	1:L:122:ILE:HA	1.96	0.47
1:C:318:LEU:HD13	1:D:315:ARG:CB	2.44	0.47
1:F:216:ASP:O	1:F:220:VAL:HG12	2.14	0.47
1:E:304:LYS:CB	1:E:363:ASN:HD21	2.27	0.47
1:A:334:GLY:O	1:A:336:ASP:N	2.47	0.47
1:G:379:VAL:HA	1:G:383:MSE:HE3	1.95	0.47
1:B:213:LEU:HD13	1:B:223:PRO:HG2	1.96	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:155:ILE:HG21	1:C:197:GLY:HA3	1.95	0.47
1:F:359:LYS:HE2	1:F:367:ILE:HD12	1.96	0.47
1:J:137:VAL:HG12	1:J:138:ILE:HG12	1.95	0.47
1:J:318:LEU:C	1:J:318:LEU:HD12	2.34	0.47
1:G:231:TYR:CE2	1:G:277:SER:HA	2.49	0.47
1:G:333:SER:HB2	3:G:507:LYS:NZ	2.30	0.47
1:E:320:ILE:HA	1:E:323:MSE:HE3	1.95	0.47
1:B:381:THR:HA	1:B:414:ILE:HG22	1.97	0.47
1:H:250:ILE:HG12	1:H:250:ILE:O	2.15	0.47
1:F:35:ILE:HB	1:F:166:VAL:HG22	1.95	0.47
1:K:409:GLN:HE21	1:K:416:VAL:HG22	1.79	0.47
1:I:335:VAL:CG2	1:J:239:TYR:CB	2.92	0.47
1:K:82:VAL:HG23	1:K:87:ILE:HB	1.97	0.47
1:G:152:TYR:CE1	1:G:196:ALA:HB3	2.49	0.47
1:I:229:ILE:HD11	1:I:237:LEU:HD12	1.96	0.47
1:F:323:MSE:HE2	1:H:316:LYS:NZ	2.30	0.47
1:G:359:LYS:CE	1:G:367:ILE:HD12	2.45	0.47
1:J:397:LEU:HD22	1:J:402:VAL:HG11	1.96	0.47
1:J:397:LEU:O	1:J:402:VAL:CG1	2.62	0.47
1:E:36:ILE:N	1:E:36:ILE:CD1	2.77	0.47
1:L:341:VAL:HG21	1:L:406:MSE:SE	2.65	0.47
1:E:253:VAL:O	1:E:256:SER:O	2.33	0.47
1:C:113:SER:OG	1:C:114:ARG:NH1	2.48	0.47
1:L:58:ASN:HD21	1:L:62:LYS:CE	2.28	0.47
1:J:431:SER:O	1:J:435:ALA:HB2	2.15	0.47
1:I:234:LEU:HD23	1:I:234:LEU:C	2.35	0.47
1:F:250:ILE:C	1:F:250:ILE:HD12	2.35	0.47
1:C:35:ILE:N	1:C:35:ILE:HD12	2.29	0.47
1:I:137:VAL:HG13	1:I:155:ILE:CG1	2.45	0.47
1:H:231:TYR:OH	1:H:253:VAL:HG12	2.15	0.47
1:E:78:TYR:O	1:E:82:VAL:HG12	2.15	0.47
1:E:155:ILE:O	1:E:159:VAL:HG13	2.14	0.47
1:D:251:PHE:CG	1:D:252:PRO:HD3	2.49	0.47
1:H:358:ILE:C	1:H:360:LYS:H	2.19	0.47
1:J:424:ASP:O	1:J:425:PHE:C	2.53	0.47
1:K:35:ILE:C	1:K:36:ILE:HD12	2.35	0.47
1:E:262:ILE:O	1:E:272:GLY:HA3	2.15	0.47
1:A:33:LYS:O	1:A:164:LYS:HA	2.15	0.47
1:H:240:MSE:SE	1:H:377:ALA:HB2	2.64	0.47
1:C:212:PHE:CD2	1:C:273:THR:HG21	2.49	0.47
1:J:155:ILE:HD13	1:J:198:VAL:HG13	1.92	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:212:PHE:H	1:I:273:THR:HG23	1.79	0.47
1:J:241:GLY:HA2	1:J:292:ALA:HB1	1.97	0.47
1:A:110:TYR:CZ	1:A:114:ARG:HD2	2.50	0.47
1:A:213:LEU:O	1:A:240:MSE:HE2	2.15	0.47
1:B:9:GLY:HA2	1:B:38:SER:HG	1.79	0.47
1:J:412:SER:HB3	1:J:415:ASN:HD22	1.79	0.47
1:F:134:ALA:HB3	1:F:171:TYR:CE1	2.50	0.47
1:I:238:SER:HA	1:I:245:LEU:CD1	2.45	0.46
1:E:239:TYR:CE2	1:E:240:MSE:HE2	2.50	0.46
1:J:82:VAL:O	1:J:85:LEU:O	2.32	0.46
1:A:34:TYR:CD1	1:A:165:ALA:HB3	2.50	0.46
1:D:229:ILE:HG22	1:D:274:LEU:O	2.14	0.46
1:G:362:CYS:O	1:G:364:PRO:HD3	2.14	0.46
1:L:114:ARG:CA	1:L:114:ARG:NE	2.78	0.46
1:H:82:VAL:O	1:H:85:LEU:O	2.33	0.46
1:A:313:PHE:CE1	1:A:317:ILE:HD11	2.50	0.46
1:E:362:CYS:O	1:E:364:PRO:HD3	2.14	0.46
1:E:284:ASN:O	1:E:287:THR:HG22	2.14	0.46
1:K:215:ALA:HB3	1:K:220:VAL:HG11	1.97	0.46
1:G:359:LYS:HE3	1:G:367:ILE:HD12	1.97	0.46
1:C:3:ILE:CG1	1:C:3:ILE:O	2.64	0.46
1:K:182:PHE:CE1	1:K:190:THR:HG22	2.50	0.46
3:C:503:LYS:NZ	1:D:329:GLU:O	2.43	0.46
1:A:339:SER:O	1:A:340:LEU:HD12	2.14	0.46
1:B:65:ILE:HG22	1:B:66:PRO:CD	2.46	0.46
1:B:234:LEU:HD11	1:B:244:VAL:HB	1.96	0.46
1:H:33:LYS:O	1:H:164:LYS:HA	2.16	0.46
1:L:198:VAL:O	1:L:199:ASN:C	2.54	0.46
1:K:378:THR:HG21	1:K:393:ILE:HD13	1.96	0.46
1:J:236:GLU:HB3	1:J:379:VAL:HG21	1.97	0.46
1:I:207:THR:OG1	1:I:208:ASP:N	2.46	0.46
1:D:221:GLU:C	1:D:223:PRO:HD3	2.35	0.46
1:G:192:SER:HB2	1:G:253:VAL:HG23	1.97	0.46
1:B:181:THR:HG23	1:B:182:PHE:O	2.16	0.46
1:F:155:ILE:CG2	1:F:156:LYS:N	2.79	0.46
1:B:220:VAL:HG13	1:B:223:PRO:HB3	1.97	0.46
1:H:256:SER:CB	1:H:258:ILE:HD12	2.45	0.46
1:I:287:THR:HG23	1:I:288:ILE:O	2.16	0.46
1:J:321:LEU:HD12	1:J:340:LEU:HD23	1.97	0.46
1:C:311:VAL:HG13	1:C:312:GLY:HA2	1.96	0.46
1:C:330:HIS:ND1	1:C:406:MSE:HE1	2.31	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:245:LEU:HB3	1:J:246:HIS:CA	2.46	0.46
1:F:60:HIS:CE1	1:G:60:HIS:HE1	2.33	0.46
1:G:61:VAL:HG21	1:G:102:ILE:O	2.16	0.46
1:D:167:ILE:N	1:D:167:ILE:HD12	2.30	0.46
1:J:298:THR:HG23	1:J:371:PRO:HA	1.98	0.46
1:G:379:VAL:N	1:G:383:MSE:HE1	2.30	0.46
1:E:335:VAL:HG22	1:F:239:TYR:CD2	2.51	0.46
1:C:320:ILE:HD13	1:C:358:ILE:HG22	1.98	0.46
1:H:198:VAL:O	1:H:198:VAL:HG12	2.15	0.46
1:E:60:HIS:O	1:E:65:ILE:HG22	2.15	0.46
1:I:53:LEU:CD1	1:L:65:ILE:HD11	2.46	0.46
