



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 12:59 am GMT

PDB ID : 2WQZ  
Title : Crystal structure of synaptic protein neuroligin-4 in complex with neurexin-beta 1: alternative refinement  
Authors : Fabrichny, I.P.; Leone, P.; Sulzenbacher, G.; Comoletti, D.; Miller, M.T.; Taylor, P.; Bourne, Y.; Marchot, P.  
Deposited on : 2009-08-28  
Resolution : 3.90 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

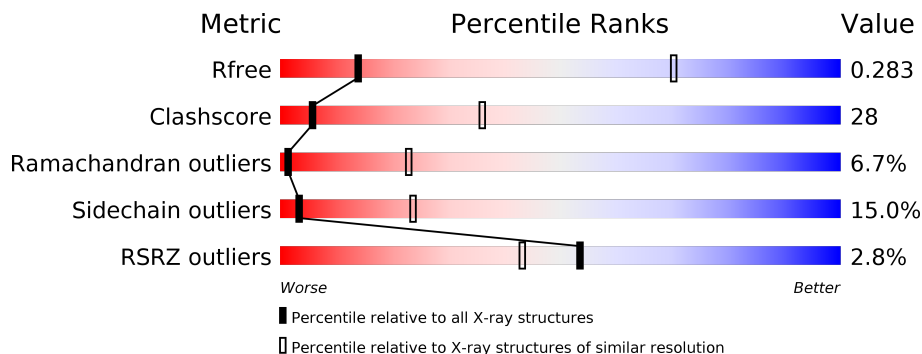
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.90 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))
$R_{free}$	100719	1007 (4.20-3.60)
Clashscore	112137	1103 (4.20-3.60)
Ramachandran outliers	110173	1062 (4.20-3.60)
Sidechain outliers	110143	1053 (4.20-3.60)
RSRZ outliers	101464	1020 (4.20-3.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	588	<div> <div>0%</div> <div> <div>42%</div> <div>38%</div> <div>11%</div> <div>7%</div> </div> </div>
1	B	588	<div> <div>3%</div> <div> <div>47%</div> <div>36%</div> <div>8%</div> <div>7%</div> </div> </div>
2	C	179	<div> <div>3%</div> <div> <div>54%</div> <div>36%</div> <div>9%</div> <div>2%</div> </div> </div>
2	D	179	<div> <div>9%</div> <div> <div>54%</div> <div>36%</div> <div>8%</div> <div>1%</div> </div> </div>

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11360 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 NEUROLIGIN 4, X-LINKED.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	545	Total	C	N	O	S	0	0	0
			4310	2756	712	821	21			
1	B	544	Total	C	N	O	S	0	0	0
			4302	2749	713	819	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	561	ARG	LYS	CONFLICT	UNP Q8N0W4
B	561	ARG	LYS	CONFLICT	UNP Q8N0W4

- Molecule 2 is a protein called NEUREXIN-1-BETA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	177	Total	C	N	O	S	0	0	0
			1359	857	243	258	1			
2	D	177	Total	C	N	O	S	0	0	0
			1359	857	243	258	1			

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

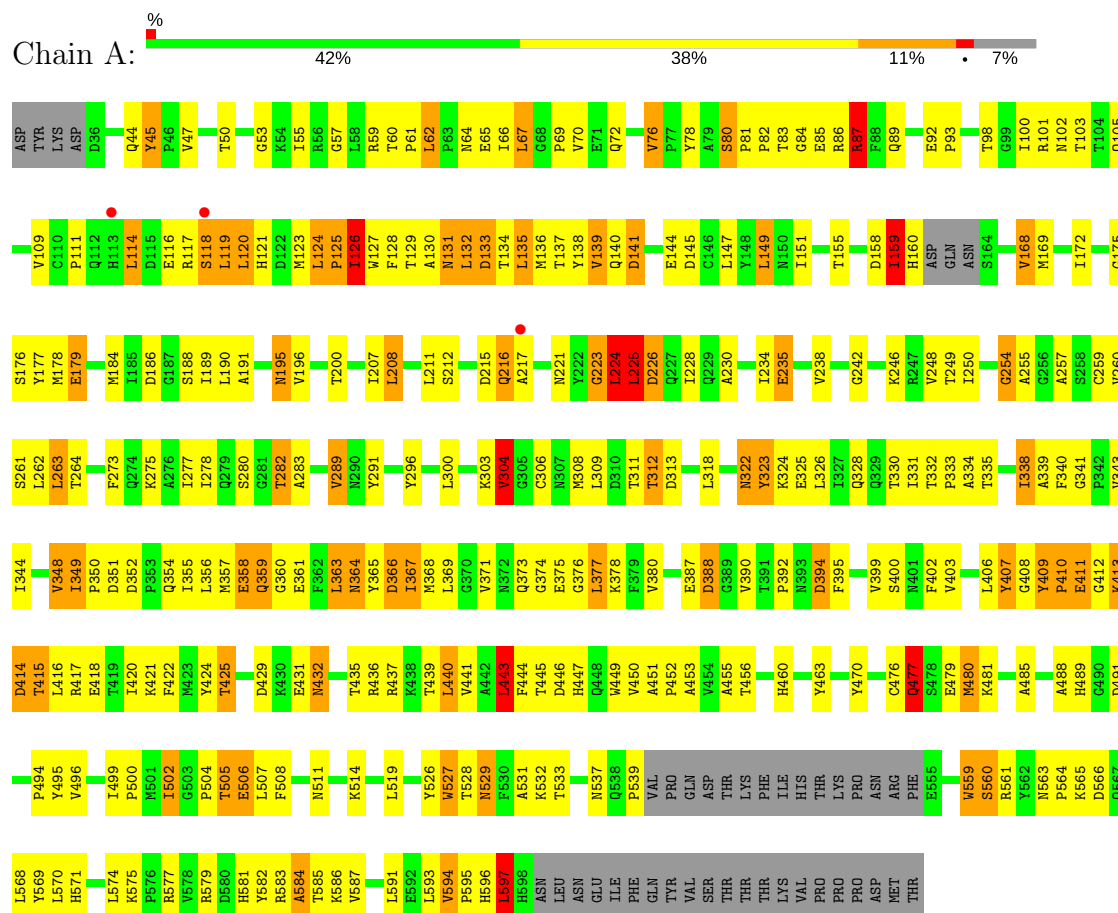
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		

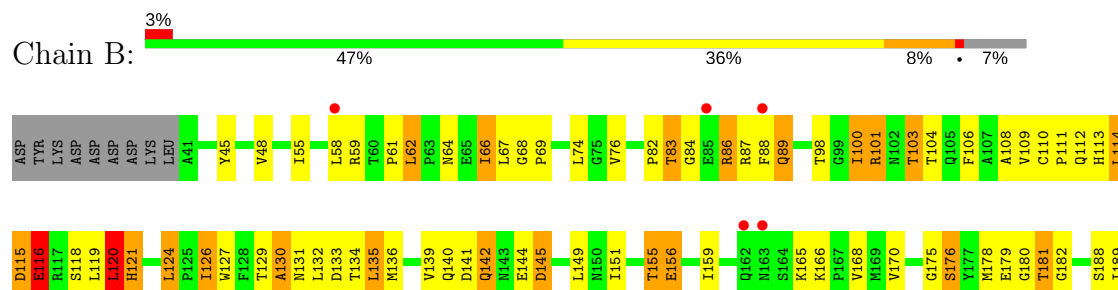
### 3 Residue-property plots

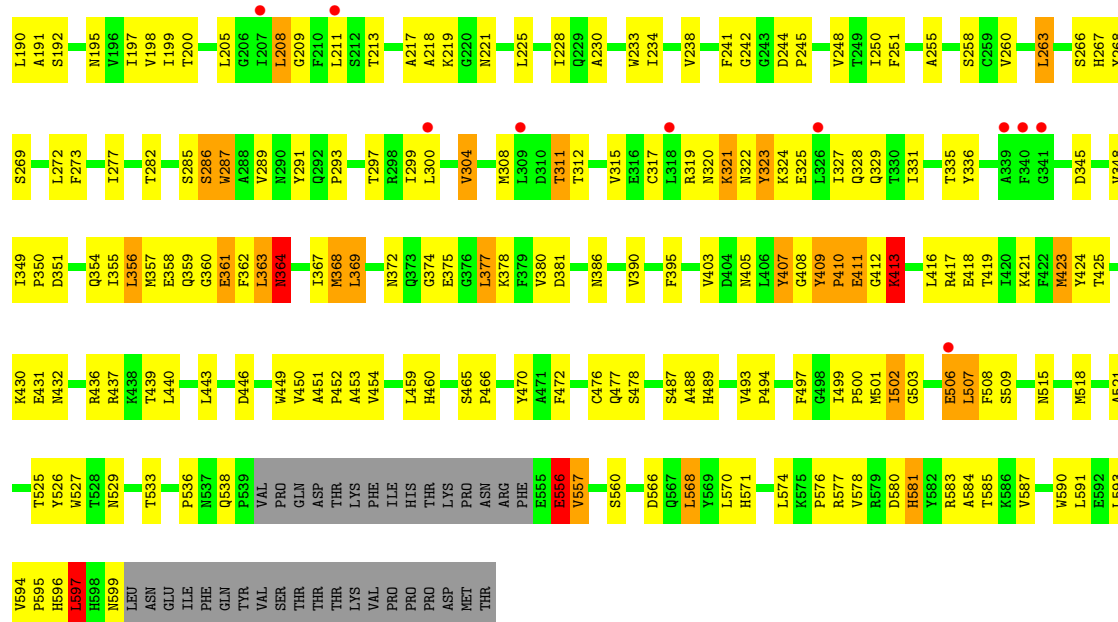
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: NEUROLIGIN 4, X-LINKED

