



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:24 AM GMT

PDB ID : 3IB9
Title : Propionyl-CoA Carboxylase Beta Subunit, D422L
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Deposited on : 2009-07-15
Resolution : 2.00 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

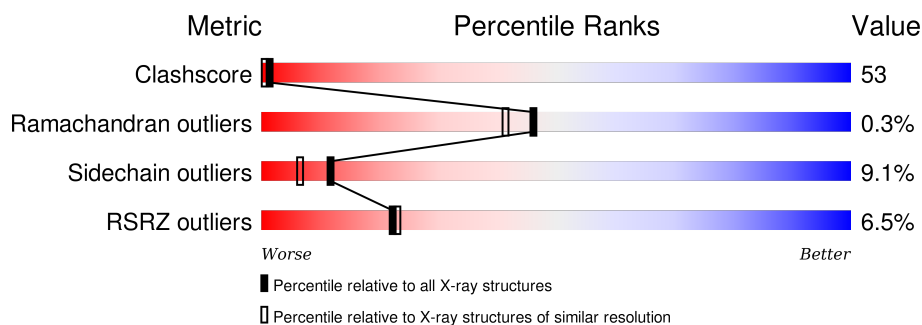
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	530	
1	B	530	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 8285 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.

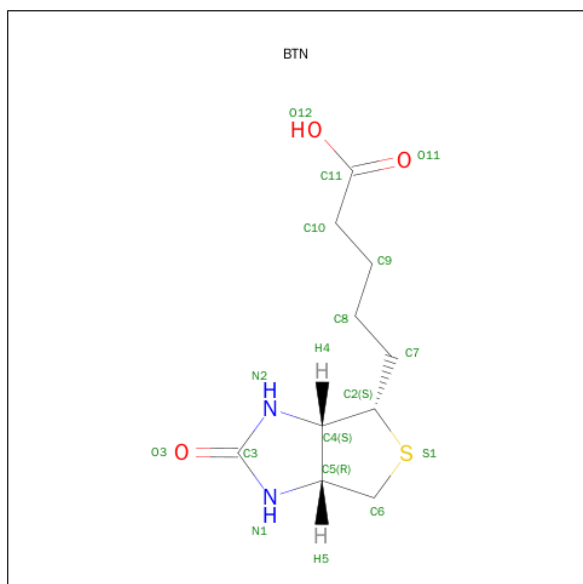
- Molecule 1 is a protein called Propionyl-CoA carboxylase complex B subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	521	Total	C	N	O	S	0	0	0
			3952	2483	698	758	13			
1	B	521	Total	C	N	O	S	0	0	0
			3952	2483	698	758	13			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	422	LEU	ASP	ENGINEERED	UNP Q9X4K7
B	422	LEU	ASP	ENGINEERED	UNP Q9X4K7

- Molecule 2 is BIOTIN (three-letter code: BTN) (formula: C₁₀H₁₆N₂O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			16	10	2	3	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			16	10	2	3	1		

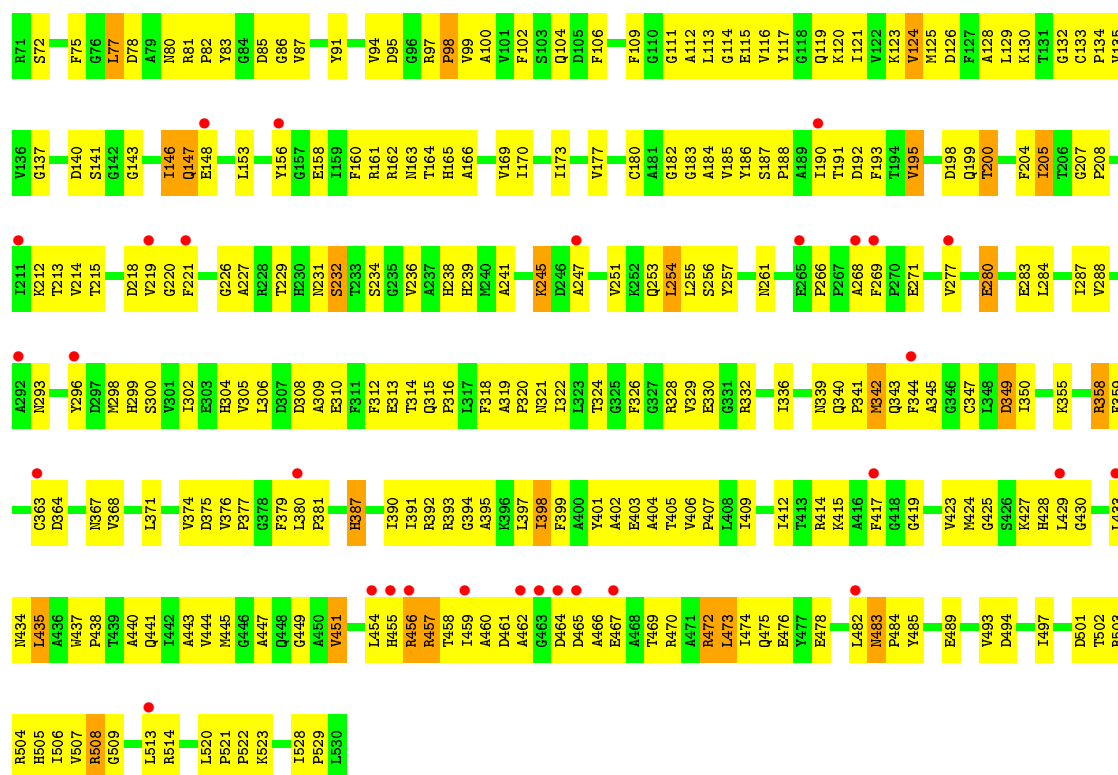
- Molecule 3 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	167	Total	O	0	0
			167	167		
4	B	172	Total	O	0	0
			172	172		



4 Data and refinement statistics

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	168.49 Å 168.49 Å 80.31 Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	50.00 – 2.00 29.60 – 1.90	Depositor EDS
% Data completeness (in resolution range)	75.7 (50.00-2.00) 70.8 (29.60-1.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.86 (at 1.89 Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.246 , 0.274 0.302 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	18.9	Xtriage
Anisotropy	0.168	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 31.2	EDS
Estimated twinning fraction	0.018 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.53$, $\langle L^2 \rangle = 0.37$	Xtriage
Outliers	10 of 91097 reflections (0.011%)	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	8285	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.00% 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: BTN, SO4

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	0.23	0/4032	0.49	2/5478 (0.0%)
1	B	0.24	0/4032	0.49	0/5478
All	All	0.24	0/8064	0.49	2/10956 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	178	GLY	C-N-CD	-5.88	107.67	120.60
1	A	149	GLY	N-CA-C	5.04	125.69	113.10

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	3952	0	3887	461	0
1	B	3952	0	3887	432	0
2	A	16	0	15	2	0
2	B	16	0	15	2	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	167	0	0	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	172	0	0	13	0
All	All	8285	0	7804	842	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 53.

