



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:49 AM GMT

PDB ID : 2IU3
Title : CRYSTAL STRUCTURES OF TRANSITION STATE ANALOGUE INHIBITORS OF INOSINE MONOPHOSPHATE CYCLOHYDROLASE
Authors : Xu, L.; Chong, Y.; Hwang, I.; D'Onofrio, A.; Amore, K.; Beardsley, G.P.; Li, C.; Olson, A.J.; Boger, D.L.; Wilson, I.A.
Deposited on : 2006-05-27
Resolution : 2.90 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

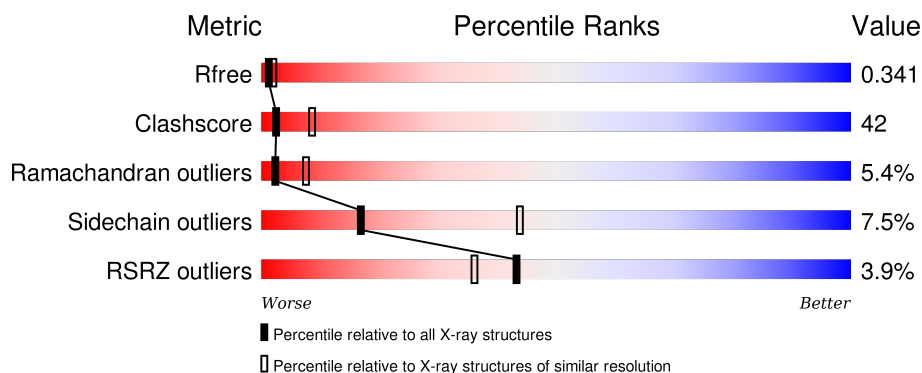
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1451 (2.90-2.90)
Clashscore	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)
RSRZ outliers	91569	1456 (2.90-2.90)

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	593	<div> <div>3%</div> <div>36% 55% 8% ..</div> </div>
1	B	593	<div> <div>5%</div> <div>39% 53% 7% ..</div> </div>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9145 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.

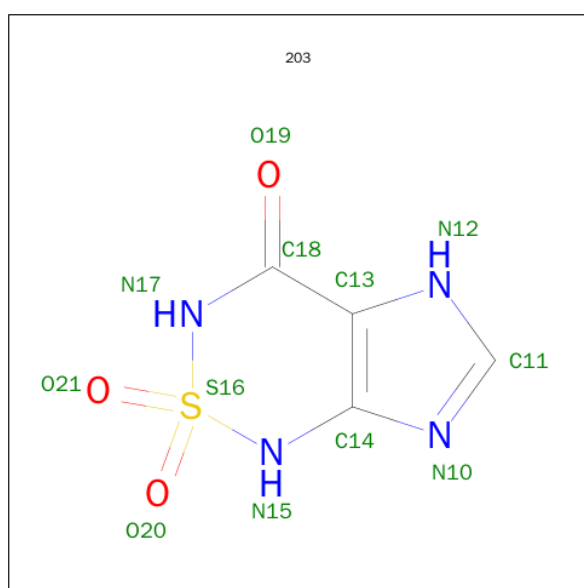
- Molecule 1 is a protein called BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	590	Total	C	N	O	S	0	1	0
			4523	2852	801	851	19			
1	B	590	Total	C	N	O	S	0	0	0
			4511	2843	800	849	19			

- Molecule 2 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	K	0	0
			1	1		
2	A	1	Total	K	0	0
			1	1		

- Molecule 3 is 1,5-DIHYDROIMIDAZO[4,5-C][1,2,6]THIADIAZIN-4(3H)-ONE 2,2-DIOXIDE (three-letter code: 203) (formula: C₄H₄N₄O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			12	4	4	3	1		

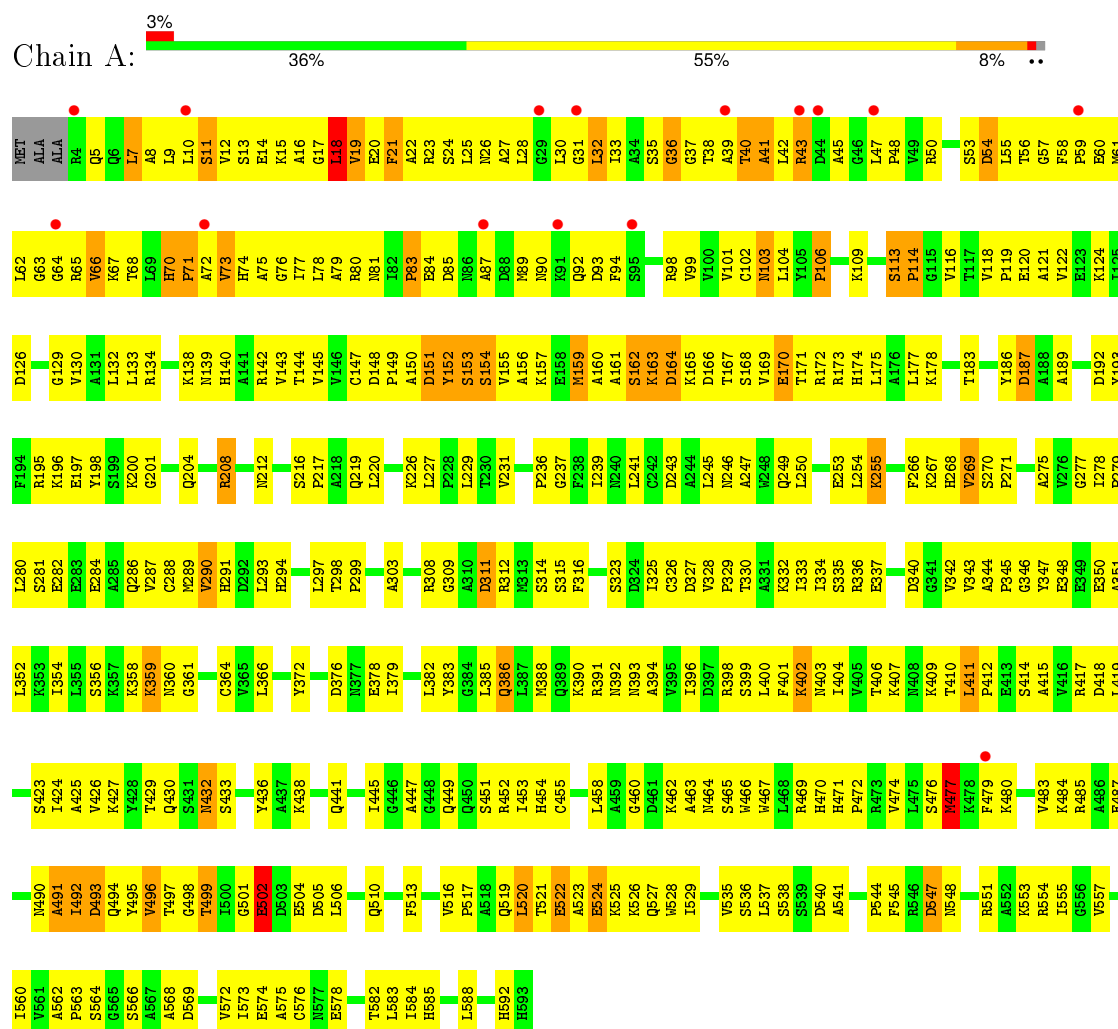
- Molecule 4 is water.

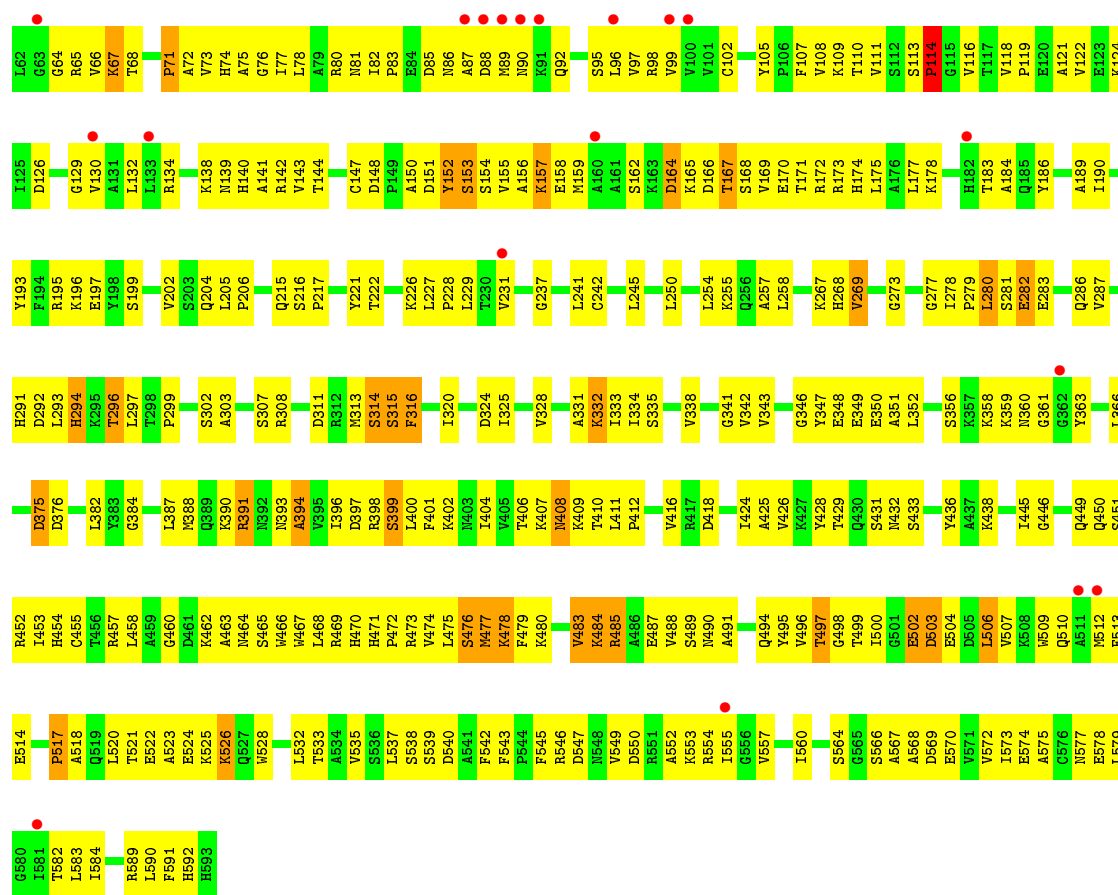
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	52	Total	O	0	0
			52	52		
4	B	45	Total	O	0	0
			45	45		

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: BIFUNCTIONAL PURINE BIOSYNTHESIS PROTEIN PURH





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	387.00Å 57.00Å 62.10Å 90.00° 98.90° 90.00°	Depositor
Resolution (Å)	35.20 – 2.90 35.13 – 2.87	Depositor EDS
% Data completeness (in resolution range)	91.5 (35.20-2.90) 90.9 (35.13-2.87)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.41 (at 2.85Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.215 , 0.300 0.285 , 0.341	Depositor DCC
R_{free} test set	1095 reflections (3.96%)	DCC
Wilson B-factor (Å ²)	50.6	Xtriage
Anisotropy	0.315	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 30.1	EDS
Estimated twinning fraction	0.027 for -h-2*k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	1 of 30321 reflections (0.003%)	Xtriage
F_o, F_c correlation	0.86	EDS
Total number of atoms	9145	wwPDB-VP
Average B, all atoms (Å ²)	45.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.98% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: 203, K

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	0.61	0/4608	0.75	1/6249 (0.0%)
1	B	0.59	0/4595	0.75	0/6230
All	All	0.60	0/9203	0.75	1/12479 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	45	ALA	N-CA-C	-5.98	94.86	111.00

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	4523	0	4570	434	0
1	B	4511	0	4561	363	4
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	B	12	0	4	1	0
4	A	52	0	0	2	0
4	B	45	0	0	3	0
All	All	9145	0	9135	763	4

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 42.