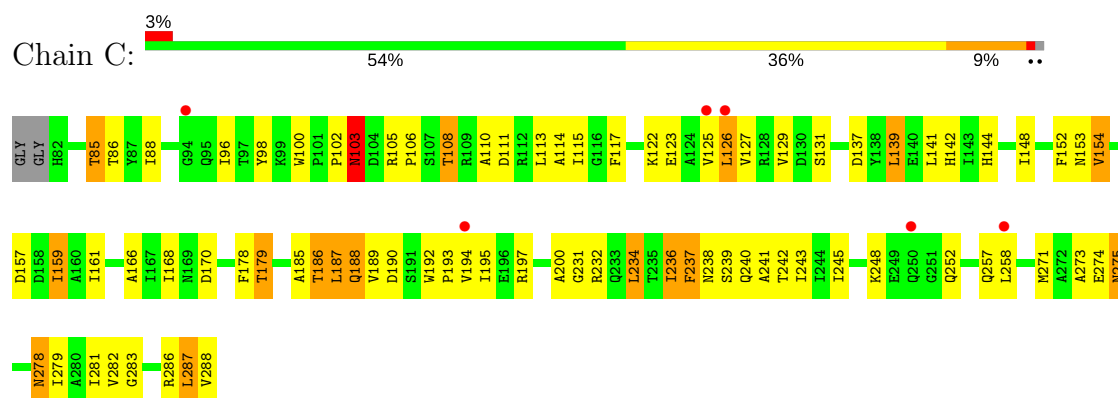


#### • Molecule 1: NEUROLIGIN 4, X-LINKED

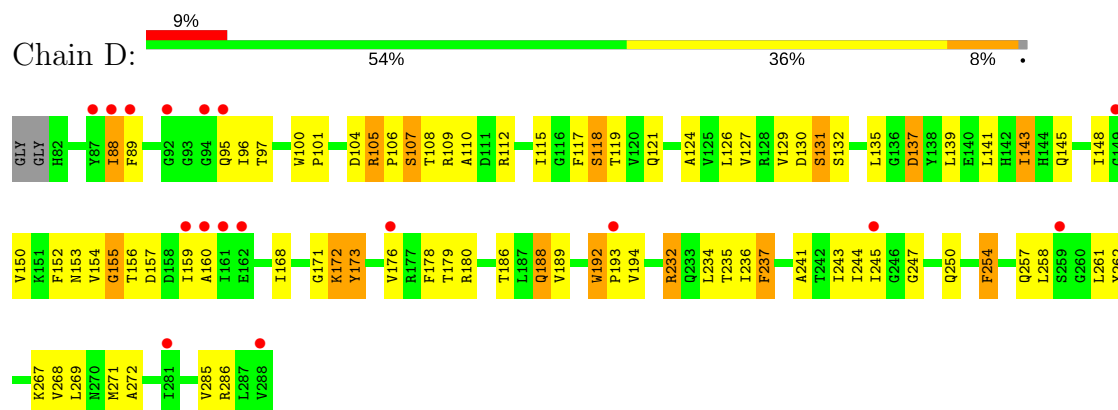




### • Molecule 2: NEUREXIN-1-BETA



### • Molecule 2: NEUREXIN-1-BETA



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	158.52Å 198.67Å 85.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.90 47.40 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.90) 96.2 (47.40-3.20)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.43 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, $R_{free}$	0.205 , 0.276 0.212 , 0.283	Depositor DCC
$R_{free}$ test set	1263 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	92.0	Xtriage
Anisotropy	0.258	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 93.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.39$ , $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.90	EDS
Total number of atoms	11360	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	72.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.35% of the height of the origin peak. No significant pseudotranslation is detected.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

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

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	0.54	0/4429	0.70	1/6040 (0.0%)
1	B	0.50	0/4422	0.66	0/6033
2	C	0.47	0/1384	0.67	0/1874
2	D	0.59	0/1384	0.68	0/1874
All	All	0.53	0/11619	0.68	1/15821 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	3
All	All	0	8

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	597	LEU	CA-CB-CG	5.89	128.85	115.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	360	GLY	Peptide
1	A	410	PRO	Peptide
1	A	411	GLU	Peptide

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Mol	Chain	Res	Type	Group
1	A	537	ASN	Peptide
1	A	597	LEU	Peptide
1	B	556	GLU	Peptide
1	B	596	HIS	Peptide
1	B	597	LEU	Peptide

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4310	0	4133	277	0
1	B	4302	0	4122	211	0
2	C	1359	0	1346	69	0
2	D	1359	0	1346	88	0
3	A	28	0	26	8	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
All	All	11360	0	10973	625	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 28.