All (842) 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:87:VAL:HB	1:A:117:TYR:CE2	1.33	1.57
1:A:456:ARG:NH1	1:A:457:ARG:HH22	1.30	1.29
1:A:87:VAL:HB	1:A:117:TYR:CD2	1.68	1.26
1:B:113:LEU:HD13	1:B:156:TYR:CE1	1.72	1.25
1:A:456:ARG:NH1	1:A:457:ARG:NH2	1.91	1.18
1:A:212:LYS:HD3	1:A:218:ASP:OD1	1.40	1.18
1:A:397:LEU:HD23	1:A:423:VAL:CG1	1.73	1.17
1:B:113:LEU:HD22	1:B:156:TYR:CE1	1.81	1.15
1:A:87:VAL:CB	1:A:117:TYR:CE2	2.30	1.15
1:B:113:LEU:CD1	1:B:156:TYR:HE1	1.62	1.13
1:A:362:THR:O	1:A:366:PHE:HD2	1.33	1.11
1:B:21:LEU:O	1:B:25:ILE:HG22	1.50	1.11
1:B:193:PHE:HA	1:B:238:HIS:CE1	1.87	1.10
1:B:457:ARG:CG	1:B:457:ARG:HH11	1.65	1.10
1:B:397:LEU:HD23	1:B:423:VAL:CG1	1.82	1.09
1:A:187:SER:HB3	1:A:188:PRO:HD3	1.34	1.09
1:A:146:ILE:HG22	1:B:454:LEU:HD11	1.35	1.08
1:A:203:MET:HB2	1:A:230:HIS:NE2	1.68	1.08
1:A:160:PHE:HE1	1:A:187:SER:HB2	1.18	1.08
1:B:113:LEU:HB3	1:B:156:TYR:OH	1.53	1.08
1:A:104:GLN:HG2	1:A:117:TYR:OH	1.54	1.07
1:A:478:GLU:HA	1:A:482:LEU:CD1	1.84	1.07
1:B:349:ASP:CB	1:B:380:LEU:HD12	1.85	1.07
1:A:478:GLU:CA	1:A:482:LEU:HD13	1.85	1.07
1:A:390:ILE:HG21	1:B:205:ILE:HD11	1.12	1.07
1:A:87:VAL:CB	1:A:117:TYR:CD2	2.38	1.05
1:B:392:ARG:HG3	1:B:393:ARG:HG3	1.39	1.05
1:B:113:LEU:HD13	1:B:156:TYR:HE1	0.89	1.04
1:A:146:ILE:CG2	1:B:454:LEU:HD11	1.86	1.04
1:A:478:GLU:HA	1:A:482:LEU:HD13	1.04	1.03
1:A:87:VAL:HB	1:A:117:TYR:HE2	1.21	1.02
1:B:397:LEU:HD23	1:B:423:VAL:HG11	1.39	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:457:ARG:HG2	1:B:457:ARG:HH11	0.88	1.02
1:B:509:GLY:O	1:B:513:LEU:HG	1.60	1.00
1:B:347:CYS:SG	1:B:377:PRO:HG2	2.01	0.99
1:A:215:THR:HG21	4:A:575:HOH:O	1.62	0.99
1:A:397:LEU:HD23	1:A:423:VAL:HG11	1.44	0.99
1:A:160:PHE:CE1	1:A:187:SER:HB2	1.98	0.98
1:A:32:GLY:HA3	1:A:107:THR:HG21	1.43	0.98
1:B:349:ASP:HB2	1:B:380:LEU:HD12	1.42	0.98
1:A:32:GLY:HA3	1:A:107:THR:CG2	1.94	0.97
1:A:10:ASP:O	1:A:16:GLY:HA3	1.63	0.97
1:A:395:ALA:O	1:A:398:ILE:HG23	1.63	0.96
1:A:113:LEU:HD12	1:A:117:TYR:HD1	1.30	0.96
1:B:87:VAL:HB	1:B:117:TYR:CE2	2.00	0.96
1:B:257:TYR:CE1	1:B:328:ARG:NH1	2.34	0.95
1:B:98:PRO:O	1:B:99:VAL:HG23	1.67	0.94
1:A:405:THR:HG21	1:A:518:GLU:O	1.66	0.94
1:A:231:ASN:OD1	1:A:240:MET:HB2	1.66	0.94
1:B:326:PHE:HE1	1:B:363:CYS:HG	0.94	0.94
1:A:377:PRO:HG3	1:A:415:LYS:HD3	1.50	0.93
1:A:392:ARG:HG3	1:A:393:ARG:HG3	1.48	0.93
1:A:390:ILE:HG21	1:B:205:ILE:CD1	1.96	0.93
1:A:99:VAL:HG22	1:A:134:PRO:HB2	1.50	0.93
1:B:470:ARG:O	1:B:474:ILE:HG13	1.69	0.93
1:B:445:MET:HE2	1:B:449:GLY:C	1.88	0.93
1:B:198:ASP:OD1	1:B:199:GLN:HG2	1.67	0.93
1:A:362:THR:O	1:A:366:PHE:CD2	2.22	0.92
1:B:187:SER:HB3	1:B:188:PRO:HD3	1.51	0.92
1:A:193:PHE:HA	1:A:238:HIS:CE1	2.04	0.92
1:A:483:ASN:HB2	1:A:484:PRO:HD2	1.50	0.92
1:A:451:VAL:HG21	1:A:474:ILE:HG12	1.51	0.91
1:B:440:ALA:O	1:B:484:PRO:HD3	1.71	0.91
1:B:200:THR:HG23	1:B:200:THR:O	1.70	0.91
1:B:113:LEU:CD2	1:B:156:TYR:CE1	2.54	0.91
1:A:380:LEU:HD22	1:A:381:PRO:HD2	1.49	0.90
1:A:467:GLU:HG3	1:A:470:ARG:HH21	1.34	0.90
1:B:457:ARG:HG2	1:B:457:ARG:NH1	1.62	0.90
1:A:87:VAL:CG1	1:A:117:TYR:CD2	2.54	0.90
1:B:241:ALA:HB3	1:B:247:ALA:HB2	1.53	0.89
1:A:457:ARG:CG	1:A:457:ARG:HH11	1.85	0.88
1:B:409:ILE:HD11	1:B:513:LEU:HD12	1.54	0.88
1:A:196:MET:SD	1:A:203:MET:HE2	2.13	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:ASN:HB3	1:B:190:ILE:HG21	1.55	0.88
1:B:315:GLN:OE1	1:B:355:LYS:HG3	1.74	0.88
1:A:265:GLU:HG2	1:A:266:PRO:HD2	1.56	0.88
1:A:398:ILE:CD1	1:B:160:PHE:HB3	2.03	0.88
1:B:528:ILE:HG12	1:B:529:PRO:HD2	1.56	0.87
1:A:447:ALA:HB2	1:A:482:LEU:HD21	1.57	0.87
1:A:113:LEU:HD12	1:A:117:TYR:CD1	2.09	0.87
1:A:212:LYS:CD	1:A:218:ASP:OD1	2.23	0.87
1:B:113:LEU:CD1	1:B:156:TYR:CE1	2.47	0.87
1:A:147:GLN:H	1:A:147:GLN:HE21	1.15	0.87
1:B:528:ILE:CG1	1:B:529:PRO:HD2	2.04	0.86
1:A:456:ARG:HH11	1:A:457:ARG:HH22	0.86	0.86
1:A:397:LEU:CD2	1:A:423:VAL:CG1	2.53	0.86
1:A:405:THR:CG2	1:A:518:GLU:O	2.22	0.86
1:A:391:ILE:HG13	4:A:602:HOH:O	1.75	0.86
1:A:86:GLY:O	1:A:117:TYR:CE2	2.29	0.86
1:A:511:ARG:O	1:A:514:ARG:HG2	1.75	0.86
1:B:397:LEU:CD2	1:B:423:VAL:CG1	2.53	0.85
1:B:113:LEU:HB3	1:B:156:TYR:CZ	2.11	0.85
1:A:447:ALA:O	1:A:451:VAL:HG13	1.76	0.85
1:A:104:GLN:CG	1:A:117:TYR:OH	2.25	0.85
1:A:451:VAL:HG11	1:A:474:ILE:HA	1.59	0.85
1:B:245:LYS:HB2	1:B:245:LYS:HZ3	1.42	0.85
1:A:85:ASP:O	1:A:117:TYR:HB2	1.77	0.84
1:A:459:ILE:CD1	1:A:470:ARG:HB2	2.06	0.84
1:B:113:LEU:HG	1:B:117:TYR:CD1	2.11	0.84
1:B:25:ILE:HD12	4:B:644:HOH:O	1.77	0.84
1:A:117:TYR:O	1:A:117:TYR:CD1	2.30	0.84
1:B:70:HIS:CE1	1:B:81:ARG:HG2	2.14	0.83
1:A:503:ARG:O	1:A:507:VAL:HG23	1.80	0.82
1:B:98:PRO:O	1:B:99:VAL:CG2	2.27	0.82
1:B:269:PHE:CD2	1:B:269:PHE:O	2.32	0.82
1:B:302:ILE:O	1:B:305:VAL:HG22	1.80	0.82
1:A:456:ARG:HH11	1:A:457:ARG:NH2	1.60	0.82
1:A:315:GLN:OE1	1:A:355:LYS:HG3	1.79	0.81
1:B:102:PHE:CZ	1:B:137:GLY:HA3	2.14	0.81
1:A:287:ILE:HG12	1:A:287:ILE:O	1.79	0.81
1:B:455:HIS:NE2	1:B:473:LEU:HG	1.95	0.81
1:B:170:ILE:HG22	1:B:261:ASN:HB3	1.62	0.81
1:A:341:PRO:HG3	1:A:375:ASP:OD2	1.81	0.81
1:B:86:GLY:O	1:B:117:TYR:HE2	1.64	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:149:GLY:O	1:B:444:VAL:HG23	1.81	0.81
1:A:113:LEU:O	1:A:145:ARG:HB2	1.79	0.80
1:A:70:HIS:HD2	1:A:72:SER:H	1.30	0.80
1:B:398:ILE:HG13	1:B:399:PHE:N	1.95	0.80
1:B:326:PHE:HE1	1:B:363:CYS:SG	2.05	0.80
1:A:175:LEU:HD22	1:A:177:VAL:HG13	1.63	0.80
1:B:475:GLN:HA	1:B:478:GLU:OE1	1.82	0.80
1:A:520:LEU:HD22	1:B:165:HIS:CD2	2.16	0.79
1:B:200:THR:CG2	1:B:200:THR:O	2.30	0.79
1:A:98:PRO:O	1:A:99:VAL:HG23	1.83	0.79
1:A:149:GLY:O	1:B:444:VAL:CG2	2.30	0.79
1:A:371:LEU:HD21	1:A:510:LEU:HD11	1.65	0.79
1:A:113:LEU:HD23	1:A:156:TYR:CZ	2.18	0.79
1:B:23:ARG:O	1:B:23:ARG:CD	2.31	0.78
1:A:113:LEU:HD23	1:A:156:TYR:CE2	2.18	0.78
1:B:113:LEU:CG	1:B:156:TYR:CE1	2.67	0.78
1:B:115:GLU:HG2	1:B:119:GLN:OE1	1.82	0.78
1:A:145:ARG:HD2	1:A:148:GLU:OE2	1.82	0.78
1:A:146:ILE:HG22	1:B:454:LEU:CD1	2.13	0.78
1:A:474:ILE:O	1:A:478:GLU:HG3	1.84	0.78
1:B:445:MET:HE3	1:B:449:GLY:HA3	1.66	0.78
1:A:380:LEU:HD13	1:A:380:LEU:C	2.05	0.77
1:B:35:ARG:O	1:B:39:LYS:HG2	1.85	0.77
1:A:398:ILE:HG13	1:A:399:PHE:N	1.98	0.77
1:A:147:GLN:NE2	1:A:147:GLN:H	1.81	0.77
1:B:415:LYS:HG2	1:B:417:PHE:HE2	1.49	0.77
1:A:362:THR:HG23	1:A:366:PHE:HE2	1.50	0.76
1:A:470:ARG:O	1:A:474:ILE:HG13	1.85	0.76
1:A:302:ILE:O	1:A:305:VAL:HG22	1.85	0.76
1:B:379:PHE:O	1:B:381:PRO:HD3	1.84	0.76
1:B:23:ARG:HD2	1:B:27:GLU:OE1	1.85	0.76
1:B:121:ILE:O	1:B:125:MET:HG3	1.84	0.76
1:A:160:PHE:HB3	1:B:398:ILE:HD13	1.65	0.76
1:B:316:PRO:HD2	4:B:547:HOH:O	1.85	0.76
1:A:467:GLU:HG3	1:A:470:ARG:NH2	2.01	0.75
1:A:350:ILE:H	1:A:385:GLN:HE22	1.34	0.75
1:A:459:ILE:HD13	1:A:470:ARG:HB2	1.66	0.75
1:A:10:ASP:O	1:A:16:GLY:CA	2.34	0.75
1:A:457:ARG:HH11	1:A:457:ARG:HG2	1.49	0.75
1:A:113:LEU:HD22	1:A:156:TYR:CE1	2.21	0.75
1:B:409:ILE:HD11	1:B:513:LEU:CD1	2.16	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:ASN:HB2	1:A:375:ASP:O	1.87	0.75
1:B:113:LEU:HD22	1:B:156:TYR:CD1	2.22	0.74
1:B:445:MET:CE	1:B:449:GLY:C	2.55	0.74
1:A:520:LEU:CD2	1:B:165:HIS:NE2	2.50	0.74
1:A:87:VAL:HG12	1:A:117:TYR:CD2	2.21	0.74
1:B:70:HIS:CD2	4:B:566:HOH:O	2.39	0.74
1:A:275:LEU:HD21	1:A:507:VAL:HG11	1.68	0.74
1:A:513:LEU:O	1:A:516:LYS:N	2.20	0.74
1:A:10:ASP:O	1:A:10:ASP:OD1	2.06	0.74
1:A:187:SER:HB3	1:A:188:PRO:CD	2.17	0.74
1:B:70:HIS:CE1	1:B:77:LEU:O	2.41	0.74