All (763) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:510:GLN:HE21	1:A:516:VAL:HG21	1.19	1.04
1:B:485:ARG:HG2	1:B:485:ARG:HH11	1.22	1.04
1:A:379:ILE:HG12	1:A:388:MET:HG3	1.34	1.04
1:A:510:GLN:NE2	1:A:516:VAL:HG21	1.76	1.00
1:B:479:PHE:HA	1:B:513:PHE:HA	1.46	0.97
1:A:502:GLU:HA	1:A:506:LEU:HB2	1.45	0.97
1:A:9:LEU:HD23	1:A:33:ILE:HB	1.45	0.95
1:B:407:LYS:O	1:B:409:LYS:HG3	1.67	0.93
1:A:520:LEU:H	1:A:520:LEU:HD12	1.33	0.92
1:B:80:ARG:HB2	1:B:82:ILE:HG12	1.51	0.92
1:B:408:ASN:HD21	1:B:577:ASN:HA	1.32	0.91
1:A:65:ARG:HD3	1:B:78:LEU:HD22	1.52	0.91
1:B:484:LYS:HB2	1:B:487:GLU:HG3	1.53	0.91
1:A:545:PHE:HB2	1:A:547:ASP:OD1	1.70	0.90
1:A:212:ASN:OD1	1:B:589:ARG:HD2	1.72	0.90
1:B:61:MET:H	1:B:61:MET:HE2	1.36	0.89
1:A:106:PRO:HD2	1:A:109:LYS:HE2	1.54	0.89
1:B:468:LEU:HD23	1:B:528:TRP:CD1	2.09	0.88
1:B:356:SER:O	1:B:361:GLY:HA2	1.74	0.87
1:B:406:THR:HG22	1:B:573:ILE:HG23	1.56	0.86
1:B:9:LEU:HD13	1:B:10:LEU:N	1.90	0.85
1:A:26:ASN:HB2	1:A:32:LEU:HD21	1.55	0.84
1:A:254:LEU:HD23	1:A:424:ILE:HD12	1.60	0.84
1:B:26:ASN:HB2	1:B:32:LEU:HD11	1.58	0.84
1:A:118:VAL:O	1:A:122:VAL:HG23	1.78	0.84
1:A:148:ASP:OD1	1:A:150:ALA:HB3	1.78	0.83
1:B:129:GLY:HA2	1:B:132:LEU:HD12	1.57	0.83
1:B:22:ALA:HA	1:B:25:LEU:HD21	1.60	0.82
1:B:12:VAL:HG12	1:B:102:CYS:HA	1.60	0.82
1:B:121:ALA:O	1:B:124:LYS:HB2	1.78	0.82
1:B:283:GLU:HG3	4:B:2018:HOH:O	1.80	0.81
1:B:485:ARG:HH11	1:B:485:ARG:CG	1.93	0.81
1:B:535:VAL:HB	1:B:557:VAL:HA	1.61	0.80
1:B:43:ARG:HG3	1:B:49:VAL:CG1	2.12	0.80
1:A:270:SER:OG	1:A:430:GLN:HG2	1.82	0.80
1:B:156:ALA:HB3	1:B:157:LYS:HE3	1.61	0.79
1:B:171:THR:O	1:B:175:LEU:HD23	1.83	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:544:PRO:O	1:A:568:ALA:HB3	1.83	0.78
1:B:74:HIS:HA	1:B:77:ILE:HD12	1.64	0.78
1:A:535:VAL:HB	1:A:557:VAL:HA	1.65	0.77
1:A:208:ARG:CZ	1:A:237:GLY:HA2	2.15	0.77
1:B:566:SER:HB3	1:B:569:ASP:OD1	1.84	0.76
1:B:474:VAL:HA	1:B:477:MET:HG3	1.67	0.76
1:A:163:LYS:HG2	1:A:164:ASP:OD1	1.85	0.76
1:A:56:THR:HG22	1:A:72:ALA:HB3	1.68	0.76
1:A:583:LEU:HD12	1:A:584:ILE:N	2.01	0.76
1:B:464:ASN:ND2	1:B:555:ILE:HD13	2.01	0.76
1:B:470:HIS:O	1:B:475:LEU:HD11	1.86	0.76
1:A:28:LEU:HG	1:A:165:LYS:HE2	1.68	0.75
1:A:174:HIS:HD2	1:A:175:LEU:HD22	1.51	0.75
1:A:410:THR:O	1:A:582:THR:HG21	1.86	0.74
1:A:522:GLU:C	1:A:524:GLU:H	1.88	0.74
1:B:83:PRO:HA	1:B:86:ASN:HD22	1.52	0.74
1:A:464:ASN:ND2	1:A:555:ILE:HD13	2.02	0.74
1:B:7:LEU:HA	1:B:31:GLY:H	1.53	0.74
1:A:25:LEU:O	1:A:30:LEU:HD12	1.88	0.74
1:A:50:ARG:HD2	1:A:54:ASP:OD2	1.87	0.74
1:B:167:THR:O	1:B:172:ARG:NH1	2.21	0.73
1:A:537:LEU:C	1:A:537:LEU:HD23	2.08	0.73
1:B:56:THR:OG1	1:B:58:PHE:HB2	1.87	0.73
1:B:118:VAL:O	1:B:122:VAL:HG23	1.88	0.73
1:A:289:MET:HG3	1:A:312:ARG:CZ	2.17	0.73
1:A:200:LYS:HD3	1:A:200:LYS:C	2.07	0.73
1:A:378:GLU:HG3	1:A:391:ARG:HB3	1.71	0.73
1:A:172:ARG:HG3	1:A:172:ARG:HH11	1.53	0.73
1:B:520:LEU:HB2	1:B:525:LYS:HE2	1.70	0.73
1:B:503:ASP:O	1:B:507:VAL:HG23	1.89	0.73
1:A:522:GLU:C	1:A:526:LYS:HE2	2.09	0.72
1:B:22:ALA:HA	1:B:25:LEU:CD2	2.19	0.72
1:A:471:HIS:ND1	1:A:472:PRO:HD2	2.05	0.72
1:A:520:LEU:HD13	1:A:525:LYS:HE2	1.70	0.72
1:B:408:ASN:ND2	1:B:577:ASN:HA	2.05	0.71
1:A:241:LEU:O	1:A:245:LEU:HD23	1.88	0.71
1:B:537:LEU:HD23	1:B:537:LEU:C	2.10	0.71
1:B:410:THR:O	1:B:582:THR:HG21	1.89	0.71
1:B:280:LEU:HD11	1:B:302:SER:HB2	1.71	0.71
1:B:410:THR:HG22	1:B:412:PRO:HD3	1.73	0.71
1:B:545:PHE:HB2	1:B:547:ASP:OD1	1.90	0.70