All (625) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:119:LEU:O	1:B:120:LEU:HD22	1.53	1.08
1:A:189:ILE:HD11	1:A:502:ILE:HD12	1.28	1.08
1:A:139:VAL:HG13	1:A:140:GLN:H	1.24	0.98
1:A:149:LEU:CD1	1:A:151:ILE:HD11	1.96	0.95
2:D:141:LEU:HD11	2:D:148:ILE:HG23	1.47	0.94
2:D:95:GLN:HE21	2:D:244:ILE:HG23	1.35	0.92
1:A:367:ILE:HD12	1:A:460:HIS:CE1	2.06	0.90
1:A:168:VAL:HG11	1:A:238:VAL:HG21	1.53	0.89
2:C:179:THR:OG1	2:C:186:THR:HG23	1.74	0.87
2:D:127:VAL:HG22	2:D:245:ILE:HG23	1.55	0.87
2:D:141:LEU:HD11	2:D:148:ILE:CG2	2.03	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:432:ASN:ND2	1:A:435:THR:OG1	2.09	0.86
1:B:597:LEU:HD21	1:B:599:ASN:HD22	1.41	0.86
1:B:361:GLU:HA	2:C:236:ILE:CD1	2.06	0.86
2:C:236:ILE:N	2:C:236:ILE:HD12	1.91	0.84
1:A:149:LEU:HD13	1:A:151:ILE:CD1	2.09	0.83
1:A:149:LEU:HD13	1:A:151:ILE:HD11	1.61	0.82
2:D:95:GLN:NE2	2:D:244:ILE:HG23	1.94	0.82
1:A:175:GLY:H	1:A:255:ALA:HB3	1.47	0.80
1:B:361:GLU:HA	2:C:236:ILE:HD13	1.62	0.80
1:B:581:HIS:HB3	1:B:584:ALA:HB2	1.64	0.80
1:A:136:MET:O	1:A:139:VAL:HG12	1.82	0.80
1:B:360:GLY:O	1:B:362:PHE:N	2.16	0.79
1:B:408:GLY:O	1:B:410:PRO:HD3	1.82	0.79
2:C:102:PRO:O	2:C:103:ASN:CG	2.22	0.79
1:B:151:ILE:HG21	1:B:241:PHE:HE1	1.49	0.78
2:C:127:VAL:HG22	2:C:245:ILE:HG23	1.65	0.78
1:A:300:LEU:HD12	1:A:331:ILE:HD11	1.65	0.78
1:B:114:LEU:HD13	1:B:132:LEU:HD22	1.66	0.77
1:B:250:ILE:CD1	1:B:263:LEU:HD11	2.15	0.77
1:B:234:ILE:O	1:B:238:VAL:HG12	1.84	0.77
1:B:129:THR:HG23	1:B:129:THR:O	1.82	0.77
1:A:111:PRO:HG3	1:A:208:LEU:HD12	1.67	0.76
1:B:507:LEU:HD22	1:B:508:PHE:CD1	2.20	0.76
1:A:149:LEU:HD11	1:A:151:ILE:HD11	1.68	0.76
2:C:236:ILE:HD12	2:C:236:ILE:H	1.51	0.75
2:C:129:VAL:HG12	2:C:243:ILE:HG12	1.69	0.75
1:A:581:HIS:HB3	1:A:584:ALA:HB2	1.68	0.75
1:A:131:ASN:ND2	1:A:135:LEU:HD21	2.00	0.75
1:A:304:VAL:CG1	1:A:304:VAL:O	2.35	0.74
2:C:125:VAL:HG23	2:C:252:GLN:HE21	1.52	0.74
1:A:111:PRO:CG	1:A:208:LEU:HD12	2.16	0.74
1:A:359:GLN:O	1:A:463:TYR:CE2	2.41	0.73
1:A:189:ILE:HD11	1:A:502:ILE:CD1	2.14	0.73
1:B:55:ILE:HB	1:B:103:THR:HG21	1.69	0.73
2:D:155:GLY:HA3	2:D:234:LEU:HD12	1.68	0.73
2:D:96:ILE:HG22	2:D:245:ILE:HB	1.70	0.72
1:B:367:ILE:CG2	1:B:369:LEU:HD22	2.19	0.72
1:B:129:THR:HG21	1:B:378:LYS:HE2	1.70	0.72
1:B:351:ASP:HB3	1:B:356:LEU:HD23	1.70	0.71
1:B:368:MET:CE	1:B:536:PRO:HG3	2.21	0.71
1:A:114:LEU:HD22	1:A:114:LEU:H	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:143:ILE:HG22	2:D:143:ILE:O	1.91	0.71
1:A:86:ARG:NH1	1:A:92:GLU:OE1	2.24	0.71
1:A:505:THR:CG2	1:A:508:PHE:HB2	2.21	0.70
1:A:526:TYR:HE2	1:A:570:LEU:HD21	1.57	0.70
1:B:139:VAL:HG12	1:B:139:VAL:O	1.91	0.70
1:A:390:VAL:O	1:A:436:ARG:NH1	2.24	0.70
2:D:126:LEU:HD23	2:D:143:ILE:HD11	1.73	0.70
1:B:250:ILE:HD11	1:B:263:LEU:HD11	1.73	0.69
1:A:304:VAL:O	1:A:304:VAL:HG13	1.92	0.69
1:A:102:ASN:ND2	3:A:1599:NAG:H2	2.07	0.69
1:B:411:GLU:O	1:B:413:LYS:N	2.25	0.69
2:C:287:LEU:H	2:C:287:LEU:HD12	1.57	0.69
2:D:131:SER:O	2:D:241:ALA:HB3	1.93	0.68
1:A:413:LYS:O	1:A:416:LEU:N	2.26	0.68
1:A:207:ILE:HD11	1:A:300:LEU:CD1	2.23	0.68
1:A:402:PHE:CE1	1:A:406:LEU:HD12	2.29	0.68
1:A:66:ILE:HD12	1:A:66:ILE:O	1.94	0.68
1:B:250:ILE:HG12	1:B:260:VAL:HG13	1.75	0.68
1:B:367:ILE:HG23	1:B:369:LEU:HD22	1.74	0.68
1:B:114:LEU:CD1	1:B:132:LEU:HD22	2.24	0.68
2:C:152:PHE:CZ	2:C:159:ILE:HD12	2.29	0.67
1:A:207:ILE:HD11	1:A:300:LEU:HD11	1.75	0.67
2:C:189:VAL:HG12	2:C:190:ASP:OD2	1.94	0.67
2:C:117:PHE:CZ	2:C:168:ILE:HD13	2.29	0.67
1:A:324:LYS:O	1:A:326:LEU:N	2.26	0.67
1:B:121:HIS:HA	1:B:124:LEU:HG	1.76	0.67
2:C:98:TYR:O	2:C:242:THR:HA	1.95	0.67
1:A:131:ASN:HB3	1:A:135:LEU:HD11	1.77	0.67
2:D:261:LEU:HD23	2:D:262:TYR:N	2.11	0.66
1:A:376:GLY:O	1:A:378:LYS:N	2.28	0.66
1:A:413:LYS:O	1:A:415:THR:N	2.29	0.65
1:B:121:HIS:HA	1:B:124:LEU:CG	2.27	0.65
1:B:191:ALA:HB2	1:B:198:VAL:HG23	1.79	0.65
1:B:501:MET:O	1:B:502:ILE:HD13	1.96	0.65
1:B:556:GLU:N	1:B:556:GLU:OE2	2.30	0.65
1:A:452:PRO:O	1:A:455:ALA:O	2.16	0.64
1:A:127:TRP:CE3	1:A:127:TRP:O	2.50	0.64
2:C:152:PHE:CE1	2:C:159:ILE:HD12	2.33	0.64
1:A:139:VAL:HG13	1:A:140:GLN:N	2.05	0.64
1:A:505:THR:OG1	1:A:506:GLU:O	2.09	0.64
1:B:355:ILE:O	1:B:359:GLN:HG2	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:570:LEU:HD12	1:B:571:HIS:N	2.14	0.63
2:C:179:THR:HG1	2:C:186:THR:HG23	1.64	0.63
2:D:268:VAL:HG12	2:D:269:LEU:HG	1.80	0.63
1:B:131:ASN:HB3	1:B:134:THR:HG22	1.81	0.63
1:B:454:VAL:HG11	1:B:587:VAL:HG11	1.80	0.63
1:A:126:ILE:HG22	1:A:489:HIS:O	1.97	0.63
1:A:443:LEU:HD23	1:A:444:PHE:N	2.14	0.63
1:A:119:LEU:HD12	1:A:120:LEU:HD22	1.80	0.63
1:A:262:LEU:HD22	1:A:349:ILE:CD1	2.29	0.63
1:B:124:LEU:HD12	1:B:124:LEU:O	1.99	0.63
1:B:58:LEU:HD23	1:B:104:THR:HB	1.80	0.63
1:A:368:MET:HE1	1:A:527:TRP:CE3	2.33	0.62
1:B:64:ASN:HD21	1:B:67:LEU:HB3	1.64	0.62
1:B:151:ILE:HG21	1:B:241:PHE:CE1	2.31	0.62
1:B:515:ASN:HB3	1:B:574:LEU:HD21	1.82	0.62
2:C:161:ILE:HD11	2:C:195:ILE:O	1.98	0.62
1:A:304:VAL:HG21	1:A:326:LEU:HD23	1.81	0.61
1:A:159:ILE:H	1:A:159:ILE:HD13	1.65	0.61
1:A:250:ILE:HG13	1:A:260:VAL:HG13	1.82	0.61
1:A:81:PRO:O	1:A:83:THR:HG22	2.01	0.61
1:B:151:ILE:HD13	1:B:241:PHE:CZ	2.36	0.61
1:A:189:ILE:CD1	1:A:502:ILE:HD12	2.17	0.61
1:B:351:ASP:HB3	1:B:356:LEU:CD2	2.30	0.61
1:B:507:LEU:C	1:B:507:LEU:HD23	2.21	0.61
1:A:333:PRO:HG3	1:A:339:ALA:HB2	1.81	0.61
1:B:395:PHE:CD1	1:B:440:LEU:HD21	2.36	0.60
1:A:526:TYR:CE2	1:A:570:LEU:HD21	2.37	0.60
1:B:55:ILE:HB	1:B:103:THR:CG2	2.32	0.60
1:A:338:ILE:HD12	1:A:341:GLY:HA3	1.82	0.60
2:D:236:ILE:O	2:D:236:ILE:HD12	2.01	0.60
2:D:97:THR:OG1	2:D:244:ILE:HD12	2.01	0.60
1:A:136:MET:HB3	1:A:139:VAL:CG1	2.32	0.60
1:A:217:ALA:HB2	1:A:312:THR:HG23	1.81	0.60
1:B:132:LEU:O	1:B:135:LEU:HD22	2.01	0.60
1:A:207:ILE:CD1	1:A:300:LEU:HD11	2.31	0.60
1:B:129:THR:O	1:B:130:ALA:HB2	2.02	0.60
1:A:102:ASN:HD22	3:A:1599:NAG:H82	1.67	0.60
1:A:435:THR:O	1:A:439:THR:HG23	2.01	0.60
1:A:344:ILE:HD13	1:A:344:ILE:N	2.16	0.59
1:B:74:LEU:HD22	1:B:106:PHE:CE1	2.37	0.59
1:A:70:VAL:HG21	1:A:188:SER:CB	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:192:TRP:HB3	2:D:193:PRO:CD	2.32	0.59
1:A:149:LEU:HD13	1:A:151:ILE:HD13	1.83	0.59
2:C:102:PRO:O	2:C:103:ASN:ND2	2.35	0.59
1:B:55:ILE:HD13	1:B:76:VAL:HG22	1.84	0.59
1:A:422:PHE:HB2	1:B:593:LEU:HD13	1.84	0.59
1:B:335:THR:OG1	1:B:405:ASN:ND2	2.36	0.59
1:B:363:LEU:N	1:B:363:LEU:HD22	2.17	0.59
1:A:593:LEU:HD21	1:B:419:THR:OG1	2.03	0.59
1:A:351:ASP:OD2	1:A:352:ASP:N	2.27	0.58
1:A:505:THR:HG23	1:A:508:PHE:HB2	1.85	0.58
1:A:377:LEU:HD22	1:A:485:ALA:HB1	1.83	0.58
1:A:135:LEU:N	1:A:135:LEU:HD23	2.18	0.58
2:C:166:ALA:HB3	2:C:192:TRP:CZ3	2.38	0.58
2:C:234:LEU:HD22	2:C:236:ILE:CD1	2.34	0.58
2:D:261:LEU:HD13	2:D:268:VAL:HB	1.84	0.58
2:C:88:ILE:HG13	2:C:288:VAL:HG22	1.86	0.58
1:A:371:VAL:HG21	1:A:450:VAL:HG22	1.85	0.58
2:D:88:ILE:O	2:D:285:VAL:HG13	2.03	0.58
1:A:410:PRO:O	1:A:412:GLY:N	2.30	0.58
