



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 02:36 PM GMT

PDB ID : 3ZZT  
Title : Crystal structure of Staphylococcus aureus elongation factor G with a fusidic  
-acid-resistant mutation F88L  
Authors : Koripella, R.K.; Chen, Y.; Selmer, M.; Sanyal, S.  
Deposited on : 2011-09-05  
Resolution : 2.95 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 (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

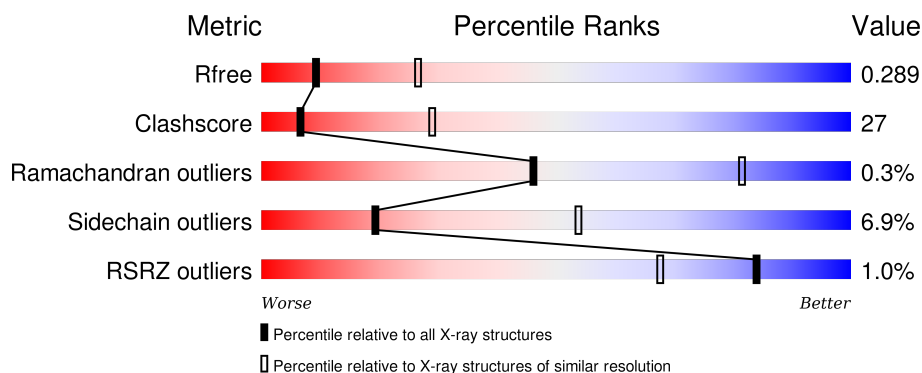
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.95 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2184 (3.00-2.92)
Clashscore	102246	2552 (3.00-2.92)
Ramachandran outliers	100387	2468 (3.00-2.92)
Sidechain outliers	100360	2471 (3.00-2.92)
RSRZ outliers	91569	2201 (3.00-2.92)

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	693	<div> <div></div> <div>55%</div> <div>35%</div> <div>6%</div> </div>
1	B	693	<div> <div></div> <div>47%</div> <div>43%</div> <div>6%</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 10059 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 ELONGATION FACTOR G.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	649	Total	C	N	O	S	0	0	1
			5018	3150	841	1000	27			
1	B	649	Total	C	N	O	S	0	0	1
			5018	3150	841	1000	27			

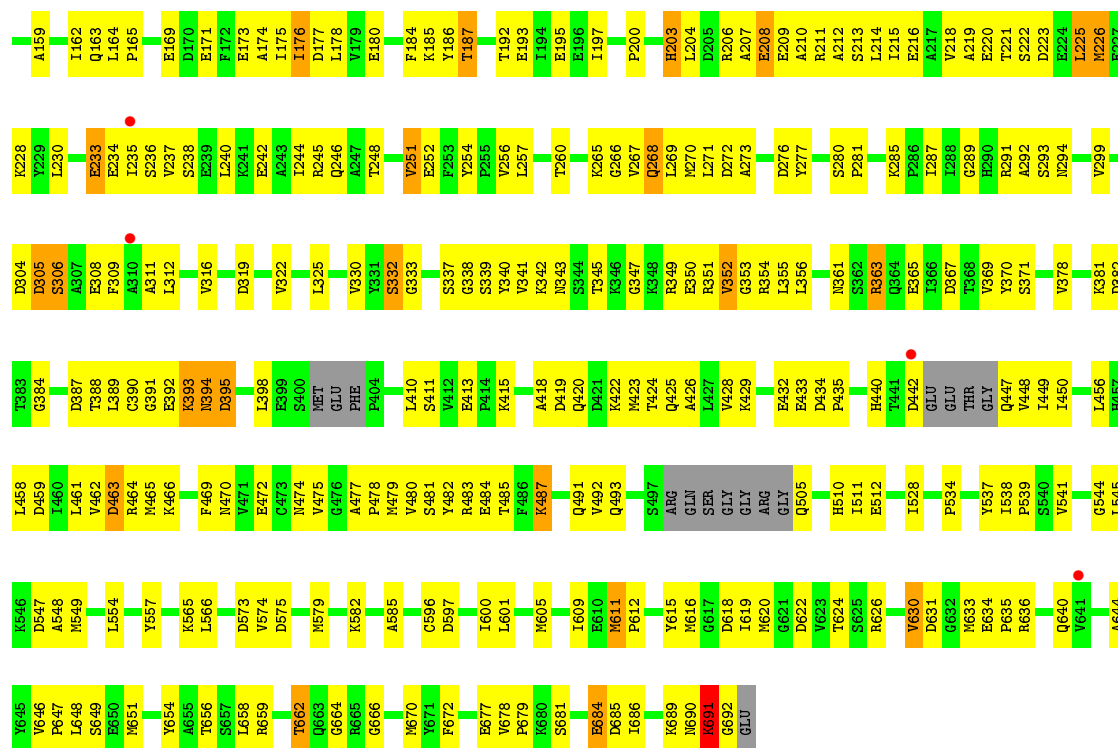
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	88	LEU	PHE	ENGINEERED MUTATION	UNP P68790
B	88	LEU	PHE	ENGINEERED MUTATION	UNP P68790