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:569:ASP:O	1:B:573:ILE:HG13	1.91	0.70
1:A:37:GLY:O	1:A:40:THR:HB	1.92	0.70
1:B:496:VAL:HG23	1:B:497:THR:H	1.56	0.70
1:B:80:ARG:HD2	1:B:82:ILE:CD1	2.22	0.70
1:A:547:ASP:OD1	1:A:547:ASP:N	2.24	0.70
1:A:458:LEU:HD21	1:A:462:LYS:HE3	1.73	0.70
1:A:38:THR:O	1:A:42:LEU:HG	1.92	0.70
1:A:70:HIS:CD2	1:A:72:ALA:H	2.10	0.70
1:A:61:MET:SD	1:B:92:GLN:HG3	2.31	0.70
1:A:106:PRO:HG2	1:A:109:LYS:HZ1	1.56	0.69
1:B:521:THR:HG23	1:B:524:GLU:OE1	1.92	0.69
1:A:169:VAL:O	1:A:173:ARG:HG3	1.91	0.69
1:B:468:LEU:HD23	1:B:528:TRP:HD1	1.57	0.69
1:A:432:ASN:HD21	1:A:449:GLN:HB2	1.56	0.69
1:B:485:ARG:NH1	1:B:485:ARG:HG2	2.03	0.69
1:B:583:LEU:HD12	1:B:584:ILE:N	2.08	0.69
1:A:418:ASP:OD2	1:A:438:LYS:HA	1.92	0.69
1:B:43:ARG:HG3	1:B:49:VAL:HG11	1.75	0.69
1:A:104:LEU:O	1:A:106:PRO:HD3	1.93	0.68
1:B:250:LEU:HD11	1:B:425:ALA:HA	1.76	0.68
1:A:9:LEU:CD2	1:A:33:ILE:HB	2.23	0.68
1:B:472:PRO:HA	1:B:475:LEU:HD12	1.74	0.68
1:B:418:ASP:OD2	1:B:438:LYS:HA	1.94	0.68
1:A:80:ARG:HG3	1:B:65:ARG:HH12	1.58	0.68
1:A:37:GLY:HA2	1:A:40:THR:HB	1.76	0.68
1:A:502:GLU:H	1:A:505:ASP:HB2	1.59	0.68
1:B:496:VAL:HG23	1:B:497:THR:N	2.09	0.68
1:A:289:MET:HG3	1:A:312:ARG:NH2	2.07	0.68
1:B:113:SER:OG	1:B:114:PRO:HD2	1.93	0.68
1:B:10:LEU:HB2	1:B:34:ALA:HB2	1.74	0.68
1:A:378:GLU:CG	1:A:391:ARG:HB3	2.23	0.67
1:A:208:ARG:NH2	1:A:237:GLY:HA2	2.10	0.67
1:B:87:ALA:HA	1:B:90:ASN:OD1	1.95	0.67
1:A:153:SER:O	1:A:157:LYS:HG3	1.95	0.67
1:B:280:LEU:HD12	1:B:280:LEU:N	2.09	0.67
1:A:200:LYS:HD3	1:A:201:GLY:N	2.09	0.67
1:A:522:GLU:OE2	1:A:522:GLU:HA	1.94	0.67
1:A:521:THR:OG1	1:A:524:GLU:HB2	1.95	0.67
1:A:53:SER:O	1:A:57:GLY:N	2.28	0.67
1:A:298:THR:HB	1:A:299:PRO:HD2	1.75	0.66
1:A:522:GLU:C	1:A:524:GLU:N	2.49	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:583:LEU:HD12	1:A:584:ILE:H	1.60	0.66
1:A:495:TYR:CE1	1:A:519:GLN:HA	2.31	0.66
1:B:335:SER:HA	1:B:358:LYS:HD2	1.78	0.66
1:A:129:GLY:HA2	1:A:132:LEU:HD12	1.76	0.66
1:A:335:SER:HA	1:A:358:LYS:HD2	1.78	0.66
1:A:282:GLU:HA	1:A:294:HIS:CE1	2.30	0.66
1:B:495:TYR:HD1	1:B:500:ILE:HD11	1.61	0.66
1:B:157:LYS:N	1:B:157:LYS:HE3	2.10	0.65
1:B:453:ILE:HD11	1:B:457:ARG:NH2	2.12	0.65
1:B:7:LEU:HA	1:B:31:GLY:N	2.11	0.65
1:A:74:HIS:HA	1:A:77:ILE:HD12	1.77	0.65
1:A:493:ASP:O	1:A:496:VAL:HG22	1.97	0.65
1:A:76:GLY:O	1:A:142:ARG:NH2	2.27	0.65
1:A:376:ASP:HB3	1:A:390:LYS:HD3	1.79	0.65
1:A:333:ILE:O	1:A:337:GLU:HG2	1.96	0.65
1:A:106:PRO:HB2	1:A:109:LYS:HZ3	1.61	0.65
1:A:55:LEU:HD22	1:A:72:ALA:HB1	1.79	0.65
1:A:61:MET:HG3	1:A:62:LEU:H	1.62	0.65
1:A:426:VAL:CG1	1:A:540:ASP:HB3	2.27	0.65
1:A:148:ASP:HB3	1:A:178:LYS:HE3	1.79	0.65
1:A:277:GLY:N	1:A:303:ALA:HB2	2.11	0.65
1:B:51:ASP:O	1:B:54:ASP:HB2	1.96	0.65
1:A:198:TYR:CE1	1:B:173:ARG:HD3	2.32	0.65
1:A:280:LEU:HB3	1:A:284:GLU:HB3	1.78	0.64
1:B:299:PRO:O	1:B:303:ALA:N	2.29	0.64
1:A:106:PRO:HG2	1:A:109:LYS:NZ	2.12	0.64
1:A:28:LEU:HA	1:A:165:LYS:NZ	2.13	0.64
1:B:85:ASP:O	1:B:89:MET:HG2	1.97	0.64
1:A:40:THR:HG22	1:A:41:ALA:N	2.12	0.64
1:A:452:ARG:NH2	1:A:541:ALA:HB3	2.13	0.64
1:A:154:SER:HA	1:A:157:LYS:HD2	1.78	0.64
1:A:401:PHE:HB3	1:A:584:ILE:HD13	1.80	0.64
1:A:171:THR:O	1:A:175:LEU:HD23	1.97	0.64
1:B:25:LEU:HA	1:B:28:LEU:HD12	1.79	0.63
1:A:61:MET:HB2	1:B:88:ASP:HB3	1.80	0.63
1:B:130:VAL:HG13	1:B:183:THR:HG22	1.78	0.63
1:B:9:LEU:C	1:B:10:LEU:HD12	2.18	0.63
1:A:451:SER:HB3	1:A:454:HIS:HB2	1.79	0.63
1:B:282:GLU:HA	1:B:294:HIS:HE1	1.62	0.63
1:B:205:LEU:HD12	1:B:206:PRO:HD2	1.80	0.63
1:B:542:PHE:HB3	1:B:564:SER:O	1.99	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:151:ASP:O	1:B:152:TYR:C	2.35	0.63
1:A:7:LEU:N	1:A:7:LEU:HD12	2.14	0.62
1:A:92:GLN:HG3	1:B:61:MET:SD	2.39	0.62
1:B:82:ILE:HG13	1:B:85:ASP:HB2	1.81	0.62
1:A:163:LYS:HG2	1:A:164:ASP:N	2.14	0.62
1:A:480:LYS:O	1:A:483:VAL:HG23	2.00	0.62
1:A:163:LYS:HG2	1:A:164:ASP:H	1.63	0.62
1:A:143:VAL:O	1:A:172:ARG:HD2	1.99	0.62
1:A:159:MET:HE2	1:A:166:ASP:HA	1.80	0.62
1:B:282:GLU:HA	1:B:294:HIS:CE1	2.35	0.62
1:A:85:ASP:O	1:A:89:MET:HG2	1.99	0.62
1:B:320:ILE:O	1:B:342:VAL:HA	2.00	0.62
1:A:196:LYS:HG2	1:A:204:GLN:NE2	2.15	0.61
1:B:471:HIS:ND1	1:B:472:PRO:HD2	2.15	0.61
1:B:254:LEU:HD23	1:B:424:ILE:HD12	1.81	0.61
1:A:220:LEU:HD13	1:B:387:LEU:HD12	1.82	0.61
1:A:37:GLY:CA	1:A:40:THR:HB	2.31	0.61
1:A:399:SER:O	1:A:402:LYS:HG3	2.00	0.61
1:A:15:LYS:O	1:A:18:LEU:HB3	1.99	0.61
1:A:208:ARG:HD3	1:A:208:ARG:H	1.66	0.61
1:B:9:LEU:HD13	1:B:10:LEU:H	1.60	0.61
1:B:480:LYS:O	1:B:483:VAL:HG12	2.00	0.61
1:A:163:LYS:HZ2	1:A:163:LYS:H	1.48	0.61
1:B:186:TYR:O	1:B:189:ALA:HB3	2.01	0.61
1:A:37:GLY:HA2	1:A:40:THR:CB	2.31	0.61
1:A:37:GLY:C	1:A:40:THR:HB	2.22	0.61
1:B:521:THR:O	1:B:525:LYS:HG3	2.01	0.61
1:A:359:LYS:C	1:A:361:GLY:H	2.03	0.61
1:A:208:ARG:NH1	1:A:237:GLY:HA2	2.15	0.60
1:A:61:MET:HG3	1:A:62:LEU:N	2.16	0.60
1:A:19:VAL:HG12	1:A:20:GLU:N	2.17	0.60
1:B:514:GLU:OE2	1:B:514:GLU:HA	2.01	0.60
1:B:547:ASP:OD1	1:B:547:ASP:N	2.35	0.60
1:B:108:VAL:HG23	1:B:109:LYS:N	2.16	0.60
1:B:446:GLY:HA2	1:B:458:LEU:HD22	1.83	0.60
1:B:7:LEU:HD13	1:B:33:ILE:HD12	1.83	0.60
1:B:126:ASP:OD1	1:B:130:VAL:HG23	2.01	0.60
1:B:108:VAL:HG23	1:B:109:LYS:H	1.67	0.59
1:B:460:GLY:O	1:B:463:ALA:HB3	2.00	0.59
1:A:7:LEU:HD23	1:A:33:ILE:CG1	2.32	0.59
1:A:152:TYR:O	1:A:155:VAL:HB	2.02	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:490:ASN:O	1:B:494:GLN:HG2	2.01	0.59
1:B:105:TYR:CE1	1:B:109:LYS:HD3	2.37	0.59
1:B:7:LEU:CD1	1:B:33:ILE:HD12	2.33	0.59
1:B:384:GLY:N	4:B:2026:HOH:O	2.33	0.59
1:A:325:ILE:HG23	1:A:346:GLY:C	2.22	0.59
1:A:98:ARG:O	1:A:98:ARG:HG2	2.01	0.59
1:A:399:SER:HB3	4:A:2030:HOH:O	2.02	0.59
1:A:520:LEU:HD13	1:A:525:LYS:CE	2.32	0.59
1:A:410:THR:O	1:A:411:LEU:HB2	2.02	0.59
1:A:159:MET:CE	1:A:166:ASP:HA	2.33	0.59
1:B:108:VAL:O	1:B:111:VAL:HG22	2.03	0.59
1:A:394:ALA:CB	1:A:588:LEU:HD11	2.32	0.59
1:A:458:LEU:HD23	1:A:458:LEU:C	2.23	0.58
1:B:164:ASP:OD1	1:B:165:LYS:N	2.36	0.58
1:A:172:ARG:HG3	1:A:172:ARG:NH1	2.16	0.58
1:A:151:ASP:O	1:A:152:TYR:C	2.40	0.58
1:A:154:SER:HA	1:A:157:LYS:CD	2.33	0.58
1:B:37:GLY:HA2	1:B:40:THR:HB	1.85	0.58
1:A:398:ARG:HB2	1:A:398:ARG:NH1	2.18	0.58
1:B:26:ASN:HB2	1:B:32:LEU:HD21	1.85	0.58
1:A:506:LEU:O	1:A:510:GLN:HG3	2.04	0.58
1:B:376:ASP:HB3	1:B:390:LYS:NZ	2.19	0.58
1:B:159:MET:HA	1:B:162:SER:OG	2.04	0.58
1:B:458:LEU:HD21	1:B:462:LYS:HE3	1.86	0.58
1:A:382:LEU:HD21	1:B:242:CYS:HA	1.85	0.58
1:A:65:ARG:CD	1:B:78:LEU:HD22	2.29	0.58
1:A:396:ILE:HG23	1:A:400:LEU:HD23	1.85	0.58
1:B:156:ALA:HB3	1:B:157:LYS:CE	2.31	0.58
1:A:495:TYR:HD1	1:A:519:GLN:HE21	1.51	0.57
1:A:139:ASN:HB3	1:A:143:VAL:HG23	1.86	0.57
1:A:10:LEU:CD1	1:A:42:LEU:HD11	2.34	0.57
1:A:171:THR:O	1:A:174:HIS:HB3	2.05	0.57
1:B:64:GLY:HA2	1:B:66:VAL:O	2.05	0.57
1:A:75:ALA:O	1:A:79:ALA:HB2	2.05	0.57
1:A:198:TYR:CD1	1:B:173:ARG:HD3	2.40	0.57
1:A:7:LEU:HD23	1:A:33:ILE:HD11	1.85	0.57
1:B:480:LYS:HA	1:B:514:GLU:CD	2.24	0.57
1:B:7:LEU:N	1:B:7:LEU:HD23	2.19	0.57
1:B:164:ASP:O	1:B:165:LYS:HG2	2.05	0.57
1:B:229:LEU:C	1:B:229:LEU:HD23	2.25	0.57
1:B:399:SER:HB2	1:B:402:LYS:NZ	2.19	0.57