1:A:64:ASN:OD1	1:A:65:GLU:N	2.37	0.58
1:B:403:VAL:HG13	1:B:416:LEU:HD23	1.84	0.58
2:D:131:SER:O	2:D:241:ALA:CB	2.51	0.58
1:A:387:GLU:O	1:A:388:ASP:HB2	2.04	0.57
1:A:569:TYR:CZ	1:A:579:ARG:HB2	2.40	0.57
1:B:364:ASN:HD22	1:B:364:ASN:H	1.51	0.57
1:A:207:ILE:CD1	1:A:300:LEU:CD1	2.82	0.57
2:C:103:ASN:HD22	2:C:103:ASN:C	2.08	0.57
2:C:154:VAL:HG12	2:C:237:PHE:HA	1.87	0.57
1:B:361:GLU:HG3	2:C:236:ILE:HD11	1.86	0.57
1:A:147:LEU:HD22	1:A:226:ASP:HB3	1.87	0.57
1:B:62:LEU:HD22	1:B:68:GLY:O	2.03	0.57
2:D:269:LEU:HD23	2:D:272:ALA:CB	2.34	0.57
1:B:87:ARG:HD3	1:B:144:GLU:OE1	2.04	0.57
1:B:359:GLN:HB3	2:C:234:LEU:HD11	1.86	0.57
1:A:134:THR:HG22	1:A:134:THR:O	2.05	0.57
1:B:151:ILE:HD13	1:B:241:PHE:HZ	1.69	0.57
2:D:121:GLN:OE1	2:D:254:PHE:HA	2.05	0.56
1:B:62:LEU:CD2	1:B:68:GLY:O	2.53	0.56
1:B:144:GLU:OE2	1:B:208:LEU:HD11	2.04	0.56
1:B:234:ILE:HG23	1:B:238:VAL:HB	1.86	0.56
1:A:368:MET:HE1	1:A:527:TRP:CZ3	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:593:LEU:HD22	1:B:419:THR:HA	1.87	0.56
1:B:304:VAL:HG13	1:B:321:LYS:HE2	1.88	0.56
1:B:127:TRP:CE3	1:B:507:LEU:HD21	2.41	0.56
2:D:172:LYS:HZ2	2:D:173:TYR:H	1.51	0.56
1:A:70:VAL:HG21	1:A:188:SER:HB2	1.88	0.56
1:B:139:VAL:CG1	1:B:139:VAL:O	2.52	0.56
1:B:48:VAL:HG13	1:B:241:PHE:HB3	1.87	0.56
2:C:113:LEU:HD12	2:C:114:ALA:N	2.21	0.56
2:D:115:ILE:HD13	2:D:258:LEU:HD22	1.87	0.56
1:A:136:MET:HB3	1:A:139:VAL:HG11	1.87	0.55
1:B:250:ILE:O	1:B:250:ILE:HG23	2.06	0.55
1:B:268:TYR:CD2	1:B:348:VAL:HG23	2.42	0.55
1:A:407:TYR:HD2	1:A:407:TYR:N	2.05	0.55
2:D:261:LEU:HD23	2:D:262:TYR:H	1.72	0.55
1:A:196:VAL:HG11	1:A:528:THR:HG23	1.88	0.55
1:A:369:LEU:H	1:A:369:LEU:HD23	1.71	0.55
1:A:559:TRP:CE3	1:A:570:LEU:HD23	2.41	0.55
2:C:168:ILE:C	2:C:168:ILE:HD12	2.27	0.55
2:D:115:ILE:CD1	2:D:258:LEU:HD22	2.36	0.55
1:A:352:ASP:HB3	1:A:355:ILE:HD12	1.89	0.55
1:A:594:VAL:HG12	1:A:595:PRO:HD3	1.88	0.55
1:A:494:PRO:HB3	1:A:499:ILE:HD12	1.89	0.54
1:B:590:TRP:CE3	1:B:594:VAL:HG21	2.42	0.54
1:A:455:ALA:O	1:A:456:THR:HB	2.07	0.54
1:A:476:CYS:O	1:A:477:GLN:O	2.25	0.54
1:A:357:MET:O	1:A:359:GLN:N	2.40	0.54
1:A:395:PHE:CD1	1:A:440:LEU:HD13	2.42	0.54
1:B:502:ILE:HG22	1:B:503:GLY:H	1.73	0.54
2:C:85:THR:HG21	2:C:273:ALA:HB2	1.88	0.54
1:A:488:ALA:N	1:A:491:ASP:OD1	2.41	0.54
1:A:114:LEU:HD22	1:A:114:LEU:N	2.22	0.54
1:B:221:ASN:O	1:B:225:LEU:HD12	2.08	0.54
2:D:88:ILE:HG22	2:D:286:ARG:HB2	1.90	0.54
1:A:273:PHE:CE2	1:A:365:TYR:CE1	2.96	0.54
1:B:139:VAL:O	1:B:142:GLN:NE2	2.41	0.54
1:A:377:LEU:H	1:A:441:VAL:HG13	1.72	0.54
1:A:407:TYR:CD2	1:A:407:TYR:N	2.75	0.54
2:D:186:THR:HG23	2:D:194:VAL:CG1	2.38	0.54
1:A:175:GLY:O	1:A:255:ALA:CB	2.57	0.53
1:A:593:LEU:O	1:A:594:VAL:HG23	2.09	0.53
1:B:62:LEU:HD23	1:B:67:LEU:HD13	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:195:ASN:HD22	1:A:195:ASN:C	2.11	0.53
1:B:67:LEU:HD22	1:B:68:GLY:H	1.73	0.53
2:D:137:ASP:HA	2:D:153:ASN:O	2.08	0.53
2:D:261:LEU:HD13	2:D:268:VAL:CG1	2.39	0.53
1:A:131:ASN:O	1:A:133:ASP:N	2.42	0.53
1:A:61:PRO:HA	1:A:69:PRO:HA	1.91	0.53
1:A:102:ASN:HD22	3:A:1599:NAG:C8	2.21	0.53
1:A:451:ALA:HA	1:A:587:VAL:HG13	1.91	0.53
1:B:67:LEU:HD11	1:B:192:SER:OG	2.09	0.53
2:C:115:ILE:HD11	2:C:258:LEU:HB3	1.90	0.53
1:A:594:VAL:HG12	1:A:595:PRO:CD	2.40	0.52
1:B:156:GLU:OE1	1:B:195:ASN:ND2	2.41	0.52
1:B:327:ILE:O	1:B:329:GLN:N	2.41	0.52
1:A:494:PRO:HB3	1:A:508:PHE:CD2	2.44	0.52
1:A:217:ALA:HB2	1:A:312:THR:CG2	2.38	0.52
1:B:251:PHE:HB2	1:B:277:ILE:HB	1.91	0.52
1:B:368:MET:HE2	1:B:536:PRO:HG3	1.91	0.52
1:A:403:VAL:HG21	1:A:417:ARG:HB2	1.91	0.52
1:B:135:LEU:HD22	1:B:136:MET:N	2.24	0.52
1:A:373:GLN:O	1:A:445:THR:HG21	2.10	0.52
1:A:506:GLU:O	1:A:507:LEU:HB2	2.08	0.52
1:A:125:PRO:O	1:A:126:ILE:C	2.48	0.52
1:A:149:LEU:O	1:A:149:LEU:HD12	2.09	0.52
1:A:82:PRO:HA	1:A:86:ARG:HB2	1.91	0.52
1:B:129:THR:HG21	1:B:378:LYS:CE	2.38	0.52
1:B:62:LEU:HD23	1:B:67:LEU:CD1	2.40	0.52
2:D:115:ILE:HD12	2:D:261:LEU:CD1	2.39	0.52
1:A:395:PHE:CZ	1:A:425:THR:HG23	2.44	0.52
1:B:357:MET:HB3	1:B:459:LEU:HD13	1.92	0.52
1:A:228:ILE:HD12	1:A:228:ILE:N	2.25	0.52
1:A:334:ALA:O	1:A:335:THR:C	2.49	0.52
1:A:277:ILE:HA	1:A:368:MET:O	2.10	0.52
1:A:413:LYS:O	1:A:414:ASP:C	2.48	0.52
1:B:82:PRO:HD2	1:B:145:ASP:HA	1.91	0.52
1:B:211:LEU:HD11	1:B:297:THR:HG23	1.92	0.52
1:B:424:TYR:CE2	1:B:443:LEU:HA	2.45	0.52
1:B:594:VAL:HG12	1:B:595:PRO:N	2.25	0.52
2:D:88:ILE:CG2	2:D:286:ARG:HB2	2.40	0.52
1:A:511:ASN:ND2	3:A:1600:NAG:C1	2.73	0.51
1:A:559:TRP:O	1:A:560:SER:CB	2.58	0.51
1:B:525:THR:HG22	1:B:529:ASN:OD1	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:115:ILE:HG12	2:D:258:LEU:HD22	1.92	0.51
1:A:402:PHE:CE1	1:A:406:LEU:CD1	2.94	0.51
1:B:131:ASN:O	1:B:134:THR:N	2.43	0.51
1:A:175:GLY:HA3	1:A:179:GLU:OE2	2.09	0.51
1:A:594:VAL:O	1:A:597:LEU:HG	2.11	0.51
1:B:581:HIS:HB3	1:B:584:ALA:CB	2.40	0.51
2:D:88:ILE:HG23	2:D:89:PHE:N	2.26	0.51
1:B:129:THR:O	1:B:130:ALA:CB	2.58	0.51
1:A:212:SER:CB	1:A:343:VAL:HG21	2.41	0.51
1:A:86:ARG:O	1:A:87:ARG:C	2.48	0.51
2:D:129:VAL:HG12	2:D:243:ILE:HG12	1.92	0.51
1:A:406:LEU:HD13	1:A:447:HIS:CE1	2.46	0.51
1:B:377:LEU:HD12	1:B:377:LEU:O	2.11	0.51
1:B:409:TYR:HB3	1:B:410:PRO:HD3	1.93	0.51
1:A:277:ILE:CG2	1:A:368:MET:HE2	2.41	0.51
1:B:217:ALA:HB2	1:B:312:THR:HG23	1.92	0.50
1:B:526:TYR:HE2	1:B:570:LEU:HD23	1.76	0.50
2:D:117:PHE:HB3	2:D:258:LEU:HD23	1.93	0.50
1:A:322:ASN:C	1:A:324:LYS:N	2.64	0.50
1:A:364:ASN:ND2	2:D:106:PRO:O	2.44	0.50
1:A:399:VAL:HG21	1:A:421:LYS:HB3	1.92	0.50
1:A:59:ARG:NH1	1:A:155:THR:HG21	2.26	0.50
2:C:271:MET:HB3	2:C:279:ILE:HD11	1.93	0.50
2:D:141:LEU:CD1	2:D:148:ILE:HG23	2.30	0.50
2:D:119:THR:O	2:D:171:GLY:N	2.44	0.50
1:A:172:ILE:HG21	1:A:259:CYS:HB2	1.93	0.50
1:A:451:ALA:O	1:A:591:LEU:HD11	2.12	0.50
1:B:55:ILE:HG22	1:B:101:ARG:HB3	1.92	0.50
1:B:369:LEU:N	1:B:369:LEU:HD23	2.26	0.50
1:A:367:ILE:HG22	1:A:367:ILE:O	2.10	0.50
1:B:268:TYR:HD2	1:B:348:VAL:HG23	1.77	0.50
2:C:234:LEU:CD2	2:C:236:ILE:CD1	2.90	0.50
1:A:223:GLY:O	1:A:225:LEU:N	2.45	0.50
2:C:192:TRP:HB3	2:C:193:PRO:CD	2.42	0.50
1:A:495:TYR:CD1	1:A:519:LEU:HD23	2.47	0.50
1:A:563:ASN:OD1	1:A:563:ASN:N	2.43	0.50
1:B:228:ILE:HG23	1:B:272:LEU:CD1	2.42	0.50
2:C:200:ALA:HA	2:C:231:GLY:N	2.27	0.50
1:B:127:TRP:CZ3	1:B:507:LEU:HD21	2.46	0.50
2:D:152:PHE:O	2:D:159:ILE:N	2.40	0.50
2:D:115:ILE:CG1	2:D:258:LEU:HD22	2.42	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:126:LEU:HD11	2:C:258:LEU:HD21	1.93	0.49
1:A:470:TYR:HB3	1:A:559:TRP:CZ2	2.47	0.49
1:B:168:VAL:CG1	1:B:199:ILE:HD12	2.42	0.49
1:B:364:ASN:N	1:B:364:ASN:HD22	2.10	0.49
2:D:129:VAL:CG2	2:D:139:LEU:HB3	2.42	0.49
2:D:186:THR:HG23	2:D:194:VAL:HG13	1.94	0.49
2:D:126:LEU:CD1	2:D:127:VAL:HG23	2.42	0.49
1:A:282:THR:OG1	1:A:283:ALA:N	2.45	0.49
1:B:129:THR:O	1:B:129:THR:CG2	2.53	0.49
2:C:234:LEU:HD22	2:C:236:ILE:HD12	1.95	0.49
1:A:234:ILE:HG23	1:A:238:VAL:HB	1.93	0.49