1:I:39:ALA:HB1	1:I:40:PRO:HD2	1.98	0.46
1:J:212:PHE:CE2	1:J:262:ILE:HD13	2.50	0.46
1:J:379:VAL:HG22	1:J:415:ASN:HB2	1.98	0.46
1:L:71:PHE:HA	1:L:74:ILE:HD12	1.98	0.46
1:A:116:GLU:HG3	1:A:170:PHE:HB3	1.97	0.46
1:C:235:ARG:O	1:C:238:SER:OG	2.32	0.46
1:G:317:ILE:CG2	1:G:340:LEU:HD21	2.45	0.46
1:E:55:TYR:CE1	1:E:112:ALA:HB2	2.51	0.46
1:D:320:ILE:HD13	1:D:358:ILE:CG2	2.41	0.46
1:D:326:VAL:HG12	1:D:346:LYS:O	2.16	0.46
1:I:288:ILE:HD11	1:I:436:PHE:CE1	2.51	0.46
1:D:251:PHE:CD2	1:D:252:PRO:HD3	2.50	0.46
1:D:384:ALA:HA	1:D:385:LYS:HA	1.74	0.46
1:L:234:LEU:HD22	1:L:275:ILE:HD13	1.98	0.46
1:L:373:MSE:HE3	1:L:405:ARG:HB3	1.98	0.46
1:B:247:GLU:HA	1:B:250:ILE:HD11	1.98	0.46
1:B:251:PHE:N	1:B:252:PRO:CD	2.78	0.46
1:D:284:ASN:O	1:D:287:THR:CG2	2.64	0.46
1:E:240:MSE:HE3	1:E:417:ILE:HD13	1.96	0.46
1:B:253:VAL:O	1:B:256:SER:O	2.33	0.46
1:B:134:ALA:HB3	1:B:171:TYR:CE1	2.50	0.46
1:F:283:ILE:N	1:F:283:ILE:HD12	2.31	0.46
1:J:167:ILE:HD12	1:J:194:ILE:HG12	1.98	0.45
1:C:318:LEU:HD23	1:C:331:MSE:CE	2.45	0.45
1:B:35:ILE:HD12	1:B:35:ILE:N	2.30	0.45
1:F:313:PHE:CE2	1:F:317:ILE:HD11	2.52	0.45
1:J:383:MSE:HB2	1:J:389:ILE:HG21	1.97	0.45
1:G:393:ILE:HG23	1:G:432:ILE:HG12	1.99	0.45
1:C:288:ILE:CG2	1:C:289:THR:N	2.79	0.45
1:B:7:LYS:HG3	1:B:8:PHE:N	2.31	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:283:ILE:HD13	1:J:228:LYS:HD3	1.97	0.45
1:J:214:MSE:HE2	1:J:433:TYR:CD2	2.51	0.45
1:I:87:ILE:CG2	1:I:89:MSE:HG2	2.46	0.45
1:L:298:THR:HG23	1:L:371:PRO:HA	1.97	0.45
1:C:13:LEU:HD22	1:C:19:PHE:CZ	2.52	0.45
1:B:231:TYR:OH	1:B:253:VAL:HG12	2.17	0.45
1:L:321:LEU:CD1	1:L:340:LEU:HD23	2.46	0.45
1:I:129:ALA:HB1	1:I:164:LYS:C	2.36	0.45
1:E:283:ILE:O	1:E:283:ILE:HG23	2.17	0.45
1:C:335:VAL:HG23	1:C:336:ASP:H	1.80	0.45
1:F:155:ILE:HG21	1:F:198:VAL:N	2.32	0.45
1:L:318:LEU:HD12	1:L:318:LEU:C	2.36	0.45
1:F:321:LEU:O	1:F:326:VAL:HG22	2.17	0.45
1:A:310:GLU:HB2	1:A:313:PHE:HB2	1.98	0.45
1:H:170:PHE:O	1:H:170:PHE:CD2	2.70	0.45
1:B:198:VAL:HG22	1:B:198:VAL:O	2.15	0.45
1:A:75:SER:O	1:A:79:THR:HG23	2.16	0.45
1:F:315:ARG:HA	1:F:318:LEU:HD12	1.97	0.45
1:K:85:LEU:CD2	1:K:87:ILE:HD11	2.46	0.45
1:K:256:SER:O	1:K:258:ILE:N	2.50	0.45
1:L:50:ILE:O	1:L:51:THR:C	2.54	0.45
1:A:284:ASN:HB2	1:A:287:THR:HG21	1.98	0.45
1:C:3:ILE:HD11	1:C:200:ALA:CA	2.43	0.45
1:A:380:GLY:N	1:A:383:MSE:HE2	2.32	0.45
1:J:85:LEU:HD23	1:J:87:ILE:HD11	1.98	0.45
1:G:19:PHE:CB	1:G:85:LEU:HD21	2.47	0.45
1:I:306:LEU:HD12	1:I:306:LEU:N	2.32	0.45
1:H:262:ILE:HD11	1:H:275:ILE:CD1	2.47	0.45
1:B:137:VAL:HG22	1:B:155:ILE:HG13	1.99	0.45
1:K:339:SER:C	1:K:340:LEU:HD12	2.36	0.45
1:C:34:TYR:CE2	1:C:198:VAL:HG11	2.52	0.45
1:C:373:MSE:HE3	1:C:375:LEU:CD2	2.47	0.45
1:J:262:ILE:HD12	1:J:275:ILE:HD11	2.00	0.45
1:G:35:ILE:C	1:G:36:ILE:HD12	2.37	0.45
1:G:321:LEU:O	1:G:326:VAL:HG22	2.16	0.45
1:I:155:ILE:HG23	1:I:159:VAL:HG22	1.96	0.44
1:J:236:GLU:CB	1:J:379:VAL:HG21	2.46	0.44
1:G:251:PHE:HB3	1:G:252:PRO:HD3	1.98	0.44
1:G:210:SER:HA	1:G:264:ASN:HB2	1.98	0.44
1:L:36:ILE:N	1:L:36:ILE:HD12	2.32	0.44
1:A:36:ILE:N	1:A:36:ILE:HD12	2.32	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:82:VAL:HG23	1:G:87:ILE:HB	1.98	0.44
1:C:397:LEU:HB3	1:C:402:VAL:HG22	1.97	0.44
1:K:406:MSE:HE2	1:K:408:ASP:CB	2.41	0.44
1:G:198:VAL:HG12	1:G:198:VAL:O	2.17	0.44
1:K:234:LEU:CD1	1:K:275:ILE:HG21	2.46	0.44
1:F:307:LEU:C	1:F:307:LEU:HD23	2.37	0.44
1:H:87:ILE:CG2	1:H:89:MSE:HG2	2.46	0.44
1:D:110:TYR:O	1:D:114:ARG:HG2	2.18	0.44
1:J:302:ILE:HD12	1:J:338:VAL:HG13	1.99	0.44
1:I:181:THR:HG22	1:I:182:PHE:O	2.18	0.44
1:L:15:ASP:O	1:L:16:SER:C	2.56	0.44
1:D:160:LEU:HG	1:D:198:VAL:HG23	2.00	0.44
1:F:304:LYS:O	1:F:336:ASP:HB3	2.18	0.44
1:A:318:LEU:HD13	1:B:315:ARG:CB	2.48	0.44
1:A:16:SER:HB2	1:A:85:LEU:CD1	2.47	0.44
1:D:141:ASP:C	1:D:141:ASP:OD1	2.56	0.44
1:H:75:SER:O	1:H:79:THR:HG23	2.17	0.44
1:K:159:VAL:O	1:K:162:CYS:HB2	2.18	0.44
1:D:315:ARG:O	1:D:318:LEU:HD12	2.17	0.44
1:H:192:SER:HB3	1:H:253:VAL:HG23	1.99	0.44
1:F:1:LEU:N	1:F:1:LEU:HD22	2.33	0.44
1:E:137:VAL:HG13	1:E:155:ILE:CG1	2.48	0.44
1:C:98:VAL:HG22	1:C:114:ARG:HD3	1.99	0.44
1:H:25:ILE:HG23	1:H:32:ARG:NH1	2.32	0.44
1:K:110:TYR:CE1	1:K:114:ARG:HD2	2.52	0.44
1:I:134:ALA:HB3	1:I:171:TYR:CZ	2.53	0.44
1:G:306:LEU:O	1:G:307:LEU:C	2.55	0.44
1:J:57:CYS:O	1:J:61:VAL:HG23	2.17	0.44
1:I:48:TYR:CE2	1:I:73:LEU:HD22	2.53	0.44
1:K:72:LYS:O	1:K:76:GLN:HB2	2.17	0.44