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:87:ALA:HA	1:A:90:ASN:OD1	2.04	0.57
1:A:36:GLY:C	1:A:38:THR:N	2.57	0.57
1:B:25:LEU:HA	1:B:28:LEU:CD1	2.35	0.57
1:A:398:ARG:HB2	1:A:398:ARG:HH11	1.69	0.57
1:A:277:GLY:HA3	1:A:299:PRO:O	2.05	0.57
1:A:7:LEU:HD23	1:A:33:ILE:HG13	1.87	0.57
1:B:80:ARG:HD2	1:B:82:ILE:HD11	1.86	0.57
1:B:453:ILE:HD11	1:B:457:ARG:CZ	2.35	0.57
1:B:231:VAL:HG22	1:B:366:LEU:CD2	2.34	0.57
1:B:10:LEU:HD12	1:B:10:LEU:N	2.20	0.56
1:A:328:VAL:HG12	1:A:332:LYS:HE3	1.87	0.56
1:A:502:GLU:HA	1:A:506:LEU:CB	2.28	0.56
1:A:36:GLY:C	1:A:38:THR:H	2.06	0.56
1:A:35:SER:O	1:A:39:ALA:HB3	2.05	0.56
1:A:495:TYR:HE1	1:A:519:GLN:HA	1.68	0.56
1:A:386:GLN:HG3	1:B:221:TYR:CZ	2.40	0.56
1:B:547:ASP:HA	1:B:550:ASP:OD2	2.04	0.56
1:B:278:ILE:HG22	1:B:279:PRO:O	2.04	0.56
1:B:483:VAL:O	1:B:484:LYS:O	2.23	0.56
1:B:506:LEU:O	1:B:510:GLN:HG3	2.05	0.56
1:A:378:GLU:CD	1:A:391:ARG:HB3	2.26	0.56
1:A:163:LYS:NZ	1:A:163:LYS:H	2.04	0.56
1:A:70:HIS:HD2	1:A:72:ALA:N	2.04	0.56
1:A:58:PHE:CD2	1:A:59:PRO:HD2	2.41	0.56
1:B:500:ILE:HG23	1:B:509:TRP:CG	2.41	0.56
1:A:522:GLU:CA	1:A:522:GLU:OE2	2.53	0.55
1:B:71:PRO:O	1:B:75:ALA:N	2.35	0.55
1:A:35:SER:O	1:A:36:GLY:O	2.23	0.55
1:B:570:GLU:O	1:B:574:GLU:HG2	2.06	0.55
1:B:61:MET:H	1:B:61:MET:CE	2.13	0.55
1:A:491:ALA:O	1:A:492:ILE:C	2.45	0.55
1:A:28:LEU:HA	1:A:165:LYS:HZ1	1.69	0.55
1:A:287:VAL:HG11	1:A:470:HIS:CE1	2.42	0.55
1:B:283:GLU:O	1:B:286:GLN:N	2.39	0.55
1:B:113:SER:O	1:B:116:VAL:HG12	2.06	0.55
1:A:126:ASP:OD1	1:A:130:VAL:HG23	2.07	0.55
1:A:106:PRO:CD	1:A:109:LYS:HE2	2.32	0.55
1:B:31:GLY:O	1:B:33:ILE:HG13	2.07	0.55
1:A:432:ASN:HD22	1:A:432:ASN:C	2.11	0.55
1:A:564:SER:HB3	1:A:585:HIS:ND1	2.22	0.55
1:B:216:SER:OG	1:B:217:PRO:HA	2.07	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:VAL:HG22	1:A:144:THR:HB	1.88	0.55
1:A:151:ASP:O	1:A:155:VAL:HG23	2.07	0.55
1:B:432:ASN:HB2	1:B:452:ARG:NH2	2.22	0.55
1:A:12:VAL:HB	1:A:103:ASN:OD1	2.06	0.54
1:A:74:HIS:O	1:A:78:LEU:HB2	2.06	0.54
1:B:148:ASP:O	1:B:151:ASP:HB2	2.07	0.54
1:B:426:VAL:CG1	1:B:540:ASP:HB3	2.37	0.54
1:B:308:ARG:NH2	1:B:316:PHE:HA	2.22	0.54
1:B:202:VAL:HG12	1:B:226:LYS:HG2	1.89	0.54
1:A:70:HIS:C	1:A:70:HIS:CD2	2.80	0.54
1:A:70:HIS:CD2	1:A:72:ALA:N	2.74	0.54
1:B:399:SER:O	1:B:402:LYS:HE2	2.07	0.54
1:A:130:VAL:HG13	1:A:183:THR:HG22	1.89	0.54
1:A:464:ASN:HD22	1:A:555:ILE:HD13	1.72	0.54
1:A:376:ASP:O	1:A:391:ARG:HG2	2.08	0.54
1:A:220:LEU:HD13	1:B:387:LEU:CD1	2.38	0.54
1:B:64:GLY:C	1:B:66:VAL:N	2.57	0.54
1:A:174:HIS:CD2	1:A:175:LEU:HD22	2.37	0.54
1:A:386:GLN:HG3	1:B:221:TYR:CE1	2.42	0.54
1:B:406:THR:HB	1:B:577:ASN:OD1	2.08	0.54
1:A:186:TYR:O	1:A:189:ALA:HB3	2.08	0.54
1:A:383:TYR:HA	1:B:391:ARG:NH2	2.23	0.54
1:A:460:GLY:O	1:A:463:ALA:HB3	2.06	0.54
1:A:254:LEU:CD2	1:A:424:ILE:HD12	2.37	0.54
1:B:172:ARG:HG3	1:B:172:ARG:HH11	1.71	0.54
1:B:411:LEU:HD11	1:B:416:VAL:HG22	1.89	0.54
1:A:492:ILE:O	1:A:493:ASP:C	2.47	0.54
1:A:32:LEU:HD12	1:A:48:PRO:O	2.08	0.53
1:A:61:MET:SD	1:B:92:GLN:CG	2.95	0.53
1:B:190:ILE:O	1:B:193:TYR:HB3	2.08	0.53
1:A:216:SER:OG	1:A:217:PRO:HA	2.09	0.53
1:B:359:LYS:HE2	1:B:363:TYR:HD1	1.73	0.53
1:A:40:THR:HA	1:A:43:ARG:CZ	2.37	0.53
1:A:220:LEU:CD1	1:B:387:LEU:HD12	2.37	0.53
1:A:113:SER:HB2	1:A:114:PRO:CD	2.39	0.53
1:A:330:THR:HG22	1:A:334:ILE:CD1	2.38	0.53
1:B:273:GLY:HA3	1:B:307:SER:O	2.08	0.53
1:A:569:ASP:O	1:A:573:ILE:HG13	2.08	0.53
1:B:484:LYS:CB	1:B:487:GLU:HG3	2.34	0.53
1:B:102:CYS:O	1:B:147:CYS:HA	2.09	0.53
1:B:83:PRO:HA	1:B:86:ASN:ND2	2.19	0.53