1:A:264:THR:HG22	1:A:365:TYR:CD2	2.47	0.49
1:A:289:VAL:HG23	1:A:291:TYR:HE2	1.77	0.49
2:C:161:ILE:HG23	2:C:187:LEU:HD22	1.94	0.49
1:B:230:ALA:O	1:B:233:TRP:HB3	2.13	0.49
1:B:300:LEU:O	1:B:300:LEU:HD23	2.12	0.49
1:B:525:THR:O	1:B:529:ASN:ND2	2.46	0.49
1:A:132:LEU:HD22	1:A:132:LEU:O	2.13	0.49
1:A:207:ILE:HG13	1:A:340:PHE:CE1	2.48	0.49
1:A:400:SER:HA	1:A:403:VAL:HG22	1.95	0.49
1:A:583:ARG:O	1:A:584:ALA:C	2.51	0.49
1:B:493:VAL:N	1:B:494:PRO:HD2	2.28	0.49
2:C:137:ASP:HA	2:C:153:ASN:O	2.13	0.49
1:A:149:LEU:HD12	1:A:149:LEU:C	2.33	0.49
1:A:50:THR:N	1:A:53:GLY:O	2.46	0.49
1:B:110:CYS:O	1:B:112:GLN:HG2	2.13	0.49
2:D:96:ILE:CG2	2:D:245:ILE:HB	2.41	0.49
1:A:390:VAL:HG23	1:A:437:ARG:HA	1.94	0.48
2:D:176:VAL:HG22	2:D:189:VAL:HG13	1.96	0.48
1:B:304:VAL:HG13	1:B:321:LYS:CE	2.43	0.48
2:D:141:LEU:HD11	2:D:148:ILE:HG22	1.92	0.48
2:D:192:TRP:CB	2:D:193:PRO:CD	2.91	0.48
2:D:117:PHE:HB2	2:D:257:GLN:O	2.13	0.48
1:B:451:ALA:HB3	1:B:452:PRO:CD	2.43	0.48
2:C:117:PHE:CE1	2:C:168:ILE:HD13	2.48	0.48
2:D:159:ILE:HG22	2:D:160:ALA:N	2.27	0.48
1:A:216:GLN:N	1:A:216:GLN:CD	2.67	0.48
1:A:76:VAL:CG2	1:A:103:THR:HG21	2.44	0.48
1:B:570:LEU:HD11	1:B:576:PRO:HB2	1.96	0.48
1:A:144:GLU:HG3	1:A:208:LEU:HD11	1.95	0.48
1:B:121:HIS:O	1:B:124:LEU:CD1	2.62	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:280:SER:OG	1:A:375:GLU:OE1	2.32	0.48
1:A:455:ALA:O	1:A:456:THR:CB	2.61	0.48
2:C:179:THR:O	2:C:185:ALA:HB1	2.13	0.48
1:B:115:ASP:O	1:B:116:GLU:C	2.52	0.47
1:B:250:ILE:HD13	1:B:263:LEU:HD11	1.95	0.47
1:B:423:MET:HE3	1:B:423:MET:HA	1.96	0.47
2:D:127:VAL:CG2	2:D:245:ILE:HG23	2.38	0.47
1:B:423:MET:CE	1:B:423:MET:HA	2.44	0.47
1:A:528:THR:O	1:A:531:ALA:N	2.46	0.47
1:B:118:SER:O	1:B:119:LEU:HD22	2.14	0.47
1:B:518:MET:O	1:B:521:ALA:HB3	2.15	0.47
1:A:59:ARG:CZ	1:A:155:THR:HG21	2.44	0.47
1:A:261:SER:O	1:A:264:THR:OG1	2.32	0.47
1:B:436:ARG:O	1:B:440:LEU:HD23	2.14	0.47
2:C:154:VAL:HG12	2:C:237:PHE:CA	2.44	0.47
1:A:304:VAL:HG12	1:A:306:CYS:SG	2.55	0.47
1:B:213:THR:HG21	1:B:311:THR:HB	1.96	0.47
1:B:213:THR:HG23	1:B:218:ALA:HB3	1.96	0.47
1:B:250:ILE:CD1	1:B:263:LEU:CD1	2.90	0.47
1:B:348:VAL:HG13	1:B:349:ILE:HG12	1.96	0.47
1:B:403:VAL:HG21	1:B:417:ARG:HA	1.97	0.47
2:C:126:LEU:HD11	2:C:258:LEU:CD2	2.44	0.47
1:B:120:LEU:N	1:B:120:LEU:HD13	2.30	0.47
1:B:189:ILE:HD11	1:B:501:MET:HB2	1.97	0.47
2:C:287:LEU:N	2:C:287:LEU:HD12	2.28	0.47
2:D:130:ASP:O	2:D:131:SER:OG	2.30	0.47
1:A:410:PRO:C	1:A:412:GLY:H	2.15	0.47
1:A:429:ASP:HB3	1:A:432:ASN:HB3	1.97	0.47
1:A:117:ARG:O	1:A:118:SER:HB3	2.15	0.47
1:A:130:ALA:O	1:A:131:ASN:CB	2.62	0.47
1:B:109:VAL:HG11	1:B:112:GLN:NE2	2.29	0.47
2:D:285:VAL:CG1	2:D:286:ARG:N	2.78	0.47
1:A:529:ASN:HB3	1:A:539:PRO:HD2	1.97	0.47
1:A:594:VAL:HG12	1:A:595:PRO:N	2.30	0.47
2:D:267:LYS:O	2:D:271:MET:HE2	2.15	0.47
1:B:248:VAL:HB	1:B:273:PHE:HA	1.97	0.46
1:B:293:PRO:O	1:B:297:THR:N	2.48	0.46
1:B:408:GLY:O	1:B:409:TYR:HB3	2.15	0.46
2:D:247:GLY:HA2	2:D:250:GLN:OE1	2.15	0.46
1:A:511:ASN:HD21	3:A:1600:NAG:C6	2.28	0.46
2:D:232:ARG:HD3	2:D:232:ARG:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:374:GLY:O	1:A:488:ALA:HA	2.16	0.46
1:B:568:LEU:N	1:B:568:LEU:HD13	2.31	0.46
1:A:136:MET:C	1:A:139:VAL:HG12	2.36	0.46
1:A:169:MET:HE2	1:A:531:ALA:HB2	1.96	0.46
1:B:354:GLN:O	1:B:355:ILE:C	2.54	0.46
1:A:125:PRO:O	1:A:127:TRP:N	2.48	0.46
1:A:135:LEU:HD22	1:A:507:LEU:H	1.80	0.46
1:A:443:LEU:O	1:A:446:ASP:N	2.49	0.46
1:B:410:PRO:O	1:B:411:GLU:C	2.54	0.46
1:A:424:TYR:CE2	1:A:443:LEU:HA	2.50	0.46
1:A:449:TRP:O	1:A:453:ALA:CB	2.64	0.46
1:A:470:TYR:CD1	1:A:470:TYR:C	2.89	0.46
1:B:418:GLU:O	1:B:421:LYS:HB3	2.15	0.46
1:A:207:ILE:HD11	1:A:300:LEU:HD13	1.98	0.46
1:A:234:ILE:O	1:A:235:GLU:C	2.55	0.46
1:B:109:VAL:HG12	1:B:110:CYS:H	1.81	0.46
1:B:587:VAL:HG12	1:B:591:LEU:HD12	1.96	0.46
1:A:137:THR:HG22	1:A:137:THR:O	2.16	0.46
1:B:526:TYR:HE2	1:B:570:LEU:CD2	2.29	0.46
2:D:117:PHE:O	2:D:173:TYR:HA	2.16	0.46
1:A:70:VAL:HG21	1:A:188:SER:HB3	1.98	0.46
1:A:132:LEU:HD22	1:A:132:LEU:C	2.37	0.45
1:A:207:ILE:HA	1:A:340:PHE:CD1	2.51	0.45
1:A:563:ASN:O	1:A:565:LYS:N	2.50	0.45
2:C:278:ASN:HD22	2:C:278:ASN:C	2.19	0.45
2:D:285:VAL:HG12	2:D:286:ARG:N	2.31	0.45
1:A:257:ALA:HB1	1:A:278:ILE:HG23	1.97	0.45
1:A:350:PRO:HD2	1:A:356:LEU:HD11	1.99	0.45
1:A:377:LEU:N	1:A:441:VAL:HG13	2.31	0.45
2:D:105:ARG:HH11	2:D:241:ALA:HB1	1.82	0.45
1:B:350:PRO:HG2	1:B:356:LEU:HD11	1.98	0.45
1:B:529:ASN:HD22	1:B:529:ASN:N	2.14	0.45
1:B:566:ASP:HB3	1:B:568:LEU:HD11	1.99	0.45
1:B:83:THR:HG23	1:B:84:GLY:N	2.31	0.45
2:C:200:ALA:CA	2:C:231:GLY:N	2.80	0.45
1:A:126:ILE:HD13	1:A:127:TRP:N	2.32	0.45
1:A:102:ASN:ND2	3:A:1599:NAG:C1	2.79	0.45
1:A:593:LEU:CD2	1:B:419:THR:HA	2.46	0.45
1:B:287:TRP:HE3	1:B:336:TYR:O	1.99	0.45
2:D:236:ILE:O	2:D:236:ILE:CD1	2.65	0.45
1:A:354:GLN:O	1:A:358:GLU:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:LEU:O	1:B:149:LEU:HD12	2.16	0.45
1:B:407:TYR:OH	1:B:594:VAL:HG11	2.17	0.45
2:C:102:PRO:O	2:C:103:ASN:CB	2.64	0.45
1:A:262:LEU:HD22	1:A:349:ILE:HD13	1.99	0.45
2:D:124:ALA:HB3	2:D:143:ILE:HB	1.98	0.45
2:D:131:SER:OG	2:D:132:SER:N	2.49	0.45
1:A:570:LEU:HD12	1:A:571:HIS:H	1.82	0.45
1:B:100:ILE:HG22	1:B:101:ARG:H	1.81	0.45
1:B:87:ARG:HG2	1:B:208:LEU:HD21	1.99	0.45
1:A:228:ILE:N	1:A:228:ILE:CD1	2.80	0.45
1:B:189:ILE:HG23	1:B:497:PHE:O	2.16	0.45
1:A:123:MET:SD	1:A:176:SER:OG	2.73	0.45
1:A:322:ASN:C	1:A:324:LYS:H	2.19	0.45
1:A:273:PHE:CE2	1:A:365:TYR:CD1	3.05	0.45
1:A:559:TRP:CD2	1:A:570:LEU:HD23	2.52	0.45
1:B:580:ASP:O	1:B:581:HIS:HB2	2.17	0.45
2:C:170:ASP:N	2:C:170:ASP:OD1	2.49	0.45
2:D:194:VAL:HG12	2:D:194:VAL:O	2.17	0.45
1:A:117:ARG:O	1:A:118:SER:CB	2.64	0.44
1:A:424:TYR:CD2	1:A:443:LEU:HB2	2.51	0.44
1:B:119:LEU:C	1:B:120:LEU:HD13	2.37	0.44
2:D:154:VAL:HG11	2:D:180:ARG:NH1	2.32	0.44
1:B:361:GLU:HA	2:C:236:ILE:CG1	2.47	0.44
1:A:169:MET:HE3	1:A:531:ALA:CB	2.48	0.44
1:A:403:VAL:CG1	1:A:420:ILE:HD12	2.48	0.44
1:A:184:MET:HB2	1:A:507:LEU:HD21	2.00	0.44
1:B:499:ILE:N	1:B:500:PRO:CD	2.80	0.44
2:D:188:GLN:HG3	2:D:194:VAL:HG22	1.99	0.44
2:C:274:GLU:O	2:C:275:ASN:HB3	2.17	0.44
2:D:101:PRO:O	2:D:104:ASP:N	2.50	0.44
2:D:126:LEU:CD2	2:D:143:ILE:HD11	2.43	0.44
1:B:114:LEU:HD12	1:B:119:LEU:HG	1.99	0.44
2:D:108:THR:HG22	2:D:109:ARG:N	2.32	0.44
2:D:115:ILE:HG23	2:D:115:ILE:O	2.16	0.44
1:A:178:MET:O	1:A:179:GLU:HB3	2.18	0.44
1:A:402:PHE:CZ	1:A:406:LEU:HD12	2.53	0.44
1:A:55:ILE:CD1	1:A:76:VAL:HG21	2.47	0.44
1:B:244:ASP:OD1	1:B:245:PRO:HD2	2.18	0.44
1:A:168:VAL:HG21	1:A:248:VAL:HG22	2.00	0.44
1:A:83:THR:O	1:A:85:GLU:N	2.50	0.44
1:B:126:ILE:HD13	1:B:126:ILE:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:590:TRP:HA	1:B:590:TRP:CE3	2.53	0.44
2:D:97:THR:OG1	2:D:244:ILE:CD1	2.65	0.44
1:A:87:ARG:HD2	1:A:144:GLU:OE2	2.18	0.44
1:A:289:VAL:CG2	1:A:291:TYR:HE2	2.30	0.44
1:A:499:ILE:N	1:A:500:PRO:CD	2.81	0.44