1:F:176:ASN:HD22	1:F:176:ASN:C	2.19	0.44
1:E:373:MSE:HE2	1:E:419:GLY:CA	2.48	0.44
1:B:170:PHE:CG	1:B:170:PHE:O	2.71	0.44
1:I:38:SER:HA	1:I:116:GLU:OE2	2.17	0.44
1:A:387:LYS:CD	1:B:401:ASN:HD22	2.31	0.44
1:J:299:VAL:HG12	1:J:370:HIS:HB2	2.00	0.44
1:D:210:SER:HA	1:D:264:ASN:HB2	1.99	0.44
1:E:216:ASP:HB3	1:E:219:ILE:HD12	2.00	0.44
1:G:25:ILE:HD13	1:G:206:TRP:CZ3	2.53	0.44
1:L:176:ASN:HD22	1:L:176:ASN:H	1.64	0.44
1:G:359:LYS:O	1:G:362:CYS:O	2.35	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:34:TYR:C	1:K:35:ILE:HD12	2.38	0.44
1:D:384:ALA:HB2	1:D:413:GLU:O	2.17	0.44
1:L:291:ILE:HG21	1:L:429:VAL:HG13	1.98	0.44
1:I:251:PHE:N	1:I:252:PRO:CD	2.80	0.44
1:F:54:LEU:HD13	1:F:111:ALA:O	2.18	0.44
1:B:100:LYS:HD2	1:B:100:LYS:N	2.33	0.44
1:H:302:ILE:CD1	1:H:358:ILE:HD12	2.47	0.44
1:H:138:ILE:HG22	1:H:172:GLY:HA3	2.00	0.44
1:L:321:LEU:O	1:L:321:LEU:HD23	2.18	0.44
1:L:261:ASN:HD22	1:L:274:LEU:HD12	1.83	0.44
1:D:55:TYR:CE1	1:D:112:ALA:HB2	2.52	0.44
1:F:376:VAL:HG11	1:F:432:ILE:HD13	1.99	0.44
1:L:299:VAL:HG22	1:L:300:ILE:N	2.33	0.44
1:E:50:ILE:HD11	1:E:77:ARG:CG	2.39	0.43
1:E:383:MSE:HE1	1:E:416:VAL:HG23	2.00	0.43
1:D:222:ASN:O	1:D:223:PRO:C	2.54	0.43
1:I:214:MSE:HE2	1:I:433:TYR:CD2	2.53	0.43
1:K:123:LEU:HA	1:K:123:LEU:HD23	1.89	0.43
1:C:3:ILE:CD1	1:C:200:ALA:HA	2.47	0.43
1:C:3:ILE:HG13	1:C:3:ILE:O	2.18	0.43
1:D:34:TYR:CE2	1:D:198:VAL:HG21	2.52	0.43
1:H:144:GLY:HA2	1:H:145:CYS:HA	1.76	0.43
1:C:407:ILE:HG21	1:D:407:ILE:HG21	1.99	0.43
1:D:113:SER:HB2	1:D:171:TYR:CD2	2.52	0.43
1:K:189:VAL:HG13	1:K:190:THR:N	2.33	0.43
1:L:114:ARG:HA	1:L:114:ARG:NE	2.33	0.43
1:J:241:GLY:HA3	1:J:292:ALA:HB1	2.00	0.43
1:C:155:ILE:CG2	1:C:156:LYS:N	2.80	0.43
1:G:39:ALA:HB2	1:G:116:GLU:OE2	2.18	0.43
1:K:318:LEU:HD13	1:L:315:ARG:CB	2.48	0.43
1:E:82:VAL:HG23	1:E:87:ILE:HB	2.00	0.43
1:E:85:LEU:HD11	1:E:126:TYR:OH	2.18	0.43
1:F:53:LEU:HD12	1:G:63:ASN:HD22	1.83	0.43
1:E:404:ILE:HD13	1:E:404:ILE:N	2.33	0.43
1:B:71:PHE:CE2	1:B:99:LYS:HB2	2.53	0.43
1:L:151:SER:O	1:L:155:ILE:HB	2.19	0.43
1:C:220:VAL:O	1:C:220:VAL:CG1	2.64	0.43
1:F:194:ILE:O	1:F:198:VAL:N	2.52	0.43
1:C:333:SER:HB2	3:C:503:LYS:HD3	2.00	0.43
1:J:116:GLU:HG3	1:J:170:PHE:HB3	2.01	0.43
1:I:378:THR:HG21	1:I:432:ILE:HD13	2.00	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:378:THR:HG21	1:K:393:ILE:CD1	2.49	0.43
1:K:56:LEU:O	1:K:59:ALA:HB3	2.18	0.43
1:H:344:ASP:O	1:H:347:LEU:HD23	2.17	0.43
1:I:231:TYR:CE1	1:I:275:ILE:HG22	2.54	0.43
1:H:294:LYS:HB3	1:H:297:PHE:HE2	1.83	0.43
1:E:166:VAL:C	1:E:167:ILE:HG13	2.39	0.43
1:E:317:ILE:CG2	1:E:340:LEU:HD21	2.48	0.43
1:F:260:ILE:HB	1:F:275:ILE:HB	2.01	0.43
1:L:372:ASN:O	1:L:405:ARG:NH1	2.51	0.43
1:K:253:VAL:CG1	1:K:258:ILE:O	2.67	0.43
1:L:229:ILE:HG22	1:L:274:LEU:O	2.19	0.43
1:H:397:LEU:HD22	1:H:402:VAL:HG11	2.00	0.43
1:I:35:ILE:HD12	1:I:35:ILE:N	2.33	0.43
1:J:160:LEU:HB2	1:J:198:VAL:HG12	2.01	0.43
1:H:274:LEU:HD23	1:H:276:LEU:CD1	2.45	0.43
1:K:318:LEU:HD21	1:L:318:LEU:HG	2.00	0.43
1:K:212:PHE:HD1	1:K:213:LEU:N	2.15	0.43
1:B:52:ASP:HB3	1:C:63:ASN:ND2	2.31	0.43
1:B:384:ALA:CB	1:B:413:GLU:O	2.66	0.43
1:K:234:LEU:HD23	1:K:234:LEU:C	2.39	0.43
1:E:404:ILE:HD13	1:E:404:ILE:H	1.83	0.43
1:D:102:ILE:HA	1:D:106:ALA:HB3	1.99	0.43
1:B:427:LYS:O	1:B:431:SER:OG	2.35	0.43
1:L:55:TYR:CE1	1:L:112:ALA:HB2	2.53	0.43
1:F:406:MSE:HE3	1:F:408:ASP:HB2	2.00	0.43
1:E:63:ASN:HD22	1:H:53:LEU:HD12	1.82	0.43
1:E:155:ILE:HG23	1:E:159:VAL:HG13	2.01	0.43
1:J:110:TYR:O	1:J:114:ARG:HG2	2.19	0.43
1:F:39:ALA:HB1	1:F:40:PRO:CD	2.48	0.43
1:F:48:TYR:HB3	1:G:65:ILE:HD11	2.00	0.43
1:C:317:ILE:CG2	1:C:340:LEU:HD21	2.48	0.43
1:D:253:VAL:CG2	1:D:260:ILE:HD11	2.47	0.43
1:C:114:ARG:HA	1:C:114:ARG:NE	2.34	0.43
1:K:383:MSE:HE3	1:K:416:VAL:HG23	2.01	0.43
1:G:13:LEU:HD22	1:G:19:PHE:CZ	2.54	0.43
1:K:291:ILE:CD1	1:K:432:ILE:HG22	2.49	0.43
1:J:263:LYS:NZ	1:J:268:PRO:O	2.52	0.43
1:J:318:LEU:C	1:J:318:LEU:CD1	2.87	0.43
1:E:85:LEU:HD21	1:E:126:TYR:CD2	2.54	0.43
1:K:98:VAL:HG13	1:K:114:ARG:HG3	2.01	0.43
1:E:240:MSE:CE	1:E:417:ILE:HD13	2.49	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:55:TYR:CE1	1:H:112:ALA:HB2	2.54	0.43
1:G:185:GLY:O	1:G:186:GLY:C	2.58	0.43
1:L:155:ILE:HG21	1:L:197:GLY:C	2.39	0.43
1:J:116:GLU:HG3	1:J:170:PHE:CB	2.49	0.43
1:K:198:VAL:HG12	1:K:198:VAL:O	2.19	0.43
1:A:397:LEU:HB3	1:A:402:VAL:CG1	2.49	0.43
1:E:18:GLN:HE22	1:E:21:LYS:HZ2	1.66	0.43