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:156:ALA:O	1:A:157:LYS:C	2.47	0.53
1:A:396:ILE:HG23	1:A:400:LEU:CD2	2.39	0.53
1:A:326:CYS:O	1:A:348:GLU:HG3	2.09	0.53
1:B:552:ALA:O	1:B:555:ILE:HG22	2.09	0.52
1:A:328:VAL:N	1:A:329:PRO:HD2	2.23	0.52
1:B:467:TRP:O	1:B:470:HIS:HB2	2.10	0.52
1:A:169:VAL:HG12	1:A:170:GLU:OE1	2.09	0.52
1:A:328:VAL:CG1	1:A:332:LYS:HE3	2.40	0.52
1:A:490:ASN:O	1:A:493:ASP:HB3	2.09	0.52
1:A:290:VAL:HA	1:A:336:ARG:HH22	1.73	0.52
1:A:474:VAL:O	1:A:477:MET:HB2	2.10	0.52
1:B:465:SER:O	1:B:469:ARG:HG3	2.09	0.52
1:A:396:ILE:HG21	1:A:423:SER:HB2	1.91	0.52
1:A:7:LEU:HD23	1:A:33:ILE:CD1	2.40	0.52
1:A:18:LEU:O	1:A:19:VAL:C	2.47	0.52
1:B:151:ASP:O	1:B:155:VAL:HG23	2.10	0.52
1:A:12:VAL:HG12	1:A:101:VAL:HG12	1.92	0.52
1:B:490:ASN:O	1:B:491:ALA:C	2.48	0.52
1:B:458:LEU:HD23	1:B:458:LEU:C	2.30	0.52
1:A:348:GLU:O	1:A:351:ALA:HB3	2.09	0.52
1:A:290:VAL:HA	1:A:336:ARG:NH2	2.25	0.52
1:A:65:ARG:HD3	1:B:78:LEU:HB3	1.90	0.52
1:B:537:LEU:HD23	1:B:538:SER:N	2.25	0.52
1:A:537:LEU:HD23	1:A:538:SER:N	2.25	0.52
1:B:376:ASP:HB3	1:B:390:LYS:HZ3	1.74	0.52
1:A:63:GLY:O	1:B:80:ARG:NH2	2.43	0.51
1:A:103:ASN:HD22	1:A:104:LEU:N	2.08	0.51
1:A:16:ALA:C	1:A:18:LEU:H	2.13	0.51
1:A:65:ARG:HD3	1:B:78:LEU:CD2	2.34	0.51
1:B:589:ARG:HG2	1:B:590:LEU:N	2.25	0.51
1:A:516:VAL:HG23	1:A:517:PRO:HD2	1.92	0.51
1:B:10:LEU:HD22	1:B:42:LEU:HD11	1.93	0.51
1:B:589:ARG:HD3	1:B:591:PHE:CG	2.46	0.51
1:B:433:SER:HA	1:B:455:CYS:SG	2.50	0.51
1:A:576:CYS:SG	1:A:583:LEU:HD22	2.51	0.51
1:A:28:LEU:HA	1:A:165:LYS:CE	2.40	0.51
1:B:58:PHE:O	1:B:60:GLU:N	2.41	0.51
1:A:445:ILE:HG23	1:A:445:ILE:O	2.11	0.51
1:A:309:GLY:O	1:A:469:ARG:NH2	2.42	0.51
1:B:408:ASN:HD21	1:B:577:ASN:CA	2.13	0.51
1:A:325:ILE:HG23	1:A:346:GLY:O	2.11	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ASN:HB3	1:A:143:VAL:CG2	2.40	0.51
1:B:26:ASN:HB2	1:B:32:LEU:CD1	2.37	0.51
1:B:24:SER:O	1:B:28:LEU:HG	2.11	0.51
1:B:157:LYS:H	1:B:157:LYS:HE3	1.74	0.51
1:A:14:GLU:OE2	1:A:14:GLU:HA	2.11	0.51
1:A:414:SER:O	1:A:417:ARG:HB3	2.11	0.51
1:A:510:GLN:HA	1:A:513:PHE:HD1	1.76	0.50
1:A:71:PRO:O	1:A:75:ALA:CB	2.59	0.50
1:A:193:TYR:O	1:A:197:GLU:HG2	2.11	0.50
1:A:102:CYS:O	1:A:147:CYS:HA	2.11	0.50
1:A:116:VAL:HG23	1:A:120:GLU:OE2	2.10	0.50
1:B:331:ALA:O	1:B:332:LYS:C	2.49	0.50
1:A:537:LEU:C	1:A:537:LEU:CD2	2.78	0.50
1:A:84:GLU:OE1	1:A:84:GLU:N	2.38	0.50
1:A:28:LEU:HA	1:A:165:LYS:HE2	1.93	0.50
1:B:412:PRO:O	1:B:416:VAL:HG23	2.11	0.50
1:A:12:VAL:CG1	1:A:101:VAL:HG12	2.41	0.50
1:B:451:SER:HB3	1:B:454:HIS:HB2	1.92	0.50
1:A:344:ALA:HB1	1:A:345:PRO:HD2	1.94	0.50
1:B:522:GLU:O	1:B:526:LYS:HG3	2.12	0.50
1:B:82:ILE:HD11	1:B:85:ASP:CG	2.32	0.50
1:A:376:ASP:HB3	1:A:390:LYS:CD	2.42	0.50
1:A:458:LEU:CD2	1:A:462:LYS:HE3	2.39	0.50
1:A:449:GLN:HB2	1:A:455:CYS:HB2	1.92	0.50
1:B:506:LEU:HD12	1:B:506:LEU:O	2.11	0.50
1:B:432:ASN:HB2	1:B:452:ARG:HH22	1.76	0.50
1:B:341:GLY:HA2	1:B:363:TYR:CZ	2.47	0.50
1:B:18:LEU:C	1:B:18:LEU:HD12	2.32	0.50
1:B:400:LEU:HG	1:B:400:LEU:O	2.11	0.50
1:A:520:LEU:N	1:A:520:LEU:HD12	2.12	0.50
1:A:19:VAL:O	1:A:22:ALA:HB3	2.12	0.50
1:A:525:LYS:O	1:A:529:ILE:HG13	2.12	0.50
1:B:537:LEU:CD2	1:B:537:LEU:C	2.80	0.50
1:A:458:LEU:HD23	1:A:458:LEU:O	2.11	0.50
1:A:562:ALA:O	1:A:585:HIS:HA	2.11	0.50
1:A:453:ILE:HG23	1:A:454:HIS:N	2.27	0.50
1:A:523:ALA:O	1:A:527:GLN:HB2	2.12	0.49
1:B:76:GLY:HA2	1:B:89:MET:HE1	1.92	0.49
1:B:325:ILE:HA	1:B:346:GLY:O	2.11	0.49
1:A:168:SER:OG	1:A:171:THR:OG1	2.10	0.49
1:B:148:ASP:OD1	1:B:150:ALA:HB3	2.11	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:426:VAL:HG13	1:B:540:ASP:HB3	1.93	0.49
1:B:18:LEU:HG	1:B:19:VAL:N	2.26	0.49
1:A:342:VAL:HG22	1:A:343:VAL:N	2.27	0.49
1:B:172:ARG:HG3	1:B:172:ARG:NH1	2.27	0.49
1:B:523:ALA:C	1:B:525:LYS:N	2.65	0.49
1:A:116:VAL:HG23	1:A:120:GLU:CD	2.32	0.49
1:A:255:LYS:HG3	1:A:323:SER:HB2	1.92	0.49
1:B:7:LEU:HD13	1:B:33:ILE:CD1	2.42	0.49
1:A:426:VAL:HG13	1:A:540:ASP:HB3	1.94	0.49
1:A:522:GLU:O	1:A:526:LYS:HE2	2.11	0.49
1:B:572:VAL:O	1:B:575:ALA:N	2.43	0.49
1:A:520:LEU:HA	1:A:524:GLU:OE1	2.13	0.49
1:B:107:PHE:O	1:B:110:THR:HB	2.13	0.49
1:A:391:ARG:NH1	1:A:393:ASN:OD1	2.46	0.49
1:B:331:ALA:O	1:B:334:ILE:N	2.46	0.49
1:B:348:GLU:O	1:B:351:ALA:HB3	2.12	0.49
1:A:566:SER:C	1:A:568:ALA:H	2.16	0.49
1:A:496:VAL:HG23	1:A:497:THR:HG23	1.94	0.49
1:A:537:LEU:HD22	1:A:560:ILE:HG23	1.93	0.49
1:A:145:VAL:O	1:A:175:LEU:HD12	2.13	0.48
1:B:250:LEU:HD12	1:B:428:TYR:HB2	1.95	0.48
1:B:431:SER:HB2	1:B:592:HIS:H	1.78	0.48
1:B:496:VAL:O	1:B:498:GLY:N	2.46	0.48
1:B:496:VAL:CG2	1:B:497:THR:H	2.25	0.48
1:A:103:ASN:C	1:A:104:LEU:HG	2.33	0.48
1:B:71:PRO:O	1:B:72:ALA:C	2.49	0.48
1:B:255:LYS:HE2	1:B:324:ASP:OD2	2.13	0.48
1:A:161:ALA:HB3	4:A:2006:HOH:O	2.13	0.48
1:B:58:PHE:HD2	1:B:61:MET:CE	2.26	0.48
1:A:293:LEU:O	1:A:297:LEU:HG	2.14	0.48
1:B:375:ASP:OD2	1:B:375:ASP:N	2.44	0.48
1:A:25:LEU:C	1:A:27:ALA:N	2.66	0.48
1:A:471:HIS:CE1	1:A:472:PRO:HD2	2.47	0.48
1:B:496:VAL:C	1:B:498:GLY:N	2.67	0.48
1:A:275:ALA:HB2	1:A:441:GLN:HB2	1.96	0.48
1:A:485:ARG:CZ	1:A:485:ARG:HB2	2.43	0.48
1:A:226:LYS:HG2	1:A:227:LEU:N	2.29	0.48
1:A:350:GLU:O	1:A:354:ILE:HG13	2.13	0.48
1:B:22:ALA:O	1:B:25:LEU:HD23	2.13	0.48
1:A:544:PRO:HA	1:A:566:SER:OG	2.14	0.48
1:A:71:PRO:O	1:A:75:ALA:HB2	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:464:ASN:ND2	1:B:555:ILE:CD1	2.76	0.48
1:B:473:ARG:HD3	1:B:518:ALA:O	2.14	0.48
1:B:296:THR:O	1:B:297:LEU:HD23	2.14	0.48
1:A:269:VAL:HG12	1:A:269:VAL:O	2.14	0.48
1:A:471:HIS:ND1	1:A:472:PRO:CD	2.75	0.48
1:A:21:PHE:CZ	1:A:155:VAL:HB	2.49	0.48
1:A:311:ASP:OD2	1:A:314:SER:CB	2.62	0.47
1:A:392:ASN:OD1	1:A:427:LYS:HE3	2.14	0.47
1:B:485:ARG:NH1	1:B:485:ARG:CG	2.63	0.47
1:A:26:ASN:HB2	1:A:32:LEU:HD11	1.96	0.47
1:A:73:VAL:HG12	1:A:74:HIS:N	2.29	0.47
1:B:523:ALA:C	1:B:525:LYS:H	2.18	0.47
1:A:113:SER:CB	1:A:114:PRO:CD	2.92	0.47
1:B:431:SER:OG	1:B:432:ASN:HA	2.13	0.47
1:B:67:LYS:NZ	3:B:1595:203:H12	2.13	0.47
1:A:42:LEU:HD22	1:A:47:LEU:HD12	1.96	0.47
1:A:429:THR:HG22	1:A:433:SER:OG	2.15	0.47
1:A:36:GLY:O	1:A:39:ALA:N	2.47	0.47
1:B:496:VAL:CG2	1:B:497:THR:N	2.78	0.47
1:B:483:VAL:O	1:B:484:LYS:C	2.53	0.47
1:A:106:PRO:CB	1:A:109:LYS:HZ3	2.27	0.47
1:A:118:VAL:N	1:A:119:PRO:HD2	2.29	0.47