2:C:166:ALA:CB	2:C:192:TRP:CZ3	3.01	0.44
1:A:306:CYS:SG	1:A:318:LEU:HD23	2.58	0.43
2:D:261:LEU:HD13	2:D:268:VAL:CB	2.47	0.43
1:A:124:LEU:HB3	1:A:125:PRO:CD	2.49	0.43
1:A:139:VAL:CG1	1:A:140:GLN:H	2.08	0.43
1:A:221:ASN:HB3	1:A:224:LEU:CD1	2.48	0.43
1:A:177:TYR:CE2	1:A:338:ILE:HD13	2.53	0.43
1:B:354:GLN:HG2	1:B:358:GLU:OE2	2.18	0.43
1:B:431:GLU:O	1:B:432:ASN:C	2.57	0.43
1:A:331:ILE:O	1:A:333:PRO:HD3	2.18	0.43
1:B:493:VAL:N	1:B:494:PRO:CD	2.82	0.43
1:B:61:PRO:HA	1:B:69:PRO:HA	1.98	0.43
2:C:188:GLN:HB3	2:C:194:VAL:HA	2.00	0.43
1:A:277:ILE:HG21	1:A:368:MET:HE2	2.00	0.43
2:D:115:ILE:HD12	2:D:261:LEU:HD12	2.00	0.43
1:A:126:ILE:HG23	1:A:127:TRP:H	1.84	0.43
1:A:596:HIS:O	1:A:597:LEU:HD23	2.18	0.43
1:A:78:TYR:CE2	1:A:230:ALA:HB2	2.53	0.43
2:C:123:GLU:OE1	2:C:144:HIS:ND1	2.39	0.43
2:D:245:ILE:HD11	2:D:268:VAL:HG11	2.00	0.43
1:A:102:ASN:ND2	3:A:1599:NAG:C2	2.79	0.43
1:A:207:ILE:CD1	1:A:300:LEU:HD13	2.48	0.43
1:A:408:GLY:C	1:A:410:PRO:HD3	2.38	0.43
2:D:117:PHE:CZ	2:D:148:ILE:HG12	2.53	0.43
1:A:361:GLU:OE2	2:D:235:THR:N	2.51	0.43
1:A:443:LEU:O	1:A:444:PHE:C	2.56	0.43
2:D:244:ILE:HG22	2:D:244:ILE:O	2.18	0.43
1:A:348:VAL:HG12	1:A:349:ILE:N	2.33	0.43
1:A:479:GLU:OE1	1:A:479:GLU:N	2.52	0.43
1:A:377:LEU:HD23	1:A:488:ALA:HB2	2.01	0.43
1:B:144:GLU:CD	1:B:208:LEU:HD11	2.39	0.43
1:B:299:ILE:CG2	1:B:331:ILE:HG23	2.48	0.43
1:B:375:GLU:OE1	1:B:489:HIS:ND1	2.44	0.43
2:D:135:LEU:HA	2:D:135:LEU:HD23	1.80	0.43
1:A:190:LEU:O	1:A:191:ALA:C	2.56	0.43
1:A:263:LEU:O	1:A:264:THR:C	2.57	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:249:THR:HG23	1:A:275:LYS:O	2.18	0.43
1:A:169:MET:CE	1:A:531:ALA:HB2	2.48	0.43
1:B:250:ILE:HD13	1:B:263:LEU:CD1	2.48	0.43
1:B:449:TRP:O	1:B:453:ALA:CB	2.67	0.43
2:C:96:ILE:HG12	2:C:281:ILE:HG23	2.01	0.43
1:A:328:GLN:HG3	1:A:328:GLN:O	2.19	0.43
1:A:570:LEU:HD12	1:A:571:HIS:N	2.34	0.43
2:D:129:VAL:HG23	2:D:139:LEU:HB3	1.99	0.43
1:A:333:PRO:HG3	1:A:339:ALA:CB	2.49	0.42
1:B:109:VAL:HG13	1:B:181:THR:HB	2.00	0.42
1:B:317:CYS:O	1:B:320:ASN:HB2	2.19	0.42
1:B:390:VAL:HG23	1:B:437:ARG:HG3	2.01	0.42
1:B:83:THR:O	1:B:86:ARG:N	2.51	0.42
2:C:108:THR:HB	2:C:110:ALA:O	2.19	0.42
1:B:83:THR:O	1:B:87:ARG:N	2.51	0.42
2:C:85:THR:HG21	2:C:273:ALA:CB	2.48	0.42
1:A:431:GLU:O	1:A:432:ASN:C	2.58	0.42
1:B:345:ASP:OD2	1:B:348:VAL:HG12	2.18	0.42
2:C:106:PRO:HG2	2:C:240:GLN:HB2	2.02	0.42
2:C:131:SER:HA	2:C:239:SER:O	2.19	0.42
1:A:296:TYR:CD2	1:A:339:ALA:HA	2.54	0.42
1:A:440:LEU:HA	1:A:440:LEU:HD12	1.89	0.42
1:B:178:MET:C	1:B:179:GLU:HG3	2.40	0.42
1:B:315:VAL:HG11	1:B:319:ARG:HH21	1.85	0.42
1:B:372:ASN:OD1	1:B:472:PHE:HB3	2.20	0.42
1:A:207:ILE:HD13	1:A:326:LEU:O	2.20	0.42
1:A:470:TYR:CD1	1:A:470:TYR:O	2.73	0.42
1:A:533:THR:HG23	1:A:539:PRO:HG3	2.01	0.42
1:A:60:THR:HB	1:A:72:GLN:NE2	2.34	0.42
1:B:109:VAL:HG11	1:B:112:GLN:HE21	1.84	0.42
1:B:121:HIS:O	1:B:124:LEU:HD12	2.19	0.42
1:B:88:PHE:CE1	1:B:211:LEU:HD23	2.54	0.42
1:B:583:ARG:O	1:B:587:VAL:HG23	2.19	0.42
2:D:150:VAL:HG21	2:D:178:PHE:CE1	2.54	0.42
1:A:186:ASP:OD1	1:A:188:SER:OG	2.36	0.42
1:A:361:GLU:OE2	2:D:234:LEU:HB3	2.19	0.42
1:B:191:ALA:HB2	1:B:198:VAL:CG2	2.48	0.42
1:A:169:MET:HE3	1:A:531:ALA:HB3	2.02	0.42
1:A:207:ILE:HG23	1:A:208:LEU:N	2.34	0.42
1:A:443:LEU:HD23	1:A:444:PHE:CA	2.49	0.42
1:B:131:ASN:HB3	1:B:134:THR:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:LEU:CD1	1:B:151:ILE:HD11	2.49	0.42
1:B:361:GLU:CG	2:C:236:ILE:HD11	2.49	0.42
2:D:153:ASN:ND2	2:D:157:ASP:O	2.50	0.42
2:D:96:ILE:HG22	2:D:245:ILE:CB	2.45	0.42
1:A:409:TYR:N	1:A:410:PRO:CD	2.82	0.42
1:B:89:GLN:HA	1:B:89:GLN:HE21	1.84	0.42
2:C:86:THR:HG21	2:C:257:GLN:OE1	2.19	0.42
1:A:249:THR:HA	1:A:275:LYS:O	2.19	0.42
1:A:363:LEU:HD23	1:A:365:TYR:OH	2.20	0.42
1:A:418:GLU:O	1:B:593:LEU:HD11	2.20	0.42
1:B:178:MET:HB2	1:B:179:GLU:HG3	2.02	0.42
2:D:126:LEU:HB2	2:D:143:ILE:HD11	2.02	0.42
2:D:126:LEU:HD12	2:D:127:VAL:HG23	2.01	0.42
2:D:192:TRP:HB3	2:D:193:PRO:HD2	2.00	0.42
1:A:131:ASN:CB	1:A:135:LEU:HD11	2.46	0.41
1:A:359:GLN:O	1:A:463:TYR:CZ	2.73	0.41
1:B:180:GLY:O	1:B:205:LEU:HD11	2.20	0.41
1:B:322:ASN:HB2	1:B:323:TYR:CD1	2.55	0.41
1:B:446:ASP:HA	1:B:450:VAL:HB	2.02	0.41
1:B:361:GLU:CA	2:C:236:ILE:HD13	2.41	0.41
1:B:197:ILE:HD11	1:B:242:GLY:HA3	2.02	0.41
2:C:139:LEU:C	2:C:139:LEU:HD12	2.40	0.41
1:A:168:VAL:CG2	1:A:248:VAL:HG22	2.50	0.41
1:B:175:GLY:H	1:B:255:ALA:HB3	1.85	0.41
1:B:322:ASN:C	1:B:324:LYS:H	2.23	0.41
2:C:105:ARG:NH1	2:C:241:ALA:HB1	2.35	0.41
1:A:422:PHE:CG	1:B:593:LEU:HD22	2.56	0.41
1:A:215:ASP:O	1:A:217:ALA:N	2.53	0.41
1:A:406:LEU:C	1:A:407:TYR:HD2	2.24	0.41
1:A:511:ASN:ND2	3:A:1600:NAG:O6	2.51	0.41
1:B:465:SER:HA	1:B:466:PRO:HD3	1.96	0.41
2:C:274:GLU:O	2:C:275:ASN:CB	2.67	0.41
2:D:148:ILE:HD13	2:D:168:ILE:CD1	2.49	0.41
1:A:228:ILE:HD11	1:A:263:LEU:HD21	2.01	0.41
1:A:506:GLU:O	1:A:508:PHE:N	2.52	0.41
1:B:533:THR:HG21	1:B:538:GLN:C	2.40	0.41
1:A:136:MET:HB3	1:A:139:VAL:HG12	2.02	0.41
1:A:303:LYS:O	1:A:304:VAL:HG23	2.21	0.41
1:B:507:LEU:C	1:B:507:LEU:CD2	2.89	0.41
2:C:192:TRP:N	2:C:192:TRP:CD1	2.86	0.41
2:D:108:THR:HG22	2:D:110:ALA:H	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:254:GLY:O	1:A:257:ALA:HB3	2.21	0.41
1:A:277:ILE:HG23	1:A:368:MET:HE2	2.03	0.41
1:B:114:LEU:HA	1:B:119:LEU:HD21	2.02	0.41
1:B:132:LEU:HA	1:B:135:LEU:HD11	2.03	0.41
1:B:213:THR:H	1:B:218:ALA:HB3	1.85	0.41
1:B:360:GLY:CA	2:C:238:ASN:HD21	2.34	0.41
1:B:361:GLU:HB2	2:C:234:LEU:HD21	2.02	0.41
1:B:470:TYR:C	1:B:470:TYR:CD1	2.94	0.41
2:C:113:LEU:O	2:C:178:PHE:N	2.53	0.41
1:A:67:LEU:HA	1:A:67:LEU:HD23	1.78	0.41
1:B:374:GLY:O	1:B:488:ALA:HA	2.20	0.41
1:B:566:ASP:HB3	1:B:568:LEU:CD1	2.50	0.41
1:A:392:PRO:C	1:A:394:ASP:H	2.24	0.41
1:B:369:LEU:N	1:B:369:LEU:CD2	2.84	0.41
1:B:55:ILE:HD13	1:B:76:VAL:CG2	2.48	0.41
1:A:130:ALA:O	1:A:131:ASN:HB3	2.21	0.41
1:A:158:ASP:O	1:A:160:HIS:N	2.53	0.41
1:B:451:ALA:HB3	1:B:452:PRO:HD3	2.03	0.41
2:C:141:LEU:HD11	2:C:148:ILE:HD11	2.03	0.41
1:A:126:ILE:HG23	1:A:127:TRP:N	2.36	0.40
1:B:69:PRO:O	1:B:155:THR:HG23	2.21	0.40
1:B:120:LEU:HD21	1:B:176:SER:OG	2.20	0.40
1:B:289:VAL:HG11	1:B:291:TYR:CE2	2.55	0.40
1:A:377:LEU:H	1:A:441:VAL:CG1	2.34	0.40
1:A:566:ASP:HB3	1:A:568:LEU:HD12	2.03	0.40
1:A:80:SER:O	1:A:81:PRO:C	2.59	0.40
1:A:463:TYR:CE1	2:D:135:LEU:HD21	2.56	0.40
1:A:140:GLN:O	1:A:141:ASP:CB	2.69	0.40
1:A:447:HIS:O	1:A:447:HIS:CG	2.75	0.40
1:A:529:ASN:N	1:A:529:ASN:HD22	2.19	0.40
1:A:528:THR:HG22	1:A:532:LYS:NZ	2.36	0.40
1:B:83:THR:HB	1:B:86:ARG:HG3	2.04	0.40
2:C:139:LEU:HB2	2:C:152:PHE:HB3	2.02	0.40
2:D:126:LEU:HD11	2:D:258:LEU:HD21	2.02	0.40
1:A:361:GLU:HG2	2:D:236:ILE:HD11	2.03	0.40
1:A:62:LEU:HD12	1:A:62:LEU:HA	1.89	0.40
2:C:282:VAL:HG22	2:C:283:GLY:N	2.36	0.40
1:A:149:LEU:C	1:A:149:LEU:CD1	2.90	0.40
1:A:45:TYR:HB3	1:A:57:GLY:O	2.22	0.40
1:A:582:TYR:CZ	1:A:583:ARG:HD2	2.57	0.40