1:K:233:GLU:HB2	1:K:379:VAL:CG1	2.49	0.43
1:A:60:HIS:CE1	1:D:60:HIS:CE1	3.07	0.43
1:E:37:PRO:HB3	1:E:123:LEU:HD12	2.01	0.43
1:K:327:SER:O	1:K:342:ILE:HG23	2.18	0.43
1:A:262:ILE:HD12	1:A:262:ILE:N	2.34	0.43
1:F:155:ILE:HG21	1:F:197:GLY:C	2.39	0.42
1:K:155:ILE:HG22	1:K:156:LYS:N	2.33	0.42
1:D:242:ALA:O	1:D:244:VAL:HG22	2.19	0.42
1:F:226:ILE:HG22	1:F:229:ILE:HB	2.01	0.42
1:G:65:ILE:HG22	1:G:66:PRO:O	2.19	0.42
1:B:159:VAL:HG11	1:B:167:ILE:HD11	2.01	0.42
1:F:409:GLN:HE21	1:F:409:GLN:C	2.22	0.42
1:J:397:LEU:O	1:J:400:GLU:O	2.37	0.42
1:H:253:VAL:HG11	1:H:260:ILE:HD11	2.00	0.42
1:J:350:LYS:O	1:J:351:CYS:C	2.56	0.42
1:K:300:ILE:HG22	1:K:302:ILE:CG1	2.49	0.42
1:I:87:ILE:HD11	1:I:126:TYR:HB2	2.02	0.42
1:K:192:SER:HB3	1:K:253:VAL:HG23	2.01	0.42
1:F:397:LEU:HD22	1:F:402:VAL:HG11	2.01	0.42
1:J:86:ASN:HD22	1:J:86:ASN:N	2.17	0.42
1:E:316:LYS:NZ	1:G:323:MSE:HE2	2.33	0.42
1:C:318:LEU:CD2	1:C:331:MSE:HE1	2.48	0.42
1:H:110:TYR:CE1	1:H:114:ARG:HD2	2.54	0.42
1:G:187:SER:HA	1:G:190:THR:HG23	2.00	0.42
1:J:432:ILE:O	1:J:435:ALA:HB3	2.19	0.42
1:I:87:ILE:HG22	1:I:89:MSE:HG2	2.02	0.42
1:B:137:VAL:HG22	1:B:155:ILE:CG1	2.49	0.42
1:E:277:SER:HB3	1:E:280:HIS:CD2	2.54	0.42
1:E:310:GLU:O	1:E:311:VAL:C	2.58	0.42
1:J:36:ILE:HG21	1:J:190:THR:HG22	2.01	0.42
1:J:155:ILE:O	1:J:155:ILE:HD12	2.19	0.42
1:G:226:ILE:O	1:G:273:THR:CG2	2.66	0.42
1:E:375:LEU:HD23	1:E:419:GLY:CA	2.49	0.42
1:K:318:LEU:CD2	1:L:315:ARG:HA	2.50	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:226:ILE:C	1:L:273:THR:HG22	2.40	0.42
1:G:7:LYS:NZ	1:G:188:ASP:CG	2.72	0.42
1:L:383:MSE:CE	1:L:416:VAL:HG23	2.50	0.42
1:A:321:LEU:O	1:A:326:VAL:HG23	2.18	0.42
1:C:26:ILE:HG21	1:C:127:LEU:HD13	2.02	0.42
1:E:379:VAL:HG22	1:E:415:ASN:HB2	2.01	0.42
1:D:189:VAL:HG23	1:D:249:ALA:CB	2.42	0.42
1:H:87:ILE:HG22	1:H:89:MSE:CG	2.50	0.42
1:L:116:GLU:HG3	1:L:170:PHE:HB2	2.00	0.42
1:E:321:LEU:HD23	1:E:326:VAL:O	2.19	0.42
1:D:87:ILE:HD11	1:D:126:TYR:HB2	2.01	0.42
1:E:58:ASN:HD21	1:E:62:LYS:HE3	1.83	0.42
1:I:342:ILE:HG22	1:I:343:GLU:O	2.19	0.42
1:J:276:LEU:CD1	1:J:276:LEU:N	2.83	0.42
1:J:276:LEU:HD12	1:J:276:LEU:N	2.34	0.42
1:D:212:PHE:CZ	1:D:262:ILE:CD1	3.01	0.42
1:I:291:ILE:CD1	1:I:432:ILE:HG22	2.49	0.42
1:H:207:THR:OG1	1:H:208:ASP:N	2.50	0.42
1:B:48:TYR:CD1	1:B:53:LEU:HD22	2.55	0.42
1:A:110:TYR:O	1:A:113:SER:OG	2.28	0.42
1:K:35:ILE:N	1:K:35:ILE:CD1	2.83	0.42
1:K:163:ASN:HD22	1:K:163:ASN:N	2.17	0.42
1:F:226:ILE:C	1:F:273:THR:HG22	2.39	0.42
1:D:85:LEU:HD23	1:D:126:TYR:CD1	2.54	0.42
1:E:362:CYS:C	1:E:364:PRO:HD3	2.40	0.42
1:A:37:PRO:HD2	1:A:168:PRO:HA	2.02	0.42
1:E:89:MSE:CE	1:E:125:LYS:CB	2.98	0.42
1:B:283:ILE:O	1:B:285:LEU:HD12	2.20	0.42
1:K:151:SER:O	1:K:155:ILE:HD13	2.19	0.42
1:C:283:ILE:HG21	1:J:274:LEU:HD22	2.02	0.42
1:G:213:LEU:CD1	1:G:217:PRO:HG3	2.50	0.42
1:F:25:ILE:O	1:F:32:ARG:NH1	2.49	0.42
1:G:8:PHE:CD1	1:G:22:VAL:HG22	2.55	0.42
1:D:129:ALA:HB2	1:D:164:LYS:HD3	2.01	0.42
1:F:202:LEU:HD12	1:F:203:TYR:H	1.85	0.42
1:I:245:LEU:N	1:I:245:LEU:CD2	2.71	0.42
1:K:318:LEU:HD22	1:L:315:ARG:HA	2.01	0.42
1:C:36:ILE:N	1:C:36:ILE:HD12	2.35	0.42
1:I:37:PRO:HB3	1:I:123:LEU:CD1	2.50	0.42
1:J:288:ILE:CD1	1:J:383:MSE:SE	3.18	0.42
1:I:118:LEU:O	1:I:121:VAL:HG22	2.20	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:39:ALA:HB2	1:D:116:GLU:OE2	2.19	0.42
1:B:89:MSE:HA	1:G:100:LYS:HG2	2.02	0.42
1:G:229:ILE:O	1:G:229:ILE:HG23	2.20	0.42
1:F:79:THR:HA	1:F:82:VAL:HG12	2.02	0.42
1:K:331:MSE:HE1	1:L:318:LEU:HD23	2.01	0.42
1:K:213:LEU:HD22	1:K:223:PRO:HD2	2.02	0.42
1:E:239:TYR:HD2	1:F:335:VAL:HG22	1.83	0.42
1:K:383:MSE:HB3	1:K:389:ILE:HG21	2.02	0.42
1:G:262:ILE:HD11	1:G:275:ILE:HD11	2.01	0.42
1:C:3:ILE:HD13	1:C:198:VAL:HG12	2.02	0.41
1:B:324:TYR:HB2	1:B:326:VAL:HG22	2.01	0.41
1:E:288:ILE:CG2	1:E:289:THR:N	2.82	0.41
1:J:253:VAL:CG1	1:J:258:ILE:HB	2.45	0.41
1:K:318:LEU:C	1:K:318:LEU:HD12	2.40	0.41
1:L:378:THR:O	1:L:378:THR:HG23	2.20	0.41
1:E:7:LYS:HZ1	1:E:188:ASP:CG	2.22	0.41
1:A:195:SER:O	1:A:198:VAL:O	2.38	0.41
1:F:117:TYR:O	1:F:121:VAL:HG13	2.19	0.41
1:A:394:PHE:CZ	1:A:407:ILE:HD13	2.56	0.41
1:G:274:LEU:HA	1:G:274:LEU:HD12	1.87	0.41
1:A:383:MSE:HB2	1:A:389:ILE:HG21	2.02	0.41
1:F:215:ALA:HB3	1:F:220:VAL:HG11	2.01	0.41
1:F:60:HIS:CE1	1:G:56:LEU:HD21	2.56	0.41
1:L:121:VAL:HG12	1:L:131:PHE:CE1	2.55	0.41
1:L:333:SER:HA	1:L:338:VAL:HA	2.02	0.41