1:A:25:LEU:C	1:A:27:ALA:H	2.18	0.47
1:A:58:PHE:CG	1:A:59:PRO:HD2	2.49	0.47
1:B:495:TYR:HA	1:B:500:ILE:HD11	1.97	0.47
1:B:130:VAL:O	1:B:134:ARG:HG3	2.15	0.47
1:A:231:VAL:HG22	1:A:366:LEU:CD2	2.45	0.47
1:B:99:VAL:HG22	1:B:144:THR:HB	1.95	0.47
1:A:467:TRP:O	1:A:470:HIS:HB2	2.15	0.47
1:B:53:SER:HG	1:B:60:GLU:CD	2.18	0.47
1:A:70:HIS:CD2	1:A:71:PRO:HG2	2.50	0.47
1:A:372:TYR:OH	1:B:384:GLY:HA3	2.15	0.47
1:B:193:TYR:O	1:B:197:GLU:HG2	2.15	0.47
1:A:522:GLU:O	1:A:524:GLU:N	2.48	0.47
1:A:148:ASP:O	1:A:151:ASP:HB2	2.14	0.47
1:B:466:TRP:O	1:B:469:ARG:HB2	2.15	0.47
1:B:483:VAL:HG22	1:B:483:VAL:O	2.16	0.46
1:A:25:LEU:O	1:A:28:LEU:HB2	2.14	0.46
1:B:64:GLY:C	1:B:66:VAL:H	2.18	0.46
1:B:6:GLN:OE1	1:B:98:ARG:NH2	2.47	0.46
1:B:59:PRO:O	1:B:60:GLU:C	2.53	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:TYR:CD1	1:A:519:GLN:NE2	2.82	0.46
1:B:463:ALA:O	1:B:466:TRP:HB3	2.15	0.46
1:A:22:ALA:HB1	1:A:47:LEU:HD13	1.96	0.46
1:B:280:LEU:HD12	1:B:280:LEU:H	1.79	0.46
1:A:246:ASN:HD21	1:A:592:HIS:CE1	2.32	0.46
1:B:20:GLU:OE2	1:B:20:GLU:HA	2.16	0.46
1:B:476:SER:O	1:B:478:LYS:HD2	2.15	0.46
1:A:73:VAL:O	1:A:77:ILE:HG13	2.15	0.46
1:A:330:THR:CG2	1:A:334:ILE:HD11	2.45	0.46
1:B:572:VAL:O	1:B:575:ALA:HB3	2.15	0.46
1:B:139:ASN:OD1	1:B:143:VAL:HG23	2.16	0.46
1:A:59:PRO:O	1:A:60:GLU:C	2.53	0.46
1:A:477:MET:CE	1:A:492:ILE:HG12	2.46	0.46
1:A:330:THR:HG22	1:A:334:ILE:HD11	1.96	0.46
1:A:36:GLY:O	1:A:38:THR:N	2.49	0.46
1:A:70:HIS:O	1:A:73:VAL:HB	2.16	0.46
1:B:342:VAL:HG22	1:B:343:VAL:N	2.31	0.46
1:A:278:ILE:O	1:A:279:PRO:C	2.54	0.46
1:A:18:LEU:HD12	1:A:18:LEU:C	2.36	0.46
1:B:494:GLN:HA	1:B:497:THR:HB	1.97	0.46
1:B:231:VAL:HG22	1:B:366:LEU:HD21	1.98	0.46
1:A:286:GLN:C	1:A:288:CYS:N	2.68	0.46
1:A:56:THR:O	1:A:57:GLY:C	2.54	0.46
1:A:50:ARG:HD2	1:A:54:ASP:CG	2.35	0.46
1:B:352:LEU:HD12	1:B:352:LEU:O	2.16	0.46
1:A:429:THR:CG2	1:A:433:SER:OG	2.64	0.46
1:A:492:ILE:O	1:A:495:TYR:HB3	2.16	0.46
1:B:396:ILE:O	1:B:397:ASP:HB3	2.16	0.46
1:A:106:PRO:CG	1:A:109:LYS:NZ	2.79	0.45
1:A:523:ALA:HA	1:A:526:LYS:CE	2.46	0.45
1:A:298:THR:HG23	1:A:329:PRO:HG3	1.97	0.45
1:A:359:LYS:HE3	1:A:359:LYS:HB3	1.85	0.45
1:B:397:ASP:C	1:B:397:ASP:OD1	2.55	0.45
1:B:406:THR:CG2	1:B:583:LEU:HB3	2.47	0.45
1:B:589:ARG:HG2	1:B:590:LEU:H	1.82	0.45
1:B:438:LYS:HE2	1:B:533:THR:O	2.17	0.45
1:A:476:SER:O	1:A:477:MET:C	2.53	0.45
1:A:359:LYS:C	1:A:361:GLY:N	2.68	0.45
1:B:575:ALA:O	1:B:579:LEU:HG	2.16	0.45
1:A:38:THR:O	1:A:42:LEU:CG	2.64	0.45
1:A:25:LEU:O	1:A:28:LEU:N	2.44	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:LYS:O	1:B:215:GLN:HG2	2.17	0.45
1:A:492:ILE:O	1:A:495:TYR:N	2.49	0.45
1:B:44:ASP:C	1:B:46:GLY:N	2.70	0.45
1:A:287:VAL:O	1:A:287:VAL:HG12	2.17	0.45
1:A:464:ASN:O	1:A:465:SER:C	2.54	0.45
1:B:134:ARG:CZ	1:B:134:ARG:HB3	2.46	0.45
1:B:152:TYR:O	1:B:155:VAL:HB	2.16	0.45
1:A:102:CYS:O	1:A:147:CYS:CB	2.65	0.45
1:B:158:GLU:CD	1:B:168:SER:H	2.20	0.45
1:A:551:ARG:O	1:A:554:ARG:HB2	2.16	0.45
1:A:92:GLN:O	1:A:93:ASP:HB3	2.17	0.45
1:B:5:GLN:O	1:B:5:GLN:HG3	2.16	0.45
1:A:502:GLU:N	1:A:505:ASP:HB2	2.29	0.45
1:A:208:ARG:CD	1:A:208:ARG:H	2.29	0.45
1:A:208:ARG:NH2	1:A:237:GLY:CA	2.79	0.45
1:B:509:TRP:HH2	1:B:517:PRO:HG2	1.81	0.45
1:A:563:PRO:HG3	1:A:588:LEU:O	2.17	0.45
1:B:398:ARG:O	1:B:401:PHE:HD2	1.99	0.45
1:B:14:GLU:HA	1:B:14:GLU:OE1	2.16	0.45
1:B:118:VAL:N	1:B:119:PRO:HD2	2.32	0.45
1:B:496:VAL:C	1:B:498:GLY:H	2.20	0.45
1:A:494:GLN:O	1:A:498:GLY:N	2.50	0.45
1:A:311:ASP:OD2	1:A:314:SER:HB2	2.17	0.45
1:A:229:LEU:C	1:A:229:LEU:HD23	2.37	0.45
1:A:64:GLY:C	1:A:65:ARG:HG3	2.37	0.44
1:B:49:VAL:O	1:B:49:VAL:HG13	2.17	0.44
1:B:497:THR:HG22	1:B:497:THR:O	2.17	0.44
1:B:429:THR:O	1:B:592:HIS:HB3	2.16	0.44
1:A:64:GLY:O	1:A:65:ARG:HG3	2.16	0.44
1:A:26:ASN:HB2	1:A:32:LEU:CD2	2.37	0.44
1:A:37:GLY:HA2	1:A:40:THR:OG1	2.17	0.44
1:B:44:ASP:C	1:B:46:GLY:H	2.20	0.44
1:A:501:GLY:O	1:A:502:GLU:HB3	2.18	0.44
1:A:7:LEU:CD1	1:A:7:LEU:N	2.78	0.44
1:A:429:THR:HG22	1:A:430:GLN:N	2.32	0.44
1:B:477:MET:C	1:B:478:LYS:HD2	2.37	0.44
1:A:246:ASN:ND2	1:A:592:HIS:NE2	2.62	0.44
1:B:82:ILE:HD11	1:B:85:ASP:OD1	2.17	0.44
1:A:103:ASN:O	1:A:104:LEU:HD23	2.17	0.44
1:B:495:TYR:CD1	1:B:500:ILE:HD11	2.47	0.44
1:A:98:ARG:HD3	1:A:166:ASP:OD2	2.17	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:546:ARG:O	1:B:549:VAL:N	2.50	0.44
1:A:239:ILE:HG22	1:A:243:ASP:OD2	2.17	0.44
1:A:80:ARG:HB2	1:A:80:ARG:HE	1.45	0.44
1:A:187:ASP:HB3	1:B:184:ALA:HB2	1.99	0.44
1:A:103:ASN:O	1:A:104:LEU:HG	2.17	0.44
1:B:22:ALA:CA	1:B:25:LEU:CD2	2.92	0.44
1:A:237:GLY:O	1:A:241:LEU:HG	2.18	0.44
1:B:156:ALA:CB	1:B:157:LYS:HE3	2.41	0.44
1:B:471:HIS:ND1	1:B:472:PRO:CD	2.81	0.44
1:A:436:TYR:CE2	1:A:555:ILE:HG21	2.53	0.44
1:A:102:CYS:HB3	1:A:133:LEU:HD21	2.00	0.44
1:B:257:ALA:O	1:B:258:LEU:HD23	2.18	0.44
1:A:407:LYS:O	1:A:409:LYS:HD3	2.17	0.44
1:A:250:LEU:HD11	1:A:425:ALA:HA	1.98	0.44
1:B:89:MET:HE1	1:B:96:LEU:HD23	1.99	0.44
1:B:169:VAL:O	1:B:173:ARG:HG3	2.17	0.44
1:A:10:LEU:HD13	1:A:42:LEU:HD11	2.00	0.44
1:B:467:TRP:HA	1:B:467:TRP:CE3	2.53	0.44
1:B:7:LEU:HD21	1:B:95:SER:HB3	2.00	0.44
1:B:164:ASP:OD2	1:B:166:ASP:HB3	2.17	0.44
1:A:286:GLN:C	1:A:288:CYS:H	2.21	0.44
1:B:71:PRO:O	1:B:75:ALA:CB	2.66	0.43
1:A:245:LEU:HD22	1:A:245:LEU:N	2.33	0.43
1:A:490:ASN:O	1:A:491:ALA:C	2.56	0.43
1:A:385:LEU:HD22	1:B:227:LEU:CD2	2.48	0.43
1:A:432:ASN:HD21	1:A:455:CYS:HB2	1.83	0.43
1:A:148:ASP:OD1	1:A:150:ALA:CB	2.59	0.43
1:A:163:LYS:N	1:A:163:LYS:NZ	2.66	0.43
1:B:473:ARG:HD2	1:B:520:LEU:HD21	2.01	0.43
1:A:281:SER:OG	1:A:284:GLU:HB2	2.19	0.43
1:B:509:TRP:HE3	1:B:510:GLN:HG2	1.83	0.43
1:A:192:ASP:HA	1:A:195:ARG:NH2	2.33	0.43
1:B:311:ASP:OD1	1:B:314:SER:HB2	2.17	0.43
1:A:308:ARG:HG3	1:A:315:SER:HB3	2.01	0.43
1:A:89:MET:HE3	1:A:94:PHE:HB2	2.01	0.43
1:B:21:PHE:O	1:B:25:LEU:HD23	2.17	0.43
1:A:451:SER:HB3	1:A:454:HIS:CG	2.54	0.43
1:A:219:GLN:NE2	1:B:388:MET:CE	2.82	0.43
1:B:164:ASP:C	1:B:165:LYS:HG2	2.38	0.43
1:B:328:VAL:HG21	1:B:350:GLU:OE1	2.18	0.43
1:A:352:LEU:O	1:A:352:LEU:HD12	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:286:GLN:HG2	1:B:291:HIS:HB2	2.00	0.43
1:A:298:THR:OG1	1:A:327:ASP:OD2	2.24	0.43
1:A:382:LEU:CD2	1:B:242:CYS:HA	2.48	0.43
1:B:347:TYR:OH	1:B:366:LEU:O	2.28	0.43
1:A:268:HIS:NE2	1:B:432:ASN:HB3	2.33	0.43