There are no symmetry-related clashes.



## 5.3 Torsion angles

### 5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	539/588 (92%)	388 (72%)	105 (20%)	46 (8%)	1	16
1	B	540/588 (92%)	419 (78%)	81 (15%)	40 (7%)	1	20
2	C	173/179 (97%)	142 (82%)	28 (16%)	3 (2%)	11	52
2	D	173/179 (97%)	125 (72%)	41 (24%)	7 (4%)	3	34
All	All	1425/1534 (93%)	1074 (75%)	255 (18%)	96 (7%)	1	23

All (96) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	84	GLY
1	A	87	ARG
1	A	118	SER
1	A	121	HIS
1	A	126	ILE
1	A	132	LEU
1	A	133	ASP
1	A	139	VAL
1	A	304	VAL
1	A	325	GLU
1	A	377	LEU
1	A	388	ASP
1	A	409	TYR
1	A	411	GLU
1	A	413	LYS
1	A	414	ASP
1	A	477	GLN
1	A	481	LYS
1	A	504	PRO
1	A	560	SER
1	A	564	PRO
1	B	111	PRO

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Mol	Chain	Res	Type
1	B	130	ALA
1	B	323	TYR
1	B	361	GLU
1	B	364	ASN
1	B	409	TYR
1	B	413	LYS
1	B	476	CYS
1	B	477	GLN
1	B	556	GLU
1	B	557	VAL
1	B	597	LEU
2	C	275	ASN
2	D	192	TRP
1	A	128	PHE
1	A	141	ASP
1	A	224	LEU
1	A	225	LEU
1	A	358	GLU
1	A	480	MET
1	A	559	TRP
1	A	594	VAL
1	B	66	ILE
1	B	108	ALA
1	B	120	LEU
1	B	155	THR
1	B	156	GLU
1	B	165	LYS
1	B	286	SER
1	B	304	VAL
1	B	321	LYS
1	B	328	GLN
1	B	411	GLU
1	B	412	GLY
1	B	487	SER
1	B	507	LEU
1	B	581	HIS
2	C	103	ASN
2	D	237	PHE
1	A	93	PRO
1	A	145	ASP
1	A	242	GLY
1	A	584	ALA