1:B:326:PHE:CE1	1:B:363:CYS:SG	2.80	0.74
1:A:320:PRO:HB2	1:A:343:GLN:HG3	1.68	0.74
1:A:227:ALA:HB1	1:A:240:MET:HG3	1.70	0.74
1:B:104:GLN:HG2	1:B:117:TYR:OH	1.88	0.73
1:A:154:GLY:HA2	1:B:428:HIS:CE1	2.21	0.73
1:B:528:ILE:HG12	1:B:529:PRO:CD	2.18	0.73
1:A:469:THR:O	1:A:472:ARG:HB3	1.89	0.73
1:B:287:ILE:HG23	1:B:288:VAL:N	2.03	0.73
1:A:316:PRO:HD2	4:A:600:HOH:O	1.89	0.73
1:A:265:GLU:HG2	1:A:266:PRO:CD	2.19	0.73
1:A:405:THR:O	1:A:516:LYS:CE	2.37	0.72
1:A:146:ILE:CG2	1:B:454:LEU:CD1	2.65	0.72
1:B:158:GLU:OE2	1:B:161:ARG:NH1	2.22	0.72
1:A:513:LEU:O	1:A:515:THR:N	2.23	0.72
1:B:277:VAL:HG23	1:B:277:VAL:O	1.89	0.72
1:B:87:VAL:HG12	1:B:117:TYR:CD2	2.25	0.72
1:B:113:LEU:HG	1:B:117:TYR:HD1	1.50	0.72
1:B:23:ARG:HD2	1:B:23:ARG:O	1.89	0.72
1:A:193:PHE:HD1	1:A:238:HIS:CD2	2.07	0.71
1:A:293:ASN:O	1:A:295:PRO:HD3	1.90	0.71
1:B:445:MET:HE2	1:B:449:GLY:O	1.90	0.71
1:B:254:LEU:HD13	1:B:312:PHE:HE2	1.56	0.71
1:A:299:HIS:HE1	1:A:313:GLU:OE2	1.72	0.71
1:B:339:ASN:ND2	1:B:424:MET:HE1	2.05	0.71
1:A:32:GLY:CA	1:A:107:THR:CG2	2.68	0.71
1:A:113:LEU:CD2	1:A:156:TYR:CE1	2.74	0.70
1:B:451:VAL:HB	1:B:455:HIS:HD2	1.55	0.70
1:A:215:THR:HG23	1:A:215:THR:O	1.88	0.70
1:B:339:ASN:HD21	1:B:424:MET:HE1	1.56	0.70
1:B:106:PHE:HB2	1:B:140:ASP:OD2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:398:ILE:HD13	1:B:160:PHE:HB3	1.71	0.70
1:A:292:ALA:O	1:A:414:ARG:NH1	2.25	0.70
1:A:399:PHE:CD1	1:B:164:THR:HG23	2.27	0.70
1:B:80:ASN:C	1:B:82:PRO:HD3	2.13	0.70
1:A:504:ARG:HG2	1:A:508:ARG:HD2	1.72	0.70
1:A:196:MET:O	1:A:240:MET:HA	1.92	0.70
1:B:115:GLU:O	1:B:119:GLN:HG3	1.92	0.70
1:B:298:MET:O	1:B:298:MET:HG3	1.92	0.69
1:B:485:TYR:O	1:B:489:GLU:HG3	1.92	0.69
1:A:344:PHE:O	1:A:345:ALA:HB3	1.91	0.69
1:B:374:VAL:HB	1:B:412:ILE:HA	1.72	0.69
1:B:349:ASP:HB3	1:B:380:LEU:HD12	1.72	0.69
1:A:399:PHE:CE1	1:B:164:THR:HG23	2.27	0.69
1:B:193:PHE:HD1	1:B:238:HIS:CD2	2.09	0.69
1:B:102:PHE:CZ	1:B:137:GLY:CA	2.75	0.69
1:B:339:ASN:HD21	1:B:424:MET:CE	2.06	0.69
1:A:329:VAL:O	1:A:330:GLU:HB2	1.92	0.69
1:A:354:GLU:OE2	1:B:392:ARG:NH1	2.21	0.69
1:B:10:ASP:CG	1:B:11:ILE:H	1.94	0.69
1:A:231:ASN:O	1:A:318:PHE:HB2	1.93	0.69
1:B:349:ASP:CB	1:B:380:LEU:CD1	2.68	0.69
1:A:165:HIS:CD2	1:B:520:LEU:HD22	2.28	0.69
1:B:22:ARG:HA	1:B:25:ILE:CG2	2.22	0.69
1:B:447:ALA:O	1:B:451:VAL:HG13	1.92	0.69
1:A:36:ALA:HB3	1:A:107:THR:HG23	1.74	0.69
1:B:160:PHE:HE1	1:B:187:SER:HB2	1.57	0.69
1:A:254:LEU:HD23	1:A:312:PHE:HE2	1.57	0.69
1:A:397:LEU:CD2	1:A:423:VAL:HG12	2.23	0.68
1:A:266:PRO:HG2	1:A:368:VAL:HG22	1.76	0.68
1:A:457:ARG:NH1	1:A:457:ARG:CG	2.52	0.68
1:A:266:PRO:CG	1:A:368:VAL:HG22	2.24	0.68
1:A:524:LYS:HD3	4:B:697:HOH:O	1.93	0.68
1:A:367:ASN:HA	1:A:406:VAL:HG11	1.75	0.68
1:A:32:GLY:CA	1:A:107:THR:HG21	2.22	0.68
1:A:380:LEU:HD13	1:A:380:LEU:O	1.94	0.67
1:B:438:PRO:HD3	1:B:497:ILE:O	1.94	0.67
1:A:113:LEU:CD1	1:A:117:TYR:CD1	2.77	0.67
1:A:407:PRO:HB3	1:A:513:LEU:HD23	1.76	0.67
1:B:456:ARG:O	1:B:459:ILE:CG2	2.42	0.67
1:A:455:HIS:O	1:A:459:ILE:HG22	1.95	0.67
1:A:520:LEU:CD2	1:B:165:HIS:CE1	2.77	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:207:GLY:O	1:A:211:ILE:HG23	1.95	0.67
1:B:254:LEU:HD13	1:B:312:PHE:CE2	2.29	0.67
1:A:485:TYR:O	1:A:489:GLU:HG3	1.94	0.67
1:A:221:PHE:CB	2:A:5600:BTN:H81	2.24	0.67
1:A:120:LYS:O	1:A:124:VAL:HG23	1.94	0.67
1:A:339:ASN:CB	1:A:375:ASP:O	2.43	0.67
1:A:501:ASP:O	1:A:501:ASP:OD1	2.13	0.67
1:B:113:LEU:CB	1:B:156:TYR:OH	2.40	0.67
1:A:181:ALA:CB	1:A:204:PHE:CE1	2.78	0.66
1:B:231:ASN:HD21	1:B:239:HIS:N	1.93	0.66
1:B:241:ALA:CB	1:B:247:ALA:HB2	2.23	0.66
1:B:456:ARG:O	1:B:459:ILE:HG23	1.96	0.66
1:B:339:ASN:O	1:B:341:PRO:HD3	1.96	0.66
1:A:456:ARG:O	1:A:457:ARG:HG3	1.96	0.66
1:B:459:ILE:HD13	1:B:470:ARG:HB2	1.77	0.66
1:A:482:LEU:N	1:A:482:LEU:HD12	2.10	0.66
1:B:509:GLY:O	1:B:513:LEU:CG	2.41	0.66
1:B:349:ASP:HB3	1:B:380:LEU:CD1	2.26	0.66
1:B:407:PRO:HB3	1:B:513:LEU:HB3	1.77	0.66
1:B:11:ILE:HG23	1:B:12:HIS:N	2.10	0.66
1:A:406:VAL:HG12	4:B:625:HOH:O	1.95	0.66
1:B:287:ILE:CG2	1:B:288:VAL:N	2.59	0.66
1:A:85:ASP:OD2	1:A:116:VAL:HB	1.96	0.65
1:B:392:ARG:CG	1:B:393:ARG:HG3	2.23	0.65
1:A:386:GLU:OE2	1:B:204:PHE:HA	1.96	0.65
1:A:462:ALA:O	1:A:464:ASP:N	2.29	0.65
1:A:121:ILE:HG22	1:A:121:ILE:O	1.95	0.65
1:A:113:LEU:CD2	1:A:156:TYR:CZ	2.79	0.65
1:B:41:HIS:ND1	4:B:617:HOH:O	2.28	0.65
1:A:193:PHE:CD1	1:A:238:HIS:CD2	2.84	0.65
1:A:119:GLN:NE2	1:A:119:GLN:O	2.30	0.65
1:B:508:ARG:HD3	4:B:637:HOH:O	1.96	0.65
1:A:70:HIS:CE1	1:A:81:ARG:HG2	2.32	0.65
1:A:477:TYR:HD1	1:A:482:LEU:HD11	1.61	0.65
1:B:129:LEU:HD21	1:B:166:ALA:HB2	1.78	0.65
1:A:490:ARG:NH2	1:B:115:GLU:OE1	2.30	0.65
1:B:114:GLY:HA3	1:B:148:GLU:OE2	1.97	0.65
1:B:245:LYS:HB2	1:B:245:LYS:NZ	2.11	0.64
1:A:362:THR:CG2	1:A:366:PHE:CE2	2.81	0.64
1:B:23:ARG:O	1:B:23:ARG:NE	2.30	0.64
1:A:362:THR:HG23	1:A:366:PHE:CE2	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:77:LEU:HD21	1:B:109:PHE:CE1	2.32	0.64
1:B:502:THR:O	1:B:506:ILE:HG12	1.97	0.64
1:B:347:CYS:SG	1:B:377:PRO:CG	2.83	0.64
1:B:113:LEU:HD22	1:B:156:TYR:CZ	2.33	0.64
1:B:257:TYR:HE1	1:B:328:ARG:NH1	1.94	0.64
1:A:392:ARG:HG3	1:A:393:ARG:CG	2.26	0.64
1:B:23:ARG:HH21	1:B:24:ARG:HG3	1.63	0.64
1:B:114:GLY:CA	1:B:148:GLU:OE2	2.45	0.64
1:B:402:ALA:HB2	1:B:429:LEU:HD22	1.78	0.64
1:B:336:ILE:HD13	1:B:371:LEU:HB2	1.79	0.64
1:B:528:ILE:HG13	1:B:529:PRO:HD2	1.78	0.63
1:A:520:LEU:HD22	1:B:165:HIS:NE2	2.11	0.63
1:A:126:ASP:OD1	1:A:162:ARG:HD3	1.97	0.63
1:B:457:ARG:HD3	1:B:457:ARG:N	2.14	0.63
1:B:23:ARG:C	1:B:23:ARG:HE	2.01	0.63
1:B:397:LEU:CD2	1:B:423:VAL:HG12	2.29	0.63
1:A:387:HIS:O	1:B:234:SER:CB	2.46	0.63
1:B:26:GLU:O	1:B:30:HIS:HD2	1.81	0.63
1:B:339:ASN:OD1	1:B:424:MET:HE2	1.99	0.62
1:A:181:ALA:HB2	1:A:204:PHE:CE1	2.33	0.62
1:B:86:GLY:O	1:B:117:TYR:CE2	2.50	0.62
1:B:170:ILE:HG22	1:B:261:ASN:CB	2.30	0.62
1:A:403:GLU:HA	1:A:520:LEU:HD11	1.81	0.62
1:B:147:GLN:H	1:B:147:GLN:NE2	1.96	0.62
1:B:455:HIS:O	1:B:457:ARG:N	2.32	0.62
1:A:374:VAL:HB	1:A:412:ILE:HA	1.80	0.62
1:B:417:PHE:CE1	1:B:443:ALA:HB3	2.34	0.62
1:A:87:VAL:HG12	1:A:117:TYR:HD2	1.65	0.62
1:B:455:HIS:CD2	1:B:473:LEU:HG	2.33	0.62
1:A:459:ILE:HD11	1:A:470:ARG:HB2	1.82	0.62
1:A:32:GLY:HA3	1:A:107:THR:HG22	1.80	0.62
1:A:169:VAL:HA	1:A:262:ASN:ND2	2.15	0.62
1:A:125:MET:CE	1:A:163:ASN:ND2	2.63	0.62
1:B:401:TYR:CD2	1:B:423:VAL:O	2.52	0.62
1:A:397:LEU:HD23	1:A:423:VAL:HG12	1.73	0.62
1:A:376:VAL:HG13	1:A:376:VAL:O	1.99	0.62
1:B:97:ARG:HB3	1:B:98:PRO:HD2	1.82	0.61
1:A:405:THR:O	1:A:516:LYS:NZ	2.32	0.61
1:A:117:TYR:CD1	1:A:117:TYR:C	2.74	0.61
1:A:86:GLY:O	1:A:117:TYR:CD2	2.53	0.61
1:B:340:GLN:CD	1:B:342:MET:HG3	2.21	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:528:ILE:HG12	1:A:529:PRO:HD2	1.82	0.61
1:B:462:ALA:C	1:B:464:ASP:N	2.52	0.61
1:A:117:TYR:O	1:A:117:TYR:CG	2.53	0.61
1:A:147:GLN:N	1:A:147:GLN:HE21	1.94	0.61
1:A:451:VAL:HG21	1:A:474:ILE:CG1	2.26	0.61
1:B:112:ALA:HA	1:B:143:GLY:O	2.01	0.60
1:B:113:LEU:CG	1:B:156:TYR:HE1	2.06	0.60
1:A:362:THR:CG2	1:A:366:PHE:HE2	2.13	0.60
1:B:193:PHE:CD1	1:B:238:HIS:CD2	2.88	0.60
1:A:36:ALA:CB	1:A:107:THR:HG23	2.31	0.60
1:B:113:LEU:HG	1:B:117:TYR:CE1	2.36	0.60
1:A:392:ARG:CG	1:A:393:ARG:HG3	2.26	0.60
1:B:102:PHE:CE1	1:B:137:GLY:HA3	2.36	0.60
1:A:32:GLY:CA	1:A:107:THR:HG22	2.31	0.60
1:A:525:HIS:ND1	1:A:526:GLY:O	2.35	0.60