1:A:463:ALA:O	1:A:466:TRP:HB3	2.19	0.43
1:A:197:GLU:OE1	1:A:197:GLU:HA	2.19	0.43
1:B:30:LEU:HD21	1:B:98:ARG:HD2	2.01	0.43
1:B:502:GLU:H	1:B:502:GLU:HG2	1.45	0.43
1:A:429:THR:CG2	1:A:447:ALA:HB2	2.49	0.43
1:A:27:ALA:C	1:A:28:LEU:HD12	2.38	0.43
1:B:17:GLY:O	1:B:18:LEU:C	2.57	0.43
1:B:174:HIS:O	1:B:178:LYS:HG3	2.18	0.43
1:A:484:LYS:HB2	1:A:487:GLU:HG3	2.01	0.43
1:B:478:LYS:N	1:B:478:LYS:CD	2.82	0.43
1:B:520:LEU:O	1:B:525:LYS:HE3	2.19	0.43
1:A:330:THR:O	1:A:334:ILE:HG13	2.19	0.43
1:B:445:ILE:HG23	1:B:445:ILE:O	2.18	0.43
1:A:89:MET:HE3	1:A:94:PHE:CB	2.49	0.43
1:B:474:VAL:CA	1:B:477:MET:HG3	2.45	0.43
1:A:130:VAL:O	1:A:134:ARG:HG3	2.19	0.43
1:A:385:LEU:HD21	1:B:228:PRO:HD2	2.01	0.43
1:A:81:ASN:O	1:A:81:ASN:CG	2.56	0.43
1:A:245:LEU:O	1:A:249:GLN:HG3	2.18	0.42
1:A:162:SER:O	1:A:165:LYS:N	2.51	0.42
1:B:118:VAL:HB	1:B:119:PRO:CD	2.49	0.42
1:B:195:ARG:HB3	1:B:204:GLN:HB2	2.01	0.42
1:A:419:LEU:HD23	1:A:536:SER:HB3	2.01	0.42
1:B:121:ALA:C	1:B:124:LYS:HB2	2.39	0.42
1:B:281:SER:HB2	4:B:2018:HOH:O	2.19	0.42
1:B:504:GLU:O	1:B:507:VAL:HB	2.19	0.42
1:B:18:LEU:O	1:B:19:VAL:C	2.56	0.42
1:A:89:MET:O	1:A:93:ASP:N	2.52	0.42
1:A:40:THR:HA	1:A:43:ARG:NH2	2.34	0.42
1:A:249:GLN:O	1:A:253:GLU:HG3	2.19	0.42
1:A:398:ARG:CB	1:A:398:ARG:NH1	2.83	0.42
1:B:399:SER:O	1:B:402:LYS:HG2	2.18	0.42
1:A:247:ALA:HB2	1:A:266:PHE:CD1	2.54	0.42
1:B:269:VAL:O	1:B:269:VAL:HG12	2.18	0.42
1:B:237:GLY:O	1:B:241:LEU:HG	2.19	0.42
1:A:15:LYS:O	1:A:18:LEU:CB	2.67	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:GLU:O	1:A:23:ARG:HB3	2.20	0.42
1:B:140:HIS:O	1:B:141:ALA:C	2.58	0.42
1:B:58:PHE:CD2	1:B:59:PRO:HD2	2.55	0.42
1:A:404:ILE:HG12	1:A:584:ILE:HG12	2.02	0.42
1:A:200:LYS:CD	1:A:200:LYS:C	2.85	0.42
1:A:59:PRO:HG3	1:B:92:GLN:OE1	2.20	0.42
1:A:196:LYS:HD3	1:A:219:GLN:NE2	2.34	0.42
1:A:572:VAL:O	1:A:575:ALA:HB3	2.19	0.42
1:A:523:ALA:HA	1:A:526:LYS:HE3	2.00	0.42
1:A:65:ARG:NH2	1:B:138:LYS:HE2	2.33	0.42
1:A:555:ILE:O	1:A:555:ILE:HG13	2.19	0.42
1:B:33:ILE:HD13	1:B:55:LEU:HG	2.01	0.42
1:B:98:ARG:HG2	1:B:98:ARG:O	2.20	0.42
1:B:222:THR:O	1:B:222:THR:HG23	2.18	0.42
1:A:467:TRP:CD1	1:A:529:ILE:HA	2.54	0.42
1:B:286:GLN:HG2	1:B:291:HIS:CG	2.55	0.42
1:A:553:LYS:O	1:A:554:ARG:C	2.57	0.42
1:A:452:ARG:HG3	1:A:548:ASN:OD1	2.19	0.42
1:B:267:LYS:O	1:B:268:HIS:HB2	2.20	0.42
1:A:379:ILE:CG1	1:A:388:MET:HG3	2.25	0.42
1:A:470:HIS:O	1:A:471:HIS:C	2.57	0.42
1:A:18:LEU:O	1:A:21:PHE:N	2.51	0.42
1:B:287:VAL:HG11	1:B:470:HIS:CE1	2.55	0.42
1:A:282:GLU:HG3	1:A:291:HIS:CE1	2.54	0.42
1:A:280:LEU:HD12	1:A:280:LEU:N	2.35	0.42
1:B:25:LEU:HD23	1:B:25:LEU:H	1.85	0.42
1:B:107:PHE:O	1:B:108:VAL:C	2.58	0.42
1:A:419:LEU:HA	1:A:419:LEU:HD23	1.87	0.42
1:B:80:ARG:HD2	1:B:82:ILE:HD13	2.01	0.41
1:B:71:PRO:O	1:B:75:ALA:HB2	2.20	0.41
1:A:330:THR:HG22	1:A:334:ILE:HD12	2.02	0.41
1:A:412:PRO:C	1:A:414:SER:N	2.72	0.41
1:B:196:LYS:HG2	1:B:204:GLN:NE2	2.34	0.41
1:B:97:VAL:O	1:B:142:ARG:NH1	2.53	0.41
1:A:467:TRP:NE1	1:A:528:TRP:O	2.48	0.41
1:B:89:MET:CE	1:B:96:LEU:HD23	2.50	0.41
1:B:436:TYR:CE2	1:B:555:ILE:HG21	2.55	0.41
1:B:464:ASN:HD22	1:B:555:ILE:CD1	2.33	0.41
1:B:553:LYS:O	1:B:555:ILE:N	2.52	0.41
1:B:108:VAL:CG2	1:B:109:LYS:N	2.83	0.41
1:A:386:GLN:HG2	1:B:221:TYR:O	2.20	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:574:GLU:O	1:A:578:GLU:HG2	2.20	0.41
1:B:81:ASN:CG	1:B:81:ASN:O	2.58	0.41
1:B:532:LEU:HA	1:B:532:LEU:HD12	1.74	0.41
1:A:149:PRO:C	1:A:151:ASP:N	2.73	0.41
1:A:356:SER:O	1:A:361:GLY:HA2	2.20	0.41
1:B:393:ASN:O	1:B:394:ALA:C	2.58	0.41
1:B:539:SER:HB2	1:B:543:PHE:CZ	2.55	0.41
1:A:138:LYS:C	1:A:140:HIS:H	2.23	0.41
1:B:313:MET:C	1:B:315:SER:N	2.74	0.41
1:A:520:LEU:H	1:A:520:LEU:CD1	2.13	0.41
1:B:153:SER:HA	1:B:157:LYS:HZ1	1.84	0.41
1:B:553:LYS:C	1:B:555:ILE:H	2.22	0.41
1:B:537:LEU:HD22	1:B:560:ILE:HG23	2.02	0.41
1:A:566:SER:C	1:A:568:ALA:N	2.73	0.41
1:A:493:ASP:O	1:A:494:GLN:C	2.59	0.41
1:A:87:ALA:O	1:A:90:ASN:HB2	2.20	0.41
1:A:267:LYS:HG2	1:B:450:GLN:HB3	2.02	0.41
1:A:7:LEU:HB3	1:A:8:ALA:H	1.57	0.41
1:B:480:LYS:N	1:B:512:MET:O	2.46	0.41
1:B:250:LEU:HG	1:B:424:ILE:HG22	2.03	0.41
1:B:453:ILE:HG13	1:B:453:ILE:O	2.20	0.41
1:B:108:VAL:CG2	1:B:109:LYS:H	2.33	0.41
1:A:412:PRO:HD2	1:A:415:ALA:HB2	2.02	0.41
1:B:449:GLN:NE2	1:B:449:GLN:HA	2.35	0.41
1:B:22:ALA:O	1:B:23:ARG:C	2.59	0.41
1:A:378:GLU:HG3	1:A:391:ARG:CB	2.47	0.41
1:A:495:TYR:C	1:A:497:THR:H	2.23	0.41
1:A:236:PRO:HB3	1:A:364:CYS:SG	2.61	0.41
1:A:212:ASN:OD1	1:B:591:PHE:HB2	2.21	0.41
1:B:590:LEU:HD23	1:B:590:LEU:HA	1.91	0.41
1:A:418:ASP:OD1	1:A:418:ASP:N	2.54	0.41
1:B:6:GLN:O	1:B:30:LEU:HD23	2.21	0.41
1:A:467:TRP:CE3	1:A:467:TRP:HA	2.55	0.41
1:B:566:SER:C	1:B:568:ALA:N	2.72	0.41
1:A:13:SER:HB3	1:A:103:ASN:ND2	2.36	0.41
1:B:26:ASN:CA	1:B:32:LEU:HD21	2.50	0.41
1:B:280:LEU:N	1:B:280:LEU:CD1	2.80	0.41
1:B:331:ALA:O	1:B:333:ILE:N	2.53	0.41
1:B:575:ALA:O	1:B:578:GLU:HG2	2.21	0.41
1:B:241:LEU:O	1:B:245:LEU:HG	2.20	0.41
1:B:406:THR:HG23	1:B:583:LEU:HB3	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ALA:O	1:A:124:LYS:HB2	2.21	0.41
1:A:347:TYR:CD1	1:A:347:TYR:N	2.88	0.41
1:A:16:ALA:O	1:A:18:LEU:N	2.54	0.40
1:A:10:LEU:HD12	1:A:42:LEU:HD11	2.02	0.40
1:A:271:PRO:HD2	1:A:429:THR:HA	2.03	0.40
1:A:494:GLN:HA	1:A:499:THR:OG1	2.21	0.40
1:B:575:ALA:HA	1:B:578:GLU:HG2	2.03	0.40
1:B:360:ASN:HA	1:B:360:ASN:HD22	1.70	0.40
1:A:65:ARG:HB3	1:A:66:VAL:H	1.68	0.40
1:A:254:LEU:HD23	1:A:254:LEU:HA	1.87	0.40
1:B:164:ASP:O	1:B:165:LYS:CG	2.68	0.40
1:B:35:SER:N	1:B:39:ALA:HB2	2.37	0.40
1:A:7:LEU:CD2	1:A:33:ILE:HD11	2.49	0.40
1:A:523:ALA:N	1:A:526:LYS:HE2	2.34	0.40
1:A:39:ALA:O	1:A:40:THR:C	2.59	0.40
1:B:464:ASN:HD21	1:B:555:ILE:HD13	1.79	0.40
1:A:7:LEU:HA	1:A:31:GLY:H	1.85	0.40
1:A:520:LEU:CD1	1:A:525:LYS:HE2	2.47	0.40
1:B:583:LEU:HD12	1:B:584:ILE:H	1.81	0.40
1:A:103:ASN:O	1:A:104:LEU:CD2	2.70	0.40
1:A:71:PRO:O	1:A:75:ALA:N	2.46	0.40
1:A:55:LEU:CD2	1:A:72:ALA:HB1	2.49	0.40
1:A:464:ASN:HD22	1:A:555:ILE:CD1	2.32	0.40
1:B:473:ARG:NH1	1:B:524:GLU:OE2	2.53	0.40
1:A:219:GLN:HE21	1:B:388:MET:CE	2.34	0.40
1:B:446:GLY:CA	1:B:458:LEU:HD22	2.52	0.40
1:A:144:THR:HG21	1:A:167:THR:HG21	2.04	0.40
1:A:229:LEU:HD23	1:A:229:LEU:O	2.21	0.40
1:B:546:ARG:HA	1:B:549:VAL:HG23	2.03	0.40