1:G:379:VAL:HG12	1:G:380:GLY:N	2.36	0.41
1:B:87:ILE:HD13	1:B:126:TYR:HB2	2.02	0.41
1:F:359:LYS:HG3	1:F:367:ILE:HD11	2.02	0.41
1:H:297:PHE:CE1	1:H:375:LEU:HD12	2.55	0.41
1:E:43:ARG:NH1	1:E:47:ASP:OD1	2.54	0.41
1:G:219:ILE:HG22	1:G:430:LYS:HG3	2.02	0.41
1:I:98:VAL:HG13	1:I:114:ARG:HG3	2.02	0.41
1:F:6:THR:HG22	1:F:204:GLU:HB2	2.01	0.41
1:L:178:ASP:OD1	1:L:178:ASP:N	2.53	0.41
1:E:375:LEU:HA	1:E:375:LEU:HD23	1.95	0.41
1:C:43:ARG:CD	1:C:47:ASP:OD2	2.68	0.41
1:G:253:VAL:O	1:G:254:LYS:C	2.58	0.41
1:E:89:MSE:HE1	1:E:122:ILE:HA	2.03	0.41
1:K:247:GLU:HB2	1:L:306:LEU:HD11	2.02	0.41
1:E:425:PHE:O	1:E:429:VAL:HG23	2.20	0.41
1:D:320:ILE:CG2	1:D:358:ILE:HG22	2.50	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:GLY:HA3	1:A:273:THR:HG23	2.01	0.41
1:I:214:MSE:HE2	1:I:433:TYR:CE2	2.56	0.41
1:B:159:VAL:CG1	1:B:167:ILE:HD11	2.50	0.41
1:C:134:ALA:HB3	1:C:171:TYR:CE1	2.56	0.41
1:K:207:THR:OG1	1:K:208:ASP:N	2.54	0.41
1:D:35:ILE:HD12	1:D:35:ILE:N	2.36	0.41
1:H:433:TYR:C	1:H:433:TYR:CD1	2.94	0.41
1:J:198:VAL:O	1:J:200:ALA:N	2.53	0.41
1:C:69:ASP:OD1	1:C:70:VAL:HG23	2.21	0.41
1:H:263:LYS:NZ	1:H:268:PRO:O	2.51	0.41
1:K:120:GLY:O	1:K:166:VAL:HG11	2.21	0.41
1:C:167:ILE:HD12	1:C:167:ILE:N	2.35	0.41
1:F:155:ILE:HG22	1:F:156:LYS:HD2	2.03	0.41
1:F:160:LEU:HB2	1:F:198:VAL:HG22	2.02	0.41
1:I:409:GLN:CG	1:I:416:VAL:HG22	2.51	0.41
1:L:321:LEU:C	1:L:321:LEU:HD23	2.40	0.41
1:I:326:VAL:HG13	1:I:350:LYS:HD2	2.03	0.41
1:K:78:TYR:HE2	1:K:119:ASN:OD1	2.03	0.41
1:A:299:VAL:CG1	1:A:370:HIS:HB2	2.51	0.41
1:B:118:LEU:O	1:B:121:VAL:HG22	2.20	0.41
1:D:185:GLY:HA3	1:D:189:VAL:CG1	2.51	0.41
1:G:212:PHE:HB2	1:G:273:THR:HG21	2.02	0.41
1:C:3:ILE:HD13	1:C:198:VAL:CG1	2.49	0.41
1:K:315:ARG:HA	1:L:318:LEU:HD11	2.03	0.41
1:C:65:ILE:HG23	1:C:66:PRO:HD2	2.02	0.41
1:E:251:PHE:CD2	1:E:252:PRO:HD3	2.55	0.41
1:B:381:THR:O	1:B:384:ALA:HB3	2.20	0.41
1:G:321:LEU:HG	1:G:326:VAL:HG23	2.03	0.41
1:K:233:GLU:HB2	1:K:379:VAL:HG11	2.03	0.41
1:G:262:ILE:CD1	1:G:275:ILE:HD11	2.51	0.41
1:A:322:GLU:HA	1:B:311:VAL:HG12	2.02	0.41
1:E:156:LYS:NZ	1:E:197:GLY:O	2.51	0.41
1:B:18:GLN:HE22	1:B:21:LYS:NZ	2.18	0.41
1:G:68:ASP:OD1	1:G:99:LYS:NZ	2.42	0.41
1:B:54:LEU:HD13	1:B:111:ALA:O	2.21	0.41
1:D:248:GLU:HA	1:D:249:ALA:HA	1.70	0.41
1:J:5:VAL:HG21	1:J:194:ILE:HG22	2.03	0.41
1:F:155:ILE:HG23	1:F:198:VAL:CG2	2.34	0.41
1:H:373:MSE:HE1	1:H:406:MSE:HB2	2.02	0.41
1:K:155:ILE:HG23	1:K:159:VAL:HG11	1.96	0.41
1:C:260:ILE:O	1:C:274:LEU:HD12	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:53:LEU:HD11	1:L:65:ILE:HD11	2.03	0.41
1:B:226:ILE:O	1:B:227:SER:C	2.59	0.41
1:L:321:LEU:CD2	1:L:326:VAL:HG23	2.51	0.41
1:H:214:MSE:HE1	1:H:288:ILE:HG21	2.03	0.41
1:F:18:GLN:O	1:F:22:VAL:HG23	2.21	0.41
1:G:70:VAL:O	1:G:73:LEU:HB2	2.21	0.41
1:D:228:LYS:HD3	1:D:276:LEU:HD11	2.03	0.41
1:G:134:ALA:HB3	1:G:171:TYR:CZ	2.55	0.40
1:E:375:LEU:HD23	1:E:419:GLY:HA2	2.03	0.40
1:C:156:LYS:HG3	1:C:160:LEU:HD23	2.04	0.40
1:K:194:ILE:O	1:K:197:GLY:N	2.53	0.40
1:L:339:SER:C	1:L:340:LEU:HD12	2.41	0.40
1:F:317:ILE:O	1:F:320:ILE:HB	2.21	0.40
1:B:321:LEU:HD21	1:B:340:LEU:HD23	2.02	0.40
1:K:229:ILE:O	1:K:275:ILE:HA	2.20	0.40
1:D:60:HIS:CD2	1:D:65:ILE:HD11	2.56	0.40
1:H:358:ILE:HG21	1:H:358:ILE:HD13	1.86	0.40
1:E:85:LEU:HD23	1:E:87:ILE:HD11	2.03	0.40
1:A:383:MSE:CB	1:A:389:ILE:HG21	2.52	0.40
1:E:321:LEU:HG	1:E:326:VAL:HG23	2.03	0.40
1:L:176:ASN:HD22	1:L:176:ASN:N	2.19	0.40
1:G:342:ILE:HG21	1:G:347:LEU:HD13	2.03	0.40
1:G:98:VAL:HG13	1:G:114:ARG:HG3	2.03	0.40
1:D:138:ILE:HD13	1:D:193:ILE:HG21	2.03	0.40
1:K:330:HIS:CB	1:K:406:MSE:HE1	2.51	0.40
1:G:355:ILE:HD13	1:G:369:ILE:HD11	1.99	0.40
1:I:288:ILE:HG22	1:I:289:THR:H	1.86	0.40
1:E:137:VAL:CG1	1:E:155:ILE:CG1	2.99	0.40
1:I:87:ILE:HD11	1:I:126:TYR:HD1	1.85	0.40
1:E:378:THR:HG21	1:E:393:ILE:HD13	2.03	0.40
1:I:233:GLU:CG	1:I:381:THR:HG23	2.52	0.40
1:G:373:MSE:HE1	1:G:406:MSE:CB	2.40	0.40
1:L:114:ARG:N	1:L:114:ARG:HE	2.19	0.40
1:C:331:MSE:HG3	1:C:340:LEU:HD12	2.03	0.40
1:H:94:TYR:O	1:H:98:VAL:HG23	2.21	0.40
1:F:226:ILE:HG21	1:F:229:ILE:HB	2.03	0.40
1:G:418:VAL:HG12	1:G:420:VAL:HG13	2.02	0.40
1:J:318:LEU:HD12	1:J:319:SER:N	2.37	0.40
1:C:283:ILE:CG2	1:C:284:ASN:N	2.84	0.40
1:F:75:SER:CB	1:F:95:LEU:HD13	2.51	0.40
1:G:231:TYR:CD2	1:G:277:SER:HA	2.57	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:156:LYS:HA	1:D:160:LEU:HB2	2.02	0.40
1:A:321:LEU:HG	1:A:326:VAL:HG23	2.03	0.40