1:A:221:PHE:HB2	2:A:5600:BTN:H81	1.84	0.60
1:B:344:PHE:O	1:B:345:ALA:HB3	2.01	0.60
1:A:21:LEU:O	1:A:21:LEU:HG	2.01	0.60
1:A:478:GLU:CB	1:A:482:LEU:HD22	2.32	0.60
1:B:472:ARG:HH21	1:B:473:LEU:HD11	1.67	0.60
1:B:343:GLN:O	1:B:344:PHE:HB2	2.02	0.60
1:A:141:SER:O	1:A:179:PRO:HB2	2.00	0.60
1:B:106:PHE:HB2	1:B:140:ASP:CG	2.23	0.59
1:B:104:GLN:CG	1:B:117:TYR:OH	2.50	0.59
1:A:366:PHE:O	1:A:367:ASN:HB2	2.01	0.59
1:A:266:PRO:HB2	1:A:333:PRO:HG2	1.83	0.59
1:B:269:PHE:HD2	1:B:269:PHE:O	1.82	0.59
1:A:11:ILE:HG23	1:A:12:HIS:N	2.16	0.59
1:A:520:LEU:HD21	1:B:165:HIS:NE2	2.18	0.59
1:B:451:VAL:O	1:B:455:HIS:HB2	2.02	0.59
1:A:254:LEU:CD2	1:A:312:PHE:HE2	2.15	0.59
1:A:415:LYS:HE3	1:A:417:PHE:HE2	1.67	0.59
1:A:457:ARG:NH1	1:A:457:ARG:HG3	2.18	0.59
1:B:65:ASP:HB2	1:B:120:LYS:HE3	1.84	0.58
1:B:358:ARG:HG2	4:B:567:HOH:O	2.02	0.58
1:B:299:HIS:HE1	1:B:313:GLU:OE2	1.86	0.58
1:A:215:THR:CG2	1:A:215:THR:O	2.51	0.58
1:A:169:VAL:HG12	1:A:170:ILE:HG23	1.86	0.58
1:B:65:ASP:OD2	1:B:123:LYS:HD2	2.03	0.58
1:B:87:VAL:CG1	1:B:117:TYR:CD2	2.86	0.58
1:A:477:TYR:CD1	1:A:482:LEU:HD11	2.37	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:211:ILE:HD12	1:A:211:ILE:O	2.02	0.58
1:A:386:GLU:O	1:A:386:GLU:HG3	2.02	0.58
1:B:200:THR:CG2	4:B:631:HOH:O	2.51	0.58
1:B:341:PRO:HB3	1:B:414:ARG:NH2	2.19	0.58
1:A:457:ARG:HH11	1:A:457:ARG:HG3	1.69	0.57
1:A:405:THR:HG22	1:A:518:GLU:O	2.03	0.57
1:A:86:GLY:C	1:A:117:TYR:CD2	2.78	0.57
1:A:181:ALA:HB1	1:A:204:PHE:CE1	2.38	0.57
1:B:126:ASP:OD1	1:B:162:ARG:HD3	2.04	0.57
1:A:10:ASP:C	1:A:16:GLY:HA3	2.25	0.57
1:B:173:ILE:HD12	1:B:255:LEU:HD21	1.87	0.57
1:B:124:VAL:HG12	1:B:125:MET:N	2.18	0.57
1:B:10:ASP:OD1	1:B:13:THR:HG23	2.05	0.57
1:B:478:GLU:O	1:B:482:LEU:HB2	2.05	0.57
1:A:503:ARG:O	1:A:503:ARG:HG2	2.05	0.57
1:B:113:LEU:HB3	1:B:156:TYR:CE1	2.40	0.57
1:B:214:VAL:HG12	1:B:215:THR:HG22	1.86	0.57
1:B:308:ASP:O	1:B:309:ALA:C	2.43	0.57
1:A:100:ALA:HB1	1:A:124:VAL:HG12	1.86	0.56
1:B:47:THR:OG1	1:B:50:GLU:HG3	2.04	0.56
1:B:113:LEU:CB	1:B:156:TYR:CE1	2.88	0.56
1:A:477:TYR:O	1:A:482:LEU:CD1	2.53	0.56
1:A:315:GLN:HB2	1:A:355:LYS:HE3	1.88	0.56
1:A:303:GLU:O	1:A:309:ALA:HA	2.04	0.56
1:A:405:THR:O	1:A:516:LYS:HE2	2.04	0.56
1:B:147:GLN:H	1:B:147:GLN:HE21	1.54	0.56
1:A:125:MET:HE1	1:A:163:ASN:ND2	2.20	0.56
1:B:98:PRO:C	1:B:99:VAL:HG23	2.24	0.56
1:A:462:ALA:C	1:A:464:ASP:N	2.58	0.56
1:A:149:GLY:C	1:B:444:VAL:HG23	2.25	0.56
1:A:503:ARG:O	1:A:507:VAL:CG2	2.52	0.56
1:A:390:ILE:HG23	1:A:391:ILE:N	2.21	0.56
1:A:433:LEU:HA	1:A:494:ASP:OD1	2.06	0.56
1:A:475:GLN:O	1:A:475:GLN:CD	2.45	0.56
1:B:163:ASN:HB3	1:B:190:ILE:CG2	2.34	0.55
1:A:477:TYR:O	1:A:482:LEU:HD13	2.07	0.55
1:A:462:ALA:C	1:A:464:ASP:H	2.10	0.55
1:B:462:ALA:C	1:B:464:ASP:H	2.09	0.55
1:A:340:GLN:CD	1:A:342:MET:HG3	2.26	0.55
1:B:528:ILE:HG12	1:B:529:PRO:N	2.21	0.55
1:B:339:ASN:ND2	1:B:424:MET:CE	2.68	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:271:GLU:O	1:B:271:GLU:HG3	2.07	0.55
1:B:193:PHE:CD1	1:B:238:HIS:NE2	2.75	0.55
1:B:308:ASP:O	1:B:310:GLU:N	2.39	0.55
1:B:37:VAL:HG12	1:B:37:VAL:O	2.06	0.55
1:A:176:VAL:HB	1:A:196:MET:HG2	1.89	0.55
1:A:211:ILE:HD12	1:A:215:THR:HG22	1.88	0.55
1:A:464:ASP:O	1:A:465:ASP:HB2	2.05	0.55
1:A:390:ILE:HG13	1:B:186:TYR:OH	2.07	0.55
1:B:392:ARG:HG3	1:B:393:ARG:CG	2.26	0.55
1:B:417:PHE:CD1	1:B:443:ALA:HB3	2.42	0.55
1:A:113:LEU:HD23	1:A:156:TYR:CD2	2.43	0.55
1:B:102:PHE:CE1	1:B:137:GLY:CA	2.90	0.55
1:B:13:THR:O	1:B:16:GLY:N	2.33	0.55
1:A:54:LEU:HD21	1:A:245:LYS:HD2	1.89	0.55
1:B:503:ARG:O	1:B:507:VAL:HG23	2.06	0.55
1:B:24:ARG:O	1:B:67:PHE:HE1	1.90	0.54
1:B:158:GLU:CD	1:B:161:ARG:HH12	2.11	0.54
1:B:180:CYS:O	1:B:185:VAL:HG12	2.06	0.54
1:A:350:ILE:O	1:A:354:GLU:HG3	2.07	0.54
1:A:344:PHE:O	1:A:345:ALA:CB	2.54	0.54
1:A:70:HIS:HD2	1:A:72:SER:N	2.03	0.54
1:A:87:VAL:CB	1:A:117:TYR:HD2	2.17	0.54
1:B:61:PHE:HE2	1:B:63:GLU:HB2	1.70	0.54
1:B:501:ASP:O	1:B:505:HIS:HD2	1.89	0.54
1:A:379:PHE:HZ	1:A:423:VAL:HG21	1.72	0.54
1:A:409:ILE:CD1	1:A:510:LEU:HG	2.37	0.54
1:B:219:VAL:HG22	1:B:220:GLY:N	2.22	0.54
1:B:478:GLU:HA	1:B:482:LEU:HD13	1.88	0.54
1:A:458:THR:O	1:A:458:THR:CG2	2.55	0.54
1:A:520:LEU:HD22	1:B:165:HIS:CE1	2.42	0.54
1:A:458:THR:O	1:A:458:THR:HG22	2.08	0.54
1:B:467:GLU:OE1	1:B:467:GLU:N	2.30	0.54
1:B:254:LEU:CD1	1:B:312:PHE:HE2	2.21	0.54
1:A:501:ASP:OD1	1:A:504:ARG:HB3	2.08	0.54
1:A:69:ARG:HD2	1:A:83:TYR:CE2	2.43	0.54
1:A:52:ILE:HD11	1:A:88:VAL:HB	1.89	0.54
1:B:298:MET:O	1:B:302:ILE:HD12	2.08	0.54
1:A:219:VAL:HG22	1:A:223:GLU:HG2	1.90	0.53
1:A:160:PHE:CE1	1:A:187:SER:CB	2.84	0.53
1:B:158:GLU:HB3	1:B:162:ARG:HH12	1.73	0.53
1:B:403:GLU:HA	1:B:520:LEU:HD11	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:ALA:HB2	1:A:204:PHE:CZ	2.43	0.53
1:B:462:ALA:O	1:B:464:ASP:N	2.41	0.53
1:B:94:VAL:O	1:B:95:ASP:HB2	2.09	0.53
1:A:528:ILE:HG12	1:A:529:PRO:CD	2.38	0.53
1:A:113:LEU:HD13	1:A:117:TYR:CE1	2.43	0.53
1:A:387:HIS:O	1:A:388:ASP:C	2.45	0.53
1:A:379:PHE:CE1	1:A:420:ALA:HB2	2.43	0.53
1:A:528:ILE:CG1	1:A:529:PRO:HD2	2.38	0.53
1:A:219:VAL:CG2	1:A:223:GLU:HG2	2.38	0.53
1:A:102:PHE:CZ	1:A:137:GLY:HA3	2.44	0.53
1:B:87:VAL:CB	1:B:117:TYR:CE2	2.85	0.53
1:A:254:LEU:HD23	1:A:312:PHE:CE2	2.42	0.53
1:A:178:GLY:O	1:A:201:SER:HA	2.09	0.53
1:B:91:TYR:C	1:B:91:TYR:CD1	2.81	0.53
1:A:478:GLU:HG2	1:A:482:LEU:CD2	2.39	0.53
1:B:445:MET:HE3	1:B:449:GLY:CA	2.38	0.53
1:B:277:VAL:O	1:B:277:VAL:CG2	2.57	0.53
1:A:99:VAL:CG2	1:A:134:PRO:HB2	2.32	0.52
1:B:445:MET:CE	1:B:449:GLY:O	2.57	0.52
1:B:124:VAL:CG1	1:B:125:MET:N	2.71	0.52
1:B:433:LEU:HA	1:B:494:ASP:OD1	2.10	0.52
1:A:230:HIS:CE1	1:B:391:ILE:HD12	2.44	0.52
1:A:447:ALA:CB	1:A:478:GLU:HG2	2.40	0.52
1:B:33:SER:O	1:B:36:ALA:N	2.41	0.52
1:A:63:GLU:HG2	1:A:66:GLU:HB2	1.91	0.52
1:A:165:HIS:NE2	1:B:520:LEU:CD2	2.72	0.52
1:A:170:ILE:HG22	1:A:261:ASN:HB3	1.92	0.52
1:B:528:ILE:CG1	1:B:529:PRO:CD	2.79	0.52
1:A:362:THR:HG22	1:A:366:PHE:CE2	2.45	0.52
1:A:154:GLY:CA	1:B:428:HIS:CE1	2.91	0.52
1:A:188:PRO:O	1:A:191:THR:OG1	2.26	0.52
1:A:456:ARG:CZ	1:A:457:ARG:NH2	2.69	0.52
1:B:180:CYS:O	1:B:185:VAL:CG1	2.57	0.52
1:B:69:ARG:NH1	1:B:83:TYR:OH	2.43	0.52
1:A:94:VAL:O	1:A:95:ASP:HB2	2.10	0.52
1:A:482:LEU:N	1:A:482:LEU:CD1	2.73	0.52
1:A:234:SER:HA	1:B:387:HIS:O	2.10	0.52
1:A:275:LEU:CD2	1:A:507:VAL:HG21	2.40	0.51
1:B:11:ILE:CG2	1:B:12:HIS:N	2.72	0.51
1:A:438:PRO:HD3	1:A:497:ILE:O	2.10	0.51
1:A:125:MET:HE3	1:A:163:ASN:ND2	2.26	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:ARG:CD	1:A:148:GLU:OE2	2.56	0.51
1:B:314:THR:O	1:B:315:GLN:C	2.49	0.51
1:B:324:THR:HA	1:B:336:ILE:O	2.10	0.51
1:B:111:GLY:O	1:B:141:SER:CB	2.59	0.51
1:A:113:LEU:CD1	1:A:117:TYR:HD1	2.10	0.51
1:B:326:PHE:CZ	1:B:359:PHE:CE1	2.98	0.51
1:A:381:PRO:HG2	1:B:214:VAL:HG11	1.92	0.51
1:A:340:GLN:OE1	1:A:342:MET:HG3	2.11	0.51
1:A:70:HIS:HA	1:A:116:VAL:HG21	1.92	0.51
1:B:457:ARG:NH1	1:B:457:ARG:CG	2.38	0.51
1:A:134:PRO:HG3	1:A:171:PRO:HG2	1.91	0.51
1:B:160:PHE:CE1	1:B:187:SER:HB2	2.44	0.51
1:A:380:LEU:O	1:A:380:LEU:CD1	2.59	0.51
1:A:451:VAL:HG11	1:A:474:ILE:CA	2.37	0.50
1:B:401:TYR:CE2	1:B:423:VAL:O	2.64	0.50
1:A:455:HIS:O	1:A:459:ILE:CG2	2.58	0.50
1:B:40:GLN:HE22	1:B:45:LYS:NZ	2.10	0.50
1:B:367:ASN:HA	1:B:406:VAL:HG11	1.92	0.50
1:A:299:HIS:O	1:A:303:GLU:HG3	2.11	0.50
1:A:444:VAL:HA	1:B:153:LEU:HD11	1.93	0.50
1:A:211:ILE:HD12	1:A:215:THR:CG2	2.42	0.50