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Mol	Chain	Res	Type
1	B	176	SER
1	B	182	GLY
1	B	377	LEU
1	B	407	TYR
1	B	410	PRO
1	B	506	GLU
1	A	116	GLU
1	A	216	GLN
1	A	323	TYR
1	A	363	LEU
1	A	366	ASP
1	A	432	ASN
1	B	98	THR
2	C	111	ASP
2	D	131	SER
1	A	443	LEU
1	B	116	GLU
1	B	181	THR
2	D	107	SER
2	D	118	SER
1	A	223	GLY
1	A	235	GLU
1	B	509	SER
2	D	143	ILE
2	D	155	GLY
1	B	209	GLY
1	B	380	VAL
1	B	502	ILE
1	A	125	PRO
1	A	159	ILE
1	A	380	VAL
1	A	254	GLY

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	467/510 (92%)	390 (84%)	77 (16%)	2	19
1	B	466/510 (91%)	400 (86%)	66 (14%)	4	27
2	C	143/143 (100%)	119 (83%)	24 (17%)	2	19
2	D	143/143 (100%)	127 (89%)	16 (11%)	7	35
All	All	1219/1306 (93%)	1036 (85%)	183 (15%)	3	24

All (183) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	44	GLN
1	A	45	TYR
1	A	47	VAL
1	A	62	LEU
1	A	67	LEU
1	A	76	VAL
1	A	80	SER
1	A	87	ARG
1	A	89	GLN
1	A	98	THR
1	A	100	ILE
1	A	101	ARG
1	A	105	GLN
1	A	109	VAL
1	A	114	LEU
1	A	119	LEU
1	A	120	LEU
1	A	124	LEU
1	A	126	ILE
1	A	129	THR
1	A	131	ASN
1	A	135	LEU
1	A	138	TYR
1	A	149	LEU
1	A	159	ILE
1	A	168	VAL
1	A	179	GLU
1	A	195	ASN
1	A	200	THR
1	A	208	LEU
1	A	211	LEU
1	A	224	LEU
1	A	225	LEU

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Mol	Chain	Res	Type
1	A	226	ASP
1	A	246	LYS
1	A	263	LEU
1	A	282	THR
1	A	289	VAL
1	A	304	VAL
1	A	308	MET
1	A	309	LEU
1	A	311	THR
1	A	312	THR
1	A	313	ASP
1	A	322	ASN
1	A	323	TYR
1	A	330	THR
1	A	332	THR
1	A	338	ILE
1	A	348	VAL
1	A	349	ILE
1	A	359	GLN
1	A	364	ASN
1	A	366	ASP
1	A	367	ILE
1	A	394	ASP
1	A	407	TYR
1	A	415	THR
1	A	425	THR
1	A	440	LEU
1	A	443	LEU
1	A	477	GLN
1	A	480	MET
1	A	496	VAL
1	A	502	ILE
1	A	505	THR
1	A	506	GLU
1	A	514	LYS
1	A	527	TRP
1	A	529	ASN
1	A	561	ARG
1	A	574	LEU
1	A	575	LYS
1	A	577	ARG
1	A	585	THR

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Mol	Chain	Res	Type
1	A	586	LYS
1	A	597	LEU
1	B	45	TYR
1	B	59	ARG
1	B	62	LEU
1	B	66	ILE
1	B	83	THR
1	B	86	ARG
1	B	89	GLN
1	B	100	ILE
1	B	101	ARG
1	B	103	THR
1	B	113	HIS
1	B	114	LEU
1	B	115	ASP
1	B	116	GLU
1	B	120	LEU
1	B	121	HIS
1	B	124	LEU
1	B	126	ILE
1	B	133	ASP
1	B	135	LEU
1	B	140	GLN
1	B	141	ASP
1	B	142	GLN
1	B	145	ASP
1	B	159	ILE
1	B	166	LYS
1	B	170	VAL
1	B	188	SER
1	B	190	LEU
1	B	200	THR
1	B	208	LEU
1	B	219	LYS
1	B	258	SER
1	B	263	LEU
1	B	266	SER
1	B	267	HIS
1	B	269	SER
1	B	282	THR
1	B	285	SER
1	B	286	SER

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Mol	Chain	Res	Type
1	B	287	TRP
1	B	308	MET
1	B	311	THR
1	B	325	GLU
1	B	356	LEU
1	B	363	LEU
1	B	364	ASN
1	B	368	MET
1	B	369	LEU
1	B	381	ASP
1	B	386	ASN
1	B	413	LYS
1	B	423	MET
1	B	425	THR
1	B	430	LYS
1	B	439	THR
1	B	460	HIS
1	B	478	SER
1	B	506	GLU
1	B	527	TRP
1	B	557	VAL
1	B	560	SER
1	B	568	LEU
1	B	577	ARG
1	B	578	VAL
1	B	585	THR
2	C	85	THR
2	C	100	TRP
2	C	103	ASN
2	C	108	THR
2	C	122	LYS
2	C	126	LEU
2	C	139	LEU
2	C	142	HIS
2	C	154	VAL
2	C	157	ASP
2	C	159	ILE
2	C	179	THR
2	C	186	THR
2	C	187	LEU
2	C	188	GLN
2	C	197	ARG

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Mol	Chain	Res	Type
2	C	232	ARG
2	C	234	LEU
2	C	236	ILE
2	C	237	PHE
2	C	248	LYS
2	C	278	ASN
2	C	286	ARG
2	C	287	LEU
2	D	88	ILE
2	D	100	TRP
2	D	105	ARG
2	D	107	SER
2	D	112	ARG
2	D	118	SER
2	D	137	ASP
2	D	145	GLN
2	D	156	THR
2	D	172	LYS
2	D	173	TYR
2	D	179	THR
2	D	188	GLN
2	D	232	ARG
2	D	237	PHE
2	D	254	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	89	GLN
1	A	102	ASN
1	A	131	ASN
1	A	173	HIS
1	A	195	ASN
1	A	364	ASN
1	A	432	ASN
1	A	460	HIS
1	A	489	HIS
1	A	511	ASN
1	A	529	ASN
1	B	64	ASN
1	B	89	GLN
1	B	142	GLN

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Mol	Chain	Res	Type
1	B	143	ASN
1	B	307	ASN
1	B	364	ASN
1	B	386	ASN
1	B	405	ASN
1	B	448	GLN
1	B	599	ASN
2	C	103	ASN
2	C	145	GLN
2	C	238	ASN
2	C	252	GLN
2	C	264	ASN
2	C	270	ASN
2	C	278	ASN
2	D	95	GLN
2	D	145	GLN
2	D	153	ASN
2	D	165	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](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 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	NAG	A	1599	-	14,14,15	0.39	0	15,19,21	1.10	0
3	NAG	A	1600	-	14,14,15	0.33	0	15,19,21	1.05	1 (6%)

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	NAG	A	1599	-	-	0/6/23/26	0/1/1/1
3	NAG	A	1600	-	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1600	NAG	C1-C2-N2	-2.67	105.93	110.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1599	NAG	5	0
3	A	1600	NAG	3	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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	545/588 (92%)	-0.26	3 (0%) 89 84	50, 72, 77, 86	0
1	B	544/588 (92%)	-0.05	15 (2%) 53 43	63, 73, 78, 84	0
2	C	177/179 (98%)	0.12	6 (3%) 46 36	59, 72, 81, 83	0
2	D	177/179 (98%)	0.51	17 (9%) 9 8	61, 76, 84, 86	0
All	All	1443/1534 (94%)	-0.04	41 (2%) 53 43	50, 73, 80, 86	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	94	GLY	10.8
2	D	162	GLU	6.5
2	C	94	GLY	5.7
2	D	89	PHE	4.9
2	D	176	VAL	4.0
2	D	160	ALA	4.0
2	D	288	VAL	3.9
1	B	58	LEU	3.8
1	B	340	PHE	3.7
1	B	88	PHE	3.7
1	B	326	LEU	3.7
1	B	318	LEU	3.6
2	D	88	ILE	3.6
1	A	118	SER	3.5
2	D	281	ILE	3.4
1	B	339	ALA	3.3
1	B	211	LEU	3.2
2	D	193	PRO	3.1
1	B	309	LEU	3.0
2	D	245	ILE	2.8
1	B	163	ASN	2.7

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Mol	Chain	Res	Type	RSRZ
2	C	125	VAL	2.7
2	D	161	ILE	2.6
1	B	85	GLU	2.6
1	B	207	ILE	2.6
1	B	162	GLN	2.5
2	C	258	LEU	2.5
1	A	113	HIS	2.5
1	B	341	GLY	2.5
2	D	87	TYR	2.3
2	D	259	SER	2.3
2	C	250	GLN	2.3
2	D	159	ILE	2.3
2	D	149	GLY	2.2
1	B	300	LEU	2.2
2	D	92	GLY	2.2
2	C	194	VAL	2.1
1	A	217	ALA	2.1
2	C	126	LEU	2.1
1	B	506	GLU	2.1
2	D	95	GLN	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	CA	D	1289	1/1	0.97	0.14	-1.26	134,134,134,134	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	CA	C	1289	1/1	0.99	0.07	-1.84	109,109,109,109	0
3	NAG	A	1600	14/15	0.79	0.14	-	191,192,193,193	0
3	NAG	A	1599	14/15	0.80	0.17	-	221,222,224,225	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.