1:A:198:VAL:O	1:A:200:ALA:N	2.54	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	423/446 (95%)	385 (91%)	34 (8%)	4 (1%)	21	64
1	B	436/446 (98%)	406 (93%)	28 (6%)	2 (0%)	34	76
1	C	429/446 (96%)	381 (89%)	45 (10%)	3 (1%)	26	70
1	D	435/446 (98%)	397 (91%)	33 (8%)	5 (1%)	17	58
1	E	437/446 (98%)	401 (92%)	28 (6%)	8 (2%)	11	45
1	F	430/446 (96%)	387 (90%)	38 (9%)	5 (1%)	16	56
1	G	433/446 (97%)	400 (92%)	28 (6%)	5 (1%)	16	56
1	H	433/446 (97%)	386 (89%)	40 (9%)	7 (2%)	12	48
1	I	422/446 (95%)	377 (89%)	39 (9%)	6 (1%)	14	51
1	J	429/446 (96%)	386 (90%)	36 (8%)	7 (2%)	12	48
1	K	423/446 (95%)	381 (90%)	37 (9%)	5 (1%)	16	56
1	L	422/446 (95%)	383 (91%)	36 (8%)	3 (1%)	26	70
All	All	5152/5352 (96%)	4670 (91%)	422 (8%)	60 (1%)	16	56

All (60) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	307	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	144	GLY
1	G	170	PHE
1	H	199	ASN
1	I	199	ASN
1	J	128	ASN
1	J	199	ASN
1	J	351	CYS
1	K	425	PHE
1	L	351	CYS
1	A	199	ASN
1	A	335	VAL
1	C	257	GLY
1	D	169	GLY
1	E	170	PHE
1	F	29	ASP
1	F	172	GLY
1	F	305	ALA
1	G	186	GLY
1	G	254	LYS
1	H	184	ARG
1	H	244	VAL
1	I	86	ASN
1	I	257	GLY
1	I	348	ASP
1	J	305	ALA
1	K	170	PHE
1	K	257	GLY
1	A	185	GLY
1	A	305	ALA
1	E	176	ASN
1	G	438	GLU
1	H	155	ILE
1	H	249	ALA
1	J	425	PHE
1	K	164	LYS
1	B	348	ASP
1	E	311	VAL
1	F	438	GLU
1	B	227	SER
1	C	86	ASN
1	F	16	SER
1	H	198	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	I	247	GLU
1	J	246	HIS
1	L	199	ASN
1	G	384	ALA
1	H	170	PHE
1	D	144	GLY
1	I	312	GLY
1	J	241	GLY
1	L	312	GLY
1	E	186	GLY
1	C	3	ILE
1	E	363	ASN
1	K	194	ILE
1	D	37	PRO
1	E	244	VAL
1	D	371	PRO
1	E	312	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	348/377 (92%)	318 (91%)	30 (9%)	13	44
1	B	359/377 (95%)	328 (91%)	31 (9%)	13	44
1	C	354/377 (94%)	325 (92%)	29 (8%)	14	46
1	D	358/377 (95%)	326 (91%)	32 (9%)	12	42
1	E	354/377 (94%)	320 (90%)	34 (10%)	10	38
1	F	353/377 (94%)	327 (93%)	26 (7%)	17	52
1	G	357/377 (95%)	328 (92%)	29 (8%)	15	47
1	H	338/377 (90%)	312 (92%)	26 (8%)	16	50
1	I	340/377 (90%)	326 (96%)	14 (4%)	37	76
1	J	339/377 (90%)	314 (93%)	25 (7%)	17	52
1	K	334/377 (89%)	304 (91%)	30 (9%)	12	41

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	L	341/377 (90%)	319 (94%)	22 (6%)	21	58
All	All	4175/4524 (92%)	3847 (92%)	328 (8%)	15	48

All (328) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LYS
1	A	31	ASN
1	A	53	LEU
1	A	82	VAL
1	A	100	LYS
1	A	158	LYS
1	A	176	ASN
1	A	181	THR
1	A	183	SER
1	A	184	ARG
1	A	220	VAL
1	A	246	HIS
1	A	255	ASP
1	A	269	SER
1	A	274	LEU
1	A	277	SER
1	A	282	GLU
1	A	318	LEU
1	A	323	MSE
1	A	326	VAL
1	A	329	GLU
1	A	338	VAL
1	A	339	SER
1	A	356	GLU
1	A	378	THR
1	A	386	THR
1	A	387	LYS
1	A	403	ASN
1	A	409	GLN
1	A	412	SER
1	B	46	LYS
1	B	85	LEU
1	B	114	ARG
1	B	123	LEU
1	B	143	SER
1	B	158	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	160	LEU
1	B	181	THR
1	B	189	VAL
1	B	190	THR
1	B	232	LYS
1	B	236	GLU
1	B	237	LEU
1	B	250	ILE
1	B	256	SER
1	B	269	SER
1	B	276	LEU
1	B	288	ILE
1	B	318	LEU
1	B	340	LEU
1	B	352	ASP
1	B	360	LYS
1	B	363	ASN
1	B	378	THR
1	B	385	LYS
1	B	389	ILE
1	B	400	GLU
1	B	402	VAL
1	B	409	GLN
1	B	418	VAL
1	B	431	SER
1	C	3	ILE
1	C	12	SER
1	C	43	ARG
1	C	53	LEU
1	C	88	ASP
1	C	117	TYR
1	C	155	ILE
1	C	156	LYS
1	C	158	LYS
1	C	184	ARG
1	C	201	ASP
1	C	203	TYR
1	C	207	THR
1	C	221	GLU
1	C	287	THR
1	C	299	VAL
1	C	308	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	315	ARG
1	C	318	LEU
1	C	320	ILE
1	C	329	GLU
1	C	337	SER
1	C	340	LEU
1	C	352	ASP
1	C	362	CYS
1	C	378	THR
1	C	400	GLU
1	C	409	GLN
1	C	412	SER
1	D	7	LYS
1	D	12	SER
1	D	49	LYS
1	D	82	VAL
1	D	100	LYS
1	D	108	SER
1	D	116	GLU
1	D	138	ILE
1	D	145	CYS
1	D	159	VAL
1	D	160	LEU
1	D	170	PHE
1	D	181	THR
1	D	194	ILE
1	D	195	SER
1	D	210	SER
1	D	218	ARG
1	D	248	GLU
1	D	250	ILE
1	D	254	LYS
1	D	277	SER
1	D	279	THR
1	D	318	LEU
1	D	329	GLU
1	D	339	SER
1	D	361	GLN
1	D	378	THR
1	D	381	THR
1	D	402	VAL
1	D	403	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	D	409	GLN
1	D	430	LYS
1	E	7	LYS
1	E	33	LYS
1	E	43	ARG
1	E	60	HIS
1	E	65	ILE
1	E	89	MSE
1	E	109	ASP
1	E	114	ARG
1	E	146	PHE
1	E	158	LYS
1	E	159	VAL
1	E	160	LEU
1	E	162	CYS
1	E	181	THR
1	E	184	ARG
1	E	187	SER
1	E	190	THR
1	E	230	SER
1	E	232	LYS
1	E	234	LEU
1	E	236	GLU
1	E	263	LYS
1	E	277	SER
1	E	318	LEU
1	E	321	LEU
1	E	329	GLU
1	E	338	VAL