1:A:380:LEU:HD11	4:A:623:HOH:O	2.10	0.50
1:B:146:ILE:O	1:B:147:GLN:C	2.50	0.50
1:A:69:ARG:NH1	1:A:83:TYR:CZ	2.79	0.50
1:B:91:TYR:O	1:B:91:TYR:CD1	2.65	0.50
1:A:234:SER:HB2	1:A:236:VAL:HG23	1.94	0.50
1:A:176:VAL:HB	1:A:196:MET:CG	2.41	0.50
1:A:467:GLU:N	1:A:467:GLU:OE2	2.45	0.50
1:B:208:PRO:HD2	1:B:221:PHE:CZ	2.47	0.50
1:A:160:PHE:HE1	1:A:187:SER:CB	2.08	0.50
1:A:478:GLU:HA	1:A:482:LEU:CG	2.40	0.50
1:B:305:VAL:HG23	1:B:306:LEU:N	2.26	0.50
1:A:232:SER:O	1:A:318:PHE:HD1	1.95	0.49
1:A:475:GLN:O	1:A:475:GLN:OE1	2.30	0.49
1:B:111:GLY:O	1:B:141:SER:OG	2.23	0.49
1:A:406:VAL:O	1:A:408:LEU:HG	2.13	0.49
1:B:25:ILE:HG13	1:B:25:ILE:O	2.09	0.49
1:A:207:GLY:O	1:A:211:ILE:CG2	2.60	0.49
1:B:132:GLY:C	1:B:261:ASN:HD22	2.15	0.49
1:B:10:ASP:CG	1:B:11:ILE:N	2.64	0.49
1:A:250:TYR:CE1	1:A:312:PHE:CZ	3.00	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:GLU:HB3	1:A:162:ARG:HH12	1.76	0.49
1:B:300:SER:O	1:B:304:HIS:ND1	2.40	0.49
1:A:434:ASN:HB3	4:A:656:HOH:O	2.12	0.49
1:A:121:ILE:O	1:A:125:MET:HG3	2.12	0.49
1:B:465:ASP:O	1:B:469:THR:HG23	2.12	0.49
1:A:387:HIS:O	1:B:234:SER:HB2	2.12	0.49
1:B:445:MET:CE	1:B:449:GLY:CA	2.90	0.49
1:A:483:ASN:CB	1:A:484:PRO:HD2	2.31	0.49
1:B:232:SER:O	1:B:318:PHE:HD1	1.95	0.49
1:B:435:LEU:HD13	1:B:435:LEU:N	2.27	0.49
1:A:80:ASN:N	1:A:80:ASN:ND2	2.61	0.49
1:A:113:LEU:CD1	1:A:117:TYR:CE1	2.95	0.49
1:A:175:LEU:CD2	1:A:175:LEU:C	2.81	0.49
1:A:324:THR:HA	1:A:336:ILE:O	2.13	0.49
1:B:226:GLY:O	1:B:229:THR:HB	2.13	0.49
1:B:329:VAL:O	1:B:330:GLU:HB2	2.12	0.49
1:A:265:GLU:CG	1:A:266:PRO:CD	2.90	0.49
1:B:36:ALA:HA	1:B:39:LYS:HG3	1.94	0.49
1:B:147:GLN:HE21	1:B:147:GLN:N	2.11	0.49
1:A:11:ILE:CG2	1:A:12:HIS:N	2.75	0.49
1:B:445:MET:CE	1:B:449:GLY:HA3	2.41	0.49
1:A:121:ILE:CG2	1:A:121:ILE:O	2.61	0.48
1:B:231:ASN:HD21	1:B:238:HIS:C	2.16	0.48
1:B:390:ILE:HG23	1:B:391:ILE:N	2.28	0.48
1:A:230:HIS:HE1	1:B:391:ILE:HD12	1.77	0.48
1:A:517:ARG:HD2	4:A:664:HOH:O	2.12	0.48
1:B:113:LEU:HA	1:B:117:TYR:CD1	2.48	0.48
1:B:483:ASN:HD22	1:B:483:ASN:C	2.17	0.48
1:A:340:GLN:O	1:A:340:GLN:HG3	2.12	0.48
1:B:473:LEU:HA	1:B:476:GLU:HG3	1.95	0.48
1:A:349:ASP:O	1:A:350:ILE:C	2.52	0.48
1:B:437:TRP:NE1	1:B:502:THR:OG1	2.46	0.48
1:B:268:ALA:CB	1:B:332:ARG:HG3	2.43	0.48
1:A:435:LEU:HD13	1:A:435:LEU:N	2.27	0.48
1:B:113:LEU:HD13	1:B:156:TYR:CD1	2.41	0.48
1:A:391:ILE:HA	1:B:186:TYR:CE1	2.48	0.48
1:B:208:PRO:CD	1:B:221:PHE:CE1	2.97	0.48
1:B:280:GLU:O	1:B:283:GLU:HB2	2.13	0.48
1:A:392:ARG:HG3	1:A:393:ARG:N	2.28	0.48
1:A:409:ILE:HD11	1:A:510:LEU:HG	1.95	0.48
1:A:170:ILE:HG22	1:A:261:ASN:CB	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:37:VAL:O	1:B:37:VAL:CG1	2.61	0.48
1:A:193:PHE:HA	1:A:238:HIS:ND1	2.28	0.48
1:A:459:ILE:HD11	1:A:466:ALA:O	2.14	0.48
1:B:61:PHE:CE2	1:B:63:GLU:HB2	2.48	0.48
1:B:253:GLN:O	1:B:256:SER:OG	2.22	0.48
1:A:288:VAL:HG11	1:A:439:THR:HG21	1.95	0.48
1:B:455:HIS:CE1	1:B:473:LEU:HG	2.50	0.47
1:A:159:ILE:HG22	1:A:163:ASN:OD1	2.14	0.47
1:A:85:ASP:O	1:A:117:TYR:CB	2.57	0.47
1:A:147:GLN:HG3	1:B:454:LEU:CD2	2.43	0.47
1:B:187:SER:HB3	1:B:188:PRO:CD	2.35	0.47
1:B:188:PRO:O	1:B:191:THR:OG1	2.31	0.47
1:B:266:PRO:CG	1:B:368:VAL:HG22	2.44	0.47
1:B:23:ARG:NH2	1:B:24:ARG:HG3	2.29	0.47
1:B:320:PRO:HB2	1:B:343:GLN:HG3	1.96	0.47
1:A:134:PRO:HG3	1:A:171:PRO:CG	2.45	0.47
1:B:132:GLY:HA3	1:B:261:ASN:ND2	2.29	0.47
1:B:173:ILE:HD12	1:B:255:LEU:CD2	2.43	0.47
1:A:56:LEU:HD11	1:A:101:VAL:HG11	1.96	0.47
1:A:113:LEU:HD13	1:A:117:TYR:HE1	1.78	0.47
1:B:472:ARG:HE	1:B:473:LEU:HD13	1.79	0.47
1:A:451:VAL:HG23	1:A:452:ASN:N	2.29	0.47
1:A:478:GLU:HG2	1:A:482:LEU:HD22	1.97	0.47
1:A:389:GLY:O	1:A:393:ARG:HG3	2.13	0.47
1:A:483:ASN:C	1:A:483:ASN:HD22	2.17	0.47
1:B:318:PHE:O	1:B:355:LYS:HD2	2.15	0.47
1:A:170:ILE:HG13	1:A:170:ILE:O	2.15	0.47
1:A:306:LEU:HD21	1:A:336:ILE:HD11	1.96	0.47
1:B:287:ILE:HG12	1:B:296:TYR:CD2	2.50	0.47
1:B:474:ILE:O	1:B:478:GLU:OE1	2.32	0.47
1:B:322:ILE:CG2	1:B:355:LYS:HD3	2.45	0.47
1:B:23:ARG:C	1:B:23:ARG:NE	2.68	0.47
1:A:48:ALA:O	1:A:52:ILE:HG13	2.14	0.47
1:A:193:PHE:CE2	1:A:362:THR:HG21	2.50	0.46
1:A:13:THR:O	1:A:16:GLY:N	2.48	0.46
1:B:170:ILE:O	1:B:170:ILE:HG13	2.15	0.46
1:B:25:ILE:CD1	4:B:644:HOH:O	2.45	0.46
1:B:401:TYR:CE2	1:B:425:GLY:N	2.83	0.46
1:A:227:ALA:HB3	4:A:571:HOH:O	2.14	0.46
1:A:186:TYR:OH	1:B:390:ILE:HG13	2.14	0.46
1:A:390:ILE:CG1	1:B:186:TYR:OH	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:ILE:HG13	1:A:385:GLN:NE2	2.30	0.46
1:A:10:ASP:N	1:A:13:THR:HG23	2.29	0.46
1:A:498:MET:O	1:A:499:PRO:C	2.54	0.46
1:A:503:ARG:O	1:A:503:ARG:CG	2.63	0.46
1:B:204:PHE:CE1	1:B:207:GLY:HA2	2.51	0.46
1:B:221:PHE:CB	2:B:5601:BTN:H81	2.45	0.46
1:B:284:LEU:HD21	1:B:304:HIS:CG	2.51	0.46
1:B:395:ALA:O	1:B:398:ILE:HG23	2.15	0.46
1:A:389:GLY:O	1:A:393:ARG:CG	2.64	0.46
1:B:254:LEU:HD12	1:B:254:LEU:HA	1.75	0.46
1:A:386:GLU:OE2	1:B:204:PHE:CA	2.63	0.46
1:B:221:PHE:HB2	2:B:5601:BTN:H81	1.97	0.46
1:A:284:LEU:HG	1:A:304:HIS:CD2	2.50	0.46
1:A:87:VAL:N	1:A:117:TYR:HD2	2.13	0.46
1:B:81:ARG:N	1:B:82:PRO:HD3	2.29	0.46
1:A:302:ILE:O	1:A:305:VAL:CG2	2.61	0.46
1:B:376:VAL:HG13	1:B:376:VAL:O	2.15	0.46
1:B:193:PHE:HA	1:B:238:HIS:ND1	2.26	0.46
1:B:457:ARG:O	1:B:460:ALA:N	2.48	0.46
1:B:70:HIS:C	1:B:70:HIS:CD2	2.88	0.46
1:A:102:PHE:CE1	1:A:137:GLY:HA3	2.51	0.46
1:A:469:THR:O	1:A:472:ARG:CB	2.61	0.46
1:A:128:ALA:HB1	1:A:133:CYS:O	2.16	0.46
1:A:522:PRO:O	1:A:523:LYS:HB3	2.16	0.46
1:A:398:ILE:HD11	1:B:160:PHE:HB3	1.93	0.46
1:B:128:ALA:CB	1:B:135:VAL:CG2	2.93	0.46
1:A:520:LEU:HD22	1:B:165:HIS:CG	2.50	0.46
1:B:116:VAL:O	1:B:120:LYS:N	2.46	0.46
1:A:454:LEU:HD13	1:B:75:PHE:CZ	2.51	0.46
1:B:456:ARG:O	1:B:459:ILE:HG22	2.14	0.45
1:B:187:SER:H	1:B:188:PRO:HD2	1.81	0.45
1:B:198:ASP:OD1	1:B:199:GLN:N	2.49	0.45
1:A:498:MET:O	1:A:500:SER:N	2.49	0.45
1:A:361:ARG:NH2	4:A:532:HOH:O	2.38	0.45
1:A:198:ASP:CG	1:A:199:GLN:HG2	2.36	0.45
1:B:266:PRO:HG3	1:B:368:VAL:HG22	1.99	0.45
1:A:528:ILE:HG12	1:A:529:PRO:N	2.31	0.45
1:A:284:LEU:HD21	1:A:304:HIS:CG	2.51	0.45
1:A:183:GLY:O	1:A:184:ALA:C	2.54	0.45
1:B:341:PRO:HB3	1:B:414:ARG:HH22	1.81	0.45
1:B:69:ARG:NH1	1:B:83:TYR:CZ	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:ILE:CB	1:B:454:LEU:HD11	2.44	0.45
1:A:196:MET:HE3	1:A:203:MET:HG3	1.99	0.45
1:A:165:HIS:CD2	1:B:520:LEU:CD2	2.96	0.45
1:A:493:VAL:O	1:A:493:VAL:HG23	2.17	0.45
1:B:467:GLU:CD	1:B:467:GLU:H	2.17	0.45
1:A:256:SER:O	1:A:267:PRO:HG2	2.17	0.45
1:A:113:LEU:CD2	1:A:156:TYR:CD1	2.99	0.45
1:B:87:VAL:HB	1:B:117:TYR:HE2	1.74	0.45
1:B:401:TYR:CZ	1:B:425:GLY:N	2.85	0.45
1:A:322:ILE:HG13	1:A:338:ALA:O	2.16	0.45
1:A:26:GLU:O	1:A:30:HIS:HD2	1.99	0.45
1:B:456:ARG:HB2	1:B:456:ARG:HE	1.42	0.45
1:B:195:VAL:CG2	1:B:247:ALA:HB1	2.47	0.45
1:A:102:PHE:CZ	1:A:137:GLY:CA	2.99	0.45
1:A:486:THR:HB	4:A:565:HOH:O	2.16	0.45
1:B:56:LEU:CD1	1:B:61:PHE:HD1	2.30	0.45
1:A:91:TYR:C	1:A:91:TYR:CD1	2.89	0.45
1:B:474:ILE:O	1:B:478:GLU:HG3	2.17	0.45
1:A:99:VAL:HG22	1:A:134:PRO:CB	2.32	0.45
1:B:72:SER:O	1:B:78:ASP:HB3	2.16	0.45
1:B:158:GLU:O	1:B:162:ARG:NH1	2.47	0.45
1:B:13:THR:O	1:B:14:THR:C	2.55	0.45
1:B:483:ASN:HB2	1:B:484:PRO:HD2	1.98	0.45
1:B:128:ALA:HB2	1:B:135:VAL:CG2	2.46	0.45
1:A:65:ASP:HB2	1:A:120:LYS:HE3	1.99	0.45
1:A:436:ALA:O	1:A:496:VAL:HA	2.16	0.45
1:A:327:GLY:O	1:A:328:ARG:HG2	2.17	0.45
1:B:456:ARG:C	1:B:459:ILE:HG22	2.37	0.45