All (4) 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:B:47:LEU:O	1:B:47:LEU:O[2_656]	1.94	0.26
1:B:46:GLY:O	1:B:48:PRO:C[2_656]	2.02	0.18
1:B:46:GLY:CA	1:B:49:VAL:O[2_656]	2.07	0.13
1:B:46:GLY:O	1:B:48:PRO:CA[2_656]	2.11	0.09

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	589/593 (99%)	464 (79%)	90 (15%)	35 (6%)	2	6
1	B	588/593 (99%)	484 (82%)	75 (13%)	29 (5%)	3	10
All	All	1177/1186 (99%)	948 (80%)	165 (14%)	64 (5%)	2	7

All (64) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	SER
1	A	18	LEU
1	A	19	VAL
1	A	40	THR
1	A	66	VAL
1	A	83	PRO
1	A	114	PRO
1	A	152	TYR
1	A	403	ASN
1	B	18	LEU
1	B	114	PRO
1	B	152	TYR
1	B	164	ASP
1	B	477	MET
1	B	484	LYS
1	B	503	ASP
1	A	36	GLY
1	A	67	LYS
1	A	269	VAL
1	A	402	LYS
1	A	477	MET
1	A	479	PHE
1	A	492	ILE
1	A	502	GLU
1	B	19	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	60	GLU
1	B	67	LYS
1	B	73	VAL
1	B	269	VAL
1	B	489	SER
1	B	554	ARG
1	A	41	ALA
1	A	162	SER
1	A	491	ALA
1	A	499	THR
1	B	27	ALA
1	B	316	PHE
1	A	5	GLN
1	A	17	GLY
1	A	160	ALA
1	A	311	ASP
1	A	316	PHE
1	A	493	ASP
1	B	59	PRO
1	B	394	ALA
1	B	476	SER
1	A	73	VAL
1	A	153	SER
1	A	411	LEU
1	B	153	SER
1	B	277	GLY
1	B	332	LYS
1	B	404	ILE
1	B	497	THR
1	A	113	SER
1	B	71	PRO
1	B	315	SER
1	B	526	LYS
1	B	567	ALA
1	A	496	VAL
1	B	488	VAL
1	A	290	VAL
1	A	71	PRO
1	A	106	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	485/485 (100%)	450 (93%)	35 (7%)	18	46
1	B	484/485 (100%)	446 (92%)	38 (8%)	15	41
All	All	969/970 (100%)	896 (92%)	73 (8%)	17	44

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	LEU
1	A	11	SER
1	A	18	LEU
1	A	21	PHE
1	A	24	SER
1	A	32	LEU
1	A	43	ARG
1	A	54	ASP
1	A	68	THR
1	A	70	HIS
1	A	83	PRO
1	A	103	ASN
1	A	151	ASP
1	A	154	SER
1	A	159	MET
1	A	163	LYS
1	A	164	ASP
1	A	170	GLU
1	A	177	LEU
1	A	187	ASP
1	A	208	ARG
1	A	255	LYS
1	A	340	ASP
1	A	359	LYS
1	A	360	ASN
1	A	386	GLN
1	A	406	THR

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	432	ASN
1	A	477	MET
1	A	502	GLU
1	A	504	GLU
1	A	520	LEU
1	A	522	GLU
1	A	524	GLU
1	A	547	ASP
1	B	5	GLN
1	B	7	LEU
1	B	9	LEU
1	B	11	SER
1	B	19	VAL
1	B	54	ASP
1	B	56	THR
1	B	60	GLU
1	B	61	MET
1	B	68	THR
1	B	114	PRO
1	B	154	SER
1	B	157	LYS
1	B	167	THR
1	B	170	GLU
1	B	177	LEU
1	B	199	SER
1	B	280	LEU
1	B	282	GLU
1	B	292	ASP
1	B	293	LEU
1	B	294	HIS
1	B	296	THR
1	B	314	SER
1	B	338	VAL
1	B	349	GLU
1	B	375	ASP
1	B	382	LEU
1	B	391	ARG
1	B	399	SER
1	B	408	ASN
1	B	478	LYS
1	B	483	VAL
1	B	485	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	499	THR
1	B	502	GLU
1	B	506	LEU
1	B	517	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (29) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	5	GLN
1	A	70	HIS
1	A	81	ASN
1	A	86	ASN
1	A	174	HIS
1	A	185	GLN
1	A	286	GLN
1	A	291	HIS
1	A	294	HIS
1	A	386	GLN
1	A	403	ASN
1	A	432	ASN
1	A	450	GLN
1	A	464	ASN
1	A	510	GLN
1	A	519	GLN
1	B	5	GLN
1	B	70	HIS
1	B	86	ASN
1	B	185	GLN
1	B	360	ASN
1	B	393	ASN
1	B	403	ASN
1	B	408	ASN
1	B	454	HIS
1	B	464	ASN
1	B	494	GLN
1	B	510	GLN
1	B	527	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
3	203	B	1595	-	7,13,13	9.24	5 (71%)	3,20,20	3.22	3 (100%)

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
3	203	B	1595	-	-	0/0/14/14	0/1/2/2

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1595	203	C13-C14	-2.32	1.41	1.44
3	B	1595	203	C13-C18	4.51	1.55	1.47
3	B	1595	203	C14-N15	4.68	1.42	1.37
3	B	1595	203	O21-S16	12.55	1.57	1.43
3	B	1595	203	O20-S16	19.71	1.65	1.43

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1595	203	O19-C18-C13	-4.25	117.98	124.93
3	B	1595	203	C13-C18-N17	2.45	117.49	113.69
3	B	1595	203	O19-C18-N17	2.64	124.53	120.78

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	1595	203	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	590/593 (99%)	0.43	15 (2%) 61 55	22, 43, 66, 74	0
1	B	590/593 (99%)	0.55	31 (5%) 30 23	27, 46, 63, 72	0
All	All	1180/1186 (99%)	0.49	46 (3%) 43 36	22, 45, 65, 74	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	53	SER	4.5
1	B	54	ASP	4.1
1	A	59	PRO	4.0
1	A	64	GLY	3.8
1	B	96	LEU	3.7
1	A	31	GLY	3.7
1	B	231	VAL	3.5
1	A	43	ARG	3.4
1	B	130	VAL	3.1
1	B	160	ALA	3.1
1	B	8	ALA	3.0
1	B	59	PRO	2.9
1	A	87	ALA	2.9
1	B	90	ASN	2.9
1	A	39	ALA	2.9
1	A	72	ALA	2.9
1	A	4	ARG	2.7
1	B	46	GLY	2.6
1	B	89	MET	2.6
1	A	29	GLY	2.6
1	B	10	LEU	2.6
1	B	511	ALA	2.6
1	B	512	MET	2.6
1	B	91	LYS	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	48	PRO	2.4
1	B	88	ASP	2.4
1	B	61	MET	2.4
1	B	87	ALA	2.3
1	B	100	VAL	2.3
1	B	362	GLY	2.3
1	A	44	ASP	2.3
1	A	47	LEU	2.3
1	B	133	LEU	2.3
1	A	10	LEU	2.3
1	A	95	SER	2.2
1	B	63	GLY	2.2
1	A	91	LYS	2.2
1	B	49	VAL	2.2
1	B	581	ILE	2.2
1	B	57	GLY	2.2
1	B	555	ILE	2.2
1	B	55	LEU	2.2
1	B	99	VAL	2.2
1	B	33	ILE	2.1
1	A	479	PHE	2.1
1	B	182	HIS	2.1

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 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
2	K	A	1594	1/1	0.79	0.30	1.92	56,56,56,56	0
3	203	B	1595	12/12	0.71	0.24	-0.20	68,71,74,74	0
2	K	B	1594	1/1	0.82	0.18	-1.75	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.