1	E	356	GLU
1	E	363	ASN
1	E	378	THR
1	E	404	ILE
1	E	406	MSE
1	E	409	GLN
1	E	415	ASN
1	F	1	LEU
1	F	2	LYS
1	F	46	LYS
1	F	77	ARG
1	F	116	GLU
1	F	153	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	F	155	ILE
1	F	170	PHE
1	F	175	PHE
1	F	176	ASN
1	F	190	THR
1	F	236	GLU
1	F	238	SER
1	F	245	LEU
1	F	248	GLU
1	F	299	VAL
1	F	306	LEU
1	F	311	VAL
1	F	318	LEU
1	F	333	SER
1	F	340	LEU
1	F	358	ILE
1	F	378	THR
1	F	402	VAL
1	F	409	GLN
1	F	415	ASN
1	G	7	LYS
1	G	75	SER
1	G	99	LYS
1	G	100	LYS
1	G	109	ASP
1	G	116	GLU
1	G	149	LYS
1	G	173	SER
1	G	181	THR
1	G	190	THR
1	G	192	SER
1	G	221	GLU
1	G	234	LEU
1	G	236	GLU
1	G	237	LEU
1	G	245	LEU
1	G	247	GLU
1	G	250	ILE
1	G	256	SER
1	G	263	LYS
1	G	287	THR
1	G	299	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	318	LEU
1	G	340	LEU
1	G	361	GLN
1	G	378	THR
1	G	402	VAL
1	G	409	GLN
1	G	415	ASN
1	H	44	THR
1	H	89	MSE
1	H	109	ASP
1	H	136	GLU
1	H	156	LYS
1	H	221	GLU
1	H	234	LEU
1	H	236	GLU
1	H	240	MSE
1	H	250	ILE
1	H	299	VAL
1	H	309	SER
1	H	311	VAL
1	H	315	ARG
1	H	318	LEU
1	H	327	SER
1	H	329	GLU
1	H	340	LEU
1	H	346	LYS
1	H	351	CYS
1	H	366	SER
1	H	378	THR
1	H	389	ILE
1	H	401	ASN
1	H	402	VAL
1	H	409	GLN
1	I	43	ARG
1	I	63	ASN
1	I	83	SER
1	I	85	LEU
1	I	180	LYS
1	I	202	LEU
1	I	205	ASN
1	I	207	THR
1	I	245	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	I	318	LEU
1	I	323	MSE
1	I	356	GLU
1	I	378	THR
1	I	409	GLN
1	J	7	LYS
1	J	38	SER
1	J	53	LEU
1	J	77	ARG
1	J	116	GLU
1	J	127	LEU
1	J	149	LYS
1	J	155	ILE
1	J	160	LEU
1	J	192	SER
1	J	218	ARG
1	J	236	GLU
1	J	238	SER
1	J	287	THR
1	J	299	VAL
1	J	314	CYS
1	J	318	LEU
1	J	351	CYS
1	J	352	ASP
1	J	356	GLU
1	J	361	GLN
1	J	378	THR
1	J	389	ILE
1	J	409	GLN
1	J	415	ASN
1	K	31	ASN
1	K	43	ARG
1	K	53	LEU
1	K	58	ASN
1	K	73	LEU
1	K	85	LEU
1	K	116	GLU
1	K	153	GLU
1	K	160	LEU
1	K	163	ASN
1	K	190	THR
1	K	201	ASP

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	K	212	PHE
1	K	220	VAL
1	K	229	ILE
1	K	240	MSE
1	K	245	LEU
1	K	250	ILE
1	K	284	ASN
1	K	318	LEU
1	K	345	CYS
1	K	361	GLN
1	K	372	ASN
1	K	373	MSE
1	K	383	MSE
1	K	401	ASN
1	K	403	ASN
1	K	406	MSE
1	K	409	GLN
1	K	415	ASN
1	L	31	ASN
1	L	43	ARG
1	L	86	ASN
1	L	109	ASP
1	L	114	ARG
1	L	116	GLU
1	L	149	LYS
1	L	155	ILE
1	L	158	LYS
1	L	163	ASN
1	L	171	TYR
1	L	173	SER
1	L	176	ASN
1	L	181	THR
1	L	235	ARG
1	L	250	ILE
1	L	318	LEU
1	L	333	SER
1	L	356	GLU
1	L	365	ASP
1	L	409	GLN
1	L	424	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (115) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	18	GLN
1	A	58	ASN
1	A	63	ASN
1	A	76	GLN
1	A	176	ASN
1	A	266	ASN
1	A	363	ASN
1	A	372	ASN
1	A	391	ASN
1	A	437	ASN
1	B	18	GLN
1	B	58	ASN
1	B	63	ASN
1	B	246	HIS
1	B	266	ASN
1	B	401	ASN
1	B	409	GLN
1	B	415	ASN
1	B	437	ASN
1	C	18	GLN
1	C	63	ASN
1	C	261	ASN
1	C	266	ASN
1	C	308	ASN
1	C	361	GLN
1	C	401	ASN
1	C	409	GLN
1	C	437	ASN
1	D	17	ASN
1	D	18	GLN
1	D	58	ASN
1	D	60	HIS
1	D	86	ASN
1	D	222	ASN
1	D	246	HIS
1	D	266	ASN
1	D	361	GLN
1	D	372	ASN
1	D	391	ASN
1	D	403	ASN
1	D	437	ASN
1	E	18	GLN
1	E	31	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	58	ASN
1	E	60	HIS
1	E	163	ASN
1	E	199	ASN
1	E	266	ASN
1	E	280	HIS
1	E	361	GLN
1	E	363	ASN
1	E	409	GLN
1	F	17	ASN
1	F	18	GLN
1	F	58	ASN
1	F	63	ASN
1	F	176	ASN
1	F	199	ASN
1	F	222	ASN
1	F	261	ASN
1	F	266	ASN
1	F	409	GLN
1	F	437	ASN
1	G	18	GLN
1	G	58	ASN
1	G	60	HIS
1	G	63	ASN
1	G	266	ASN
1	G	361	GLN
1	G	409	GLN
1	H	18	GLN
1	H	60	HIS
1	H	63	ASN
1	H	86	ASN
1	H	101	ASN
1	H	205	ASN
1	H	266	ASN
1	H	361	GLN
1	H	401	ASN
1	H	409	GLN
1	I	18	GLN
1	I	31	ASN
1	I	205	ASN
1	I	266	ASN
1	I	409	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	18	GLN
1	J	58	ASN
1	J	63	ASN
1	J	86	ASN
1	J	101	ASN
1	J	163	ASN
1	J	261	ASN
1	J	266	ASN
1	J	401	ASN
1	J	409	GLN
1	J	415	ASN
1	K	18	GLN
1	K	58	ASN
1	K	63	ASN
1	K	163	ASN
1	K	222	ASN
1	K	266	ASN
1	K	284	ASN
1	K	372	ASN
1	K	401	ASN
1	K	409	GLN
1	K	437	ASN
1	L	18	GLN
1	L	58	ASN
1	L	163	ASN
1	L	176	ASN
1	L	261	ASN
1	L	266	ASN
1	L	409	GLN
1	L	437	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

13 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ASP	A	451	-	2,8,8	0.48	0	0,10,10	0.00	-
3	LYS	A	501	-	6,9,9	0.14	0	4,10,10	0.44	0
3	LYS	B	502	-	6,9,9	0.33	0	4,10,10	0.25	0
3	LYS	C	503	-	6,9,9	0.29	0	4,10,10	0.36	0
2	ASP	D	454	-	2,8,8	0.45	0	0,10,10	0.00	-
3	LYS	D	504	-	6,9,9	0.19	0	4,10,10	0.42	0
2	ASP	E	455	-	2,8,8	0.54	0	0,10,10	0.00	-