1:B:349:ASP:O	1:B:350:ILE:C	2.55	0.45
1:B:399:PHE:O	1:B:399:PHE:CD2	2.69	0.44
1:A:389:GLY:O	1:A:393:ARG:HD3	2.16	0.44
1:A:262:ASN:OD1	1:A:262:ASN:O	2.36	0.44
1:A:60:SER:O	1:A:61:PHE:C	2.55	0.44
1:B:321:ASN:OD1	1:B:321:ASN:N	2.47	0.44
1:A:156:TYR:HB3	1:A:160:PHE:CE2	2.52	0.44
1:B:198:ASP:CG	1:B:199:GLN:HG2	2.35	0.44
1:A:478:GLU:HB3	1:A:482:LEU:HD22	1.98	0.44
1:B:363:CYS:HB3	1:B:368:VAL:HB	1.98	0.44
1:A:161:ARG:NH2	1:A:162:ARG:NH2	2.65	0.44
1:B:40:GLN:HE22	1:B:45:LYS:HZ1	1.63	0.44
1:A:113:LEU:O	1:A:145:ARG:CB	2.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:GLY:O	1:A:117:TYR:HE2	1.96	0.44
1:B:187:SER:N	1:B:188:PRO:CD	2.80	0.44
1:A:329:VAL:O	1:A:330:GLU:CB	2.64	0.44
1:A:288:VAL:HG22	1:A:296:TYR:CZ	2.53	0.44
1:A:196:MET:CE	1:A:230:HIS:HD2	2.31	0.44
1:B:70:HIS:HD2	1:B:72:SER:N	2.16	0.44
1:B:427:LYS:HE2	1:B:427:LYS:HB2	1.73	0.44
1:A:215:THR:CG2	1:A:217:GLU:HB3	2.47	0.44
1:A:380:LEU:C	1:A:380:LEU:CD1	2.77	0.44
1:A:376:VAL:CG1	1:A:376:VAL:O	2.64	0.44
1:B:198:ASP:HA	1:B:227:ALA:HB3	2.00	0.44
1:A:483:ASN:HB2	1:A:484:PRO:CD	2.35	0.44
1:A:433:LEU:HD12	1:A:494:ASP:OD1	2.18	0.44
1:B:493:VAL:HG23	1:B:493:VAL:O	2.16	0.44
1:B:473:LEU:HD12	1:B:473:LEU:HA	1.80	0.44
1:B:469:THR:O	1:B:473:LEU:HD22	2.18	0.44
1:A:448:GLN:O	1:A:452:ASN:OD1	2.36	0.44
1:A:158:GLU:CD	1:A:161:ARG:HH12	2.21	0.44
1:B:466:ALA:O	1:B:467:GLU:C	2.56	0.44
1:A:182:GLY:O	1:A:185:VAL:HG22	2.18	0.44
1:A:456:ARG:HD2	1:A:457:ARG:CZ	2.48	0.43
1:A:478:GLU:CG	1:A:482:LEU:HD22	2.47	0.43
1:B:204:PHE:CZ	1:B:221:PHE:HE1	2.36	0.43
1:B:208:PRO:HD2	1:B:221:PHE:CE1	2.52	0.43
1:A:21:LEU:CG	1:A:21:LEU:O	2.65	0.43
1:A:102:PHE:CE1	1:A:137:GLY:CA	3.01	0.43
1:B:364:ASP:CG	1:B:404:ALA:HA	2.38	0.43
1:B:130:LYS:HE3	1:B:130:LYS:HB2	1.67	0.43
1:A:212:LYS:CE	1:A:218:ASP:OD1	2.67	0.43
1:B:326:PHE:CE2	1:B:359:PHE:HE1	2.35	0.43
1:B:182:GLY:O	1:B:185:VAL:HG22	2.18	0.43
1:B:434:ASN:C	1:B:435:LEU:HD13	2.38	0.43
1:B:455:HIS:O	1:B:456:ARG:C	2.56	0.43
1:A:395:ALA:C	1:A:398:ILE:HG23	2.33	0.43
1:B:344:PHE:O	1:B:345:ALA:CB	2.66	0.43
1:A:475:GLN:O	1:A:475:GLN:CG	2.66	0.43
1:A:475:GLN:C	1:A:475:GLN:CD	2.77	0.43
1:B:284:LEU:HG	1:B:304:HIS:CD2	2.53	0.43
1:B:478:GLU:HG2	1:B:482:LEU:HD22	1.99	0.43
1:B:205:ILE:HG13	1:B:205:ILE:H	1.30	0.43
1:A:478:GLU:HA	1:A:482:LEU:CD2	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:433:LEU:HD12	1:A:433:LEU:HA	1.80	0.43
1:B:77:LEU:HD21	1:B:109:PHE:CZ	2.54	0.43
1:B:219:VAL:HG22	1:B:220:GLY:O	2.18	0.43
1:A:23:ARG:HH11	1:A:23:ARG:HG2	1.83	0.43
1:A:445:MET:SD	1:A:449:GLY:O	2.77	0.43
1:A:160:PHE:HB3	1:B:398:ILE:CD1	2.43	0.43
1:A:212:LYS:O	1:A:216:GLY:N	2.46	0.43
1:A:11:ILE:C	1:A:13:THR:H	2.21	0.43
1:B:200:THR:HG21	4:B:631:HOH:O	2.17	0.43
1:A:250:TYR:CZ	1:A:312:PHE:CZ	3.07	0.43
1:B:457:ARG:C	1:B:459:ILE:N	2.71	0.43
1:B:419:GLY:O	1:B:423:VAL:HG23	2.19	0.43
1:A:478:GLU:HA	1:A:482:LEU:HD22	1.99	0.43
1:B:364:ASP:OD1	1:B:405:THR:N	2.48	0.43
1:B:472:ARG:O	1:B:476:GLU:HG3	2.19	0.43
1:B:266:PRO:CD	1:B:367:ASN:O	2.67	0.43
1:A:409:ILE:HD12	1:A:510:LEU:HG	2.00	0.43
1:A:343:GLN:O	1:A:344:PHE:HB2	2.19	0.43
1:A:504:ARG:CG	1:A:508:ARG:HD2	2.45	0.43
1:B:40:GLN:NE2	1:B:45:LYS:NZ	2.66	0.43
1:A:337:VAL:O	1:A:372:THR:HA	2.18	0.43
1:A:187:SER:CB	1:A:188:PRO:HD3	2.21	0.42
1:A:10:ASP:CG	1:A:10:ASP:O	2.57	0.42
1:A:148:GLU:O	1:A:151:ALA:HB3	2.20	0.42
1:B:85:ASP:O	1:B:117:TYR:HD2	2.02	0.42
1:A:175:LEU:CD2	1:A:177:VAL:HG13	2.42	0.42
1:B:315:GLN:HB2	1:B:355:LYS:HE3	2.01	0.42
1:A:520:LEU:CD2	1:B:165:HIS:CD2	2.94	0.42
1:B:20:ASP:HB3	4:B:539:HOH:O	2.19	0.42
1:A:493:VAL:O	1:A:494:ASP:C	2.58	0.42
1:A:86:GLY:C	1:A:117:TYR:HD2	2.22	0.42
1:B:332:ARG:NH2	1:B:514:ARG:HH12	2.17	0.42
1:A:387:HIS:O	1:B:234:SER:HA	2.19	0.42
1:B:198:ASP:O	1:B:199:GLN:HB2	2.19	0.42
1:B:399:PHE:CG	1:B:528:ILE:HG13	2.54	0.42
1:A:466:ALA:O	1:A:469:THR:OG1	2.33	0.42
1:B:169:VAL:HG12	1:B:170:ILE:HG23	2.02	0.42
1:A:192:ASP:O	1:A:238:HIS:CE1	2.72	0.42
1:B:390:ILE:O	1:B:394:GLY:N	2.43	0.42
1:B:146:ILE:HG23	1:B:147:GLN:N	2.34	0.42
1:A:152:SER:O	1:A:156:TYR:CD2	2.72	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:146:ILE:HG21	1:B:454:LEU:CD1	2.45	0.42
1:A:262:ASN:OD1	1:A:262:ASN:C	2.58	0.42
1:A:87:VAL:HG21	1:A:121:ILE:HD11	2.01	0.42
1:A:459:ILE:HG13	1:A:459:ILE:O	2.20	0.42
1:B:234:SER:O	1:B:236:VAL:N	2.53	0.42
1:A:483:ASN:N	1:A:483:ASN:HD22	2.18	0.42
1:B:341:PRO:HG3	1:B:375:ASP:OD2	2.19	0.42
1:B:364:ASP:OD1	1:B:404:ALA:HA	2.19	0.42
1:B:521:PRO:HA	1:B:522:PRO:HD3	1.93	0.42
1:B:113:LEU:CG	1:B:117:TYR:CE1	3.02	0.42
1:A:451:VAL:CG2	1:A:474:ILE:HG12	2.37	0.42
1:A:161:ARG:HB2	1:B:429:LEU:HD23	2.01	0.42
1:B:22:ARG:HA	1:B:25:ILE:HG23	1.99	0.41
1:B:98:PRO:C	1:B:99:VAL:CG2	2.87	0.41
1:A:279:ASP:O	1:A:283:GLU:HG3	2.20	0.41
1:A:196:MET:SD	1:A:203:MET:CE	2.98	0.41
1:B:363:CYS:O	1:B:368:VAL:O	2.38	0.41
1:A:113:LEU:HD23	1:A:156:TYR:CE1	2.43	0.41
1:A:513:LEU:C	1:A:515:THR:H	2.23	0.41
1:B:128:ALA:HB1	1:B:170:ILE:HD12	2.03	0.41
1:A:387:HIS:O	1:A:389:GLY:N	2.54	0.41
1:B:339:ASN:OD1	1:B:424:MET:CE	2.68	0.41
1:A:40:GLN:HE22	1:A:45:LYS:NZ	2.18	0.41
1:B:523:LYS:HB3	1:B:523:LYS:HE2	1.87	0.41
1:B:457:ARG:C	1:B:459:ILE:H	2.22	0.41
1:B:435:LEU:N	1:B:435:LEU:CD1	2.83	0.41
1:B:302:ILE:O	1:B:305:VAL:CG2	2.60	0.41
1:A:403:GLU:HA	1:A:520:LEU:CD1	2.49	0.41
1:A:358:ARG:O	1:A:358:ARG:CG	2.68	0.41
1:B:133:CYS:HA	1:B:134:PRO:HD3	1.74	0.41
1:A:478:GLU:HG2	1:A:482:LEU:HD21	2.02	0.41
1:B:318:PHE:O	1:B:319:ALA:HB3	2.20	0.41
1:B:80:ASN:O	1:B:82:PRO:HD3	2.20	0.41
1:A:513:LEU:C	1:A:515:THR:N	2.71	0.41
1:B:192:ASP:O	1:B:238:HIS:CE1	2.74	0.41
1:A:211:ILE:O	1:A:215:THR:HG22	2.20	0.41
1:A:134:PRO:CB	1:A:171:PRO:HG2	2.51	0.41
1:A:380:LEU:HD13	1:A:381:PRO:O	2.21	0.41
1:B:195:VAL:HG11	1:B:251:VAL:HG22	2.03	0.41
1:B:100:ALA:O	1:B:135:VAL:HA	2.21	0.41
1:A:154:GLY:HA2	1:B:428:HIS:NE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:47:THR:O	1:B:51:ARG:HD2	2.20	0.41
1:A:69:ARG:NH1	1:A:83:TYR:OH	2.54	0.41
1:A:256:SER:HA	4:A:666:HOH:O	2.19	0.41
1:A:248:VAL:HG12	1:A:252:LYS:HD2	2.02	0.41
1:A:325:GLY:O	1:A:359:PHE:HZ	2.04	0.41
1:A:366:PHE:O	1:A:367:ASN:CB	2.65	0.41
1:B:231:ASN:ND2	1:B:238:HIS:C	2.74	0.41
1:B:451:VAL:HB	1:B:455:HIS:CD2	2.45	0.41
1:B:102:PHE:CE1	1:B:137:GLY:HA2	2.55	0.41
1:B:417:PHE:CZ	1:B:441:GLN:HB2	2.56	0.41
1:A:414:ARG:O	1:A:441:GLN:N	2.43	0.41
1:B:437:TRP:HE1	1:B:502:THR:HG1	1.67	0.41
1:B:183:GLY:O	1:B:184:ALA:C	2.60	0.41
1:A:406:VAL:HB	1:A:407:PRO:HD2	2.03	0.40
1:A:512:GLN:O	1:A:513:LEU:C	2.58	0.40
1:A:203:MET:O	1:A:225:GLY:HA3	2.21	0.40
1:A:11:ILE:O	1:A:17:LYS:HG3	2.21	0.40
1:B:166:ALA:O	1:B:169:VAL:N	2.47	0.40
1:A:284:LEU:CD2	1:A:304:HIS:CD2	3.05	0.40
1:B:266:PRO:HD3	1:B:367:ASN:O	2.21	0.40
1:A:377:PRO:HA	1:A:417:PHE:HD2	1.85	0.40
1:B:287:ILE:CG2	1:B:288:VAL:H	2.32	0.40
1:B:504:ARG:HH11	1:B:508:ARG:HH11	1.69	0.40
1:B:340:GLN:HG3	1:B:340:GLN:O	2.20	0.40
1:B:430:GLY:O	4:B:581:HOH:O	2.21	0.40
1:B:98:PRO:O	1:B:99:VAL:HG22	2.19	0.40
1:A:70:HIS:CE1	1:A:77:LEU:O	2.74	0.40
1:B:483:ASN:N	1:B:483:ASN:HD22	2.18	0.40
1:A:287:ILE:CG1	1:A:287:ILE:O	2.58	0.40
1:A:175:LEU:HD22	1:A:175:LEU:C	2.42	0.40
1:B:20:ASP:OD1	1:B:23:ARG:NH2	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	519/530 (98%)	459 (88%)	58 (11%)	2 (0%)	39	33
1	B	519/530 (98%)	458 (88%)	60 (12%)	1 (0%)	52	48
All	All	1038/1060 (98%)	917 (88%)	118 (11%)	3 (0%)	46	41

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	463	GLY
1	A	514	ARG
1	B	98	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	412/421 (98%)	374 (91%)	38 (9%)	11	6
1	B	412/421 (98%)	375 (91%)	37 (9%)	12	7
All	All	824/842 (98%)	749 (91%)	75 (9%)	12	6

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	LEU
1	A	35	ARG
1	A	40	GLN
1	A	43	LYS
1	A	53	ASP
1	A	80	ASN
1	A	117	TYR
1	A	119	GLN
1	A	129	LEU
1	A	147	GLN

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Mol	Chain	Res	Type
1	A	175	LEU
1	A	205	ILE
1	A	209	ASP
1	A	211	ILE
1	A	213	THR
1	A	215	THR
1	A	219	VAL
1	A	223	GLU
1	A	232	SER
1	A	245	LYS
1	A	263	LEU
1	A	264	SER
1	A	271	GLU
1	A	275	LEU
1	A	287	ILE
1	A	291	SER
1	A	342	MET
1	A	398	ILE
1	A	433	LEU
1	A	435	LEU
1	A	444	VAL
1	A	457	ARG
1	A	461	ASP
1	A	475	GLN
1	A	483	ASN
1	A	500	SER
1	A	527	ASN
1	A	528	ILE
1	B	23	ARG
1	B	25	ILE
1	B	35	ARG
1	B	39	LYS
1	B	40	GLN
1	B	49	ARG
1	B	77	LEU
1	B	124	VAL
1	B	146	ILE
1	B	147	GLN
1	B	177	VAL
1	B	195	VAL
1	B	200	THR
1	B	205	ILE