2	ASP	G	457	-	2,8,8	0.47	0	0,10,10	0.00	-
3	LYS	G	507	-	6,9,9	0.14	0	4,10,10	0.37	0
2	ASP	H	458	-	2,8,8	0.51	0	0,10,10	0.00	-
3	LYS	H	508	-	6,9,9	0.22	0	4,10,10	0.36	0
2	ASP	I	459	-	4,7,8	2.18	1 (25%)	2,8,10	2.55	1 (50%)
2	ASP	L	462	-	2,8,8	0.44	0	0,10,10	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ASP	A	451	-	-	0/2/8/8	0/0/0/0
3	LYS	A	501	-	-	0/5/9/9	0/0/0/0
3	LYS	B	502	-	-	0/5/9/9	0/0/0/0
3	LYS	C	503	-	-	0/5/9/9	0/0/0/0
2	ASP	D	454	-	-	0/2/8/8	0/0/0/0
3	LYS	D	504	-	-	0/5/9/9	0/0/0/0
2	ASP	E	455	-	-	0/2/8/8	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ASP	G	457	-	-	0/2/8/8	0/0/0/0
3	LYS	G	507	-	-	0/5/9/9	0/0/0/0
2	ASP	H	458	-	-	0/2/8/8	0/0/0/0
3	LYS	H	508	-	-	0/5/9/9	0/0/0/0
2	ASP	I	459	-	-	0/4/6/8	0/0/0/0
2	ASP	L	462	-	-	0/2/8/8	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	I	459	ASP	OXT-C	-4.32	1.23	1.42

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	459	ASP	OXT-C-CA	3.60	121.27	111.84

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	451	ASP	2	0
3	C	503	LYS	3	0
2	E	455	ASP	1	0
2	G	457	ASP	1	0
3	G	507	LYS	7	0
2	H	458	ASP	1	0
3	H	508	LYS	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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, 95th 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 ²)	Q<0.9
1	A	421/446 (94%)	-0.44	1 (0%) 95 87	42, 62, 111, 135	0
1	B	430/446 (96%)	-0.36	2 (0%) 91 76	43, 66, 108, 135	1 (0%)
1	C	426/446 (95%)	-0.36	1 (0%) 95 87	53, 82, 112, 133	0
1	D	429/446 (96%)	-0.40	1 (0%) 95 87	36, 58, 123, 175	1 (0%)
1	E	431/446 (96%)	-0.37	3 (0%) 89 70	48, 74, 111, 142	1 (0%)
1	F	427/446 (95%)	-0.24	2 (0%) 91 76	58, 101, 135, 154	0
1	G	429/446 (96%)	-0.50	0 100 100	39, 61, 87, 101	0
1	H	427/446 (95%)	-0.37	2 (0%) 91 76	51, 80, 110, 140	0
1	I	421/446 (94%)	-0.08	7 (1%) 73 45	67, 105, 166, 195	1 (0%)
1	J	425/446 (95%)	-0.24	6 (1%) 78 51	58, 93, 154, 194	0
1	K	421/446 (94%)	-0.06	21 (4%) 32 13	54, 97, 191, 220	1 (0%)
1	L	421/446 (94%)	0.23	32 (7%) 17 6	61, 120, 203, 273	1 (0%)
All	All	5108/5352 (95%)	-0.27	78 (1%) 76 49	36, 82, 149, 273	6 (0%)

All (78) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	L	362	CYS	9.3
1	L	347	LEU	8.6
1	L	366	SER	6.9
1	L	363	ASN	6.8
1	L	351	CYS	5.5
1	L	308	ASN	5.4
1	K	353	LYS	5.1
1	L	311	VAL	5.1
1	L	336	ASP	5.0
1	K	317	ILE	4.9
1	L	365	ASP	4.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	L	358	ILE	4.8
1	L	326	VAL	4.8
1	L	355	ILE	4.7
1	I	311	VAL	4.5
1	K	364	PRO	4.4
1	L	309	SER	4.4
1	L	370	HIS	4.3
1	K	324	TYR	4.2
1	I	369	ILE	4.0
1	J	311	VAL	3.9
1	K	285	LEU	3.9
1	L	306	LEU	3.6
1	L	368	GLU	3.6
1	J	347	LEU	3.5
1	L	361	GLN	3.5
1	D	325	GLY	3.5
1	K	325	GLY	3.4
1	I	367	ILE	3.3
1	K	345	CYS	3.3
1	I	351	CYS	3.3
1	L	305	ALA	3.3
1	K	352	ASP	3.2
1	K	369	ILE	3.2
1	L	360	LYS	3.1
1	K	326	VAL	3.1
1	E	439	GLY	3.0
1	K	349	GLY	2.9
1	L	219	ILE	2.8
1	K	307	LEU	2.8
1	J	310	GLU	2.8
1	J	309	SER	2.8
1	E	280	HIS	2.8
1	K	327	SER	2.7
1	L	334	GLY	2.7
1	L	292	ALA	2.7
1	J	294	LYS	2.7
1	I	325	GLY	2.6
1	L	412	SER	2.6
1	L	369	ILE	2.6
1	H	279	THR	2.6
1	L	31	ASN	2.6
1	L	245	LEU	2.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	L	327	SER	2.5
1	H	283	ILE	2.5
1	K	320	ILE	2.5
1	K	351	CYS	2.5
1	L	342	ILE	2.4
1	L	354	ILE	2.4
1	C	175	PHE	2.4
1	I	309	SER	2.4
1	K	367	ILE	2.4
1	L	278	ASP	2.4
1	I	365	ASP	2.3
1	J	314	CYS	2.3
1	K	311	VAL	2.2
1	K	308	ASN	2.2
1	F	165	ALA	2.2
1	K	361	GLN	2.1
1	L	328	PHE	2.1
1	A	311	VAL	2.1
1	F	210	SER	2.1
1	E	347	LEU	2.1
1	K	360	LYS	2.1
1	L	294	LYS	2.1
1	B	347	LEU	2.1
1	B	309	SER	2.0
1	K	310	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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	LYS	G	507	10/10	0.27	0.80	14.51	56,64,67,68	10
2	ASP	D	454	9/9	0.76	0.35	14.02	61,69,78,81	9
3	LYS	C	503	10/10	0.57	0.60	9.96	71,73,73,73	10
2	ASP	H	458	9/9	0.75	0.41	7.48	64,66,71,74	9
3	LYS	H	508	10/10	0.58	0.56	6.97	70,72,76,81	10
2	ASP	A	451	9/9	0.59	0.50	6.80	55,59,60,61	9
2	ASP	G	457	9/9	0.67	0.45	6.67	53,55,58,58	9
2	ASP	I	459	8/9	0.76	0.38	5.88	63,64,69,73	8
2	ASP	L	462	9/9	0.74	0.42	4.20	74,78,86,87	9
3	LYS	A	501	10/10	0.69	0.46	4.00	59,62,65,66	10
3	LYS	D	504	10/10	0.75	0.41	3.98	59,61,62,62	10
2	ASP	E	455	9/9	0.80	0.36	3.74	62,63,64,66	9
3	LYS	B	502	10/10	0.75	0.38	1.96	56,58,59,60	10

6.5 Other polymers [i](#)

There are no such residues in this entry.