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Mol	Chain	Res	Type
1	B	212	LYS
1	B	213	THR
1	B	218	ASP
1	B	232	SER
1	B	245	LYS
1	B	254	LEU
1	B	280	GLU
1	B	293	ASN
1	B	342	MET
1	B	349	ASP
1	B	358	ARG
1	B	387	HIS
1	B	398	ILE
1	B	435	LEU
1	B	451	VAL
1	B	456	ARG
1	B	457	ARG
1	B	458	THR
1	B	461	ASP
1	B	472	ARG
1	B	473	LEU
1	B	483	ASN
1	B	508	ARG

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	30	HIS
1	A	40	GLN
1	A	70	HIS
1	A	74	ASN
1	A	80	ASN
1	A	119	GLN
1	A	147	GLN
1	A	230	HIS
1	A	231	ASN
1	A	299	HIS
1	A	385	GLN
1	A	448	GLN
1	A	455	HIS
1	A	483	ASN
1	A	505	HIS

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Mol	Chain	Res	Type
1	A	512	GLN
1	A	527	ASN
1	B	30	HIS
1	B	40	GLN
1	B	70	HIS
1	B	74	ASN
1	B	147	GLN
1	B	231	ASN
1	B	293	ASN
1	B	299	HIS
1	B	455	HIS
1	B	483	ASN
1	B	505	HIS
1	B	527	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

4 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
3	SO4	A	531	-	4,4,4	0.22	0	6,6,6	0.12	0
2	BTN	A	5600	-	12,17,17	4.66	8 (66%)	13,23,23	4.00	6 (46%)
3	SO4	B	531	-	4,4,4	0.19	0	6,6,6	0.13	0
2	BTN	B	5601	-	12,17,17	4.28	8 (66%)	13,23,23	4.37	5 (38%)

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	SO4	A	531	-	-	0/0/0/0	0/0/0/0
2	BTN	A	5600	-	-	0/5/28/28	0/2/2/2
3	SO4	B	531	-	-	0/0/0/0	0/0/0/0
2	BTN	B	5601	-	-	0/5/28/28	0/2/2/2

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	5600	BTN	C3-N1	-5.88	1.27	1.35
2	B	5601	BTN	C3-N1	-5.67	1.27	1.35
2	B	5601	BTN	C5-C4	-3.07	1.51	1.56
2	A	5600	BTN	C5-C4	-3.04	1.51	1.56
2	B	5601	BTN	O3-C3	2.79	1.29	1.23
2	A	5600	BTN	O3-C3	3.42	1.30	1.23
2	B	5601	BTN	C6-S1	3.67	1.92	1.81
2	A	5600	BTN	C6-S1	3.80	1.92	1.81
2	B	5601	BTN	C4-N2	5.11	1.55	1.45
2	A	5600	BTN	C4-N2	5.51	1.56	1.45
2	B	5601	BTN	C5-N1	5.94	1.56	1.45
2	B	5601	BTN	C2-S1	6.65	1.93	1.82
2	A	5600	BTN	C2-S1	6.83	1.93	1.82
2	B	5601	BTN	C3-N2	7.02	1.45	1.35
2	A	5600	BTN	C5-N1	7.02	1.58	1.45
2	A	5600	BTN	C3-N2	7.94	1.46	1.35

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	5601	BTN	O3-C3-N2	-9.51	114.86	125.90
2	A	5600	BTN	O3-C3-N2	-8.29	116.28	125.90
2	B	5601	BTN	C4-N2-C3	-7.96	105.05	112.66

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	5600	BTN	C4-N2-C3	-7.60	105.39	112.66
2	A	5600	BTN	C7-C2-S1	2.11	117.36	112.33
2	A	5600	BTN	O3-C3-N1	4.04	130.59	125.90
2	B	5601	BTN	C5-C4-N2	4.08	106.64	102.52
2	A	5600	BTN	C5-C4-N2	4.18	106.74	102.52
2	B	5601	BTN	O3-C3-N1	4.68	131.34	125.90
2	A	5600	BTN	N2-C3-N1	6.15	113.13	108.88
2	B	5601	BTN	N2-C3-N1	7.12	113.80	108.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5600	BTN	2	0
2	B	5601	BTN	2	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	521/530 (98%)	0.50	32 (6%)	25 26	22, 30, 55, 113	0
1	B	521/530 (98%)	0.54	36 (6%)	20 21	22, 31, 56, 102	0
All	All	1042/1060 (98%)	0.52	68 (6%)	22 23	22, 30, 56, 113	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	462	ALA	6.3
1	B	464	ASP	6.1
1	B	462	ALA	5.3
1	A	463	GLY	5.2
1	A	465	ASP	4.6
1	B	463	GLY	4.5
1	B	454	LEU	4.4
1	A	117	TYR	4.3
1	A	296	TYR	4.1
1	B	156	TYR	4.0
1	A	10	ASP	3.9
1	A	459	ILE	3.8
1	A	366	PHE	3.8
1	B	455	HIS	3.8
1	B	247	ALA	3.7
1	A	464	ASP	3.6
1	B	363	CYS	3.6
1	B	467	GLU	3.3
1	B	190	ILE	3.3
1	B	465	ASP	3.3
1	B	380	LEU	3.3
1	B	417	PHE	3.3
1	A	293	ASN	3.3
1	B	277	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	482	LEU	3.2
1	A	456	ARG	3.2
1	B	269	PHE	3.2
1	B	11	ILE	3.1
1	B	429	LEU	3.1
1	A	470	ARG	3.1
1	A	34	ALA	3.0
1	B	482	LEU	2.9
1	B	38	GLU	2.8
1	A	457	ARG	2.8
1	B	296	TYR	2.7
1	A	384	ASP	2.6
1	A	513	LEU	2.5
1	B	344	PHE	2.5
1	B	219	VAL	2.5
1	B	459	ILE	2.5
1	A	467	GLU	2.5
1	B	148	GLU	2.5
1	A	304	HIS	2.5
1	A	121	ILE	2.5
1	A	461	ASP	2.4
1	B	268	ALA	2.4
1	A	11	ILE	2.4
1	B	433	LEU	2.4
1	B	48	ALA	2.3
1	B	26	GLU	2.3
1	A	433	LEU	2.3
1	B	221	PHE	2.3
1	A	265	GLU	2.3
1	B	292	ALA	2.3
1	B	265	GLU	2.2
1	B	23	ARG	2.2
1	B	456	ARG	2.2
1	A	230	HIS	2.2
1	B	513	LEU	2.2
1	A	452	ASN	2.2
1	A	292	ALA	2.2
1	A	469	THR	2.1
1	B	54	LEU	2.1
1	A	218	ASP	2.1
1	A	211	ILE	2.0
1	A	268	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	211	ILE	2.0
1	A	498	MET	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

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(Å ²)	Q<0.9
2	BTN	A	5600	16/16	0.85	0.16	0.59	54,57,69,70	0
2	BTN	B	5601	16/16	0.78	0.19	0.56	55,58,75,75	0
3	SO4	A	531	5/5	0.96	0.15	-0.08	38,38,39,41	0
3	SO4	B	531	5/5	0.98	0.12	-0.33	36,38,39,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.