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	17	Total	O	0	0
			17	17		
2	B	6	Total	O	0	0
			6	6		





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.97Å 127.93Å 107.44Å 90.00° 107.86° 90.00°	Depositor
Resolution (Å)	47.40 – 2.95 47.48 – 2.95	Depositor EDS
% Data completeness (in resolution range)	90.3 (47.40-2.95) 90.3 (47.48-2.95)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.90 (at 2.96Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.241 , 0.294 0.235 , 0.289	Depositor DCC
$R_{free}$ test set	1522 reflections (4.71%)	DCC
Wilson B-factor (Å <sup>2</sup> )	77.8	Xtriage
Anisotropy	0.213	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	(Not available) , (Not available)	EDS
Estimated twinning fraction	0.032 for h,-k,-h-l	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 32339 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	10059	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.26	1/5103 (0.0%)	0.47	0/6900
1	B	0.28	1/5103 (0.0%)	0.50	0/6900
All	All	0.27	2/10206 (0.0%)	0.49	0/13800

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	691	LYS	C-N	-5.38	1.23	1.33
1	B	691	LYS	C-N	-5.32	1.23	1.33

There are no bond angle outliers.

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	5018	0	4934	233	1
1	B	5018	0	4934	310	0
2	A	17	0	0	4	0
2	B	6	0	0	1	0
All	All	10059	0	9868	542	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 27.

All (542) 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:363:ARG:HG3	1:B:363:ARG:HH11	1.01	1.17
1:B:268:GLN:OE1	1:B:268:GLN:N	1.86	1.09
1:B:186:TYR:OH	1:B:268:GLN:NE2	1.86	1.07
1:B:242:GLU:OE1	1:B:242:GLU:N	1.91	1.03
1:B:128:VAL:O	1:B:130:ARG:NH1	1.92	1.02
1:A:128:VAL:O	1:A:130:ARG:NH1	1.93	1.00
1:A:428:VAL:O	1:A:431:GLN:NE2	1.91	1.00
1:B:222:SER:HB3	1:B:225:LEU:HD23	1.44	0.99
1:B:28:GLU:OE1	1:B:28:GLU:N	1.97	0.97
1:B:28:GLU:O	1:B:31:LEU:N	1.98	0.96
1:A:130:ARG:HG3	1:A:130:ARG:HH11	1.30	0.96
1:B:413:GLU:HB3	1:B:474:ASN:OD1	1.68	0.93
1:B:363:ARG:NH1	1:B:363:ARG:HG3	1.78	0.92
1:B:612:PRO:HG2	1:B:615:TYR:HE2	1.35	0.91
1:A:506:TYR:HE1	1:A:571:TYR:HA	1.32	0.91
1:A:568:ASP:OD1	1:A:569:GLY:N	2.05	0.89
1:B:208:GLU:H	1:B:208:GLU:CD	1.74	0.89
1:B:242:GLU:HA	1:B:245:ARG:HB3	1.54	0.87
1:A:364:GLN:NE2	1:A:365:GLU:O	2.07	0.87
1:B:88:LEU:O	1:B:88:LEU:HD12	1.72	0.87
1:B:612:PRO:HG2	1:B:615:TYR:CE2	2.10	0.86
1:B:195:GLU:OE1	1:B:195:GLU:N	2.10	0.85
1:A:342:LYS:NZ	1:A:394:ASN:O	2.08	0.85
1:B:415:LYS:HZ3	1:B:474:ASN:HB3	1.42	0.85
1:B:208:GLU:N	1:B:208:GLU:OE1	2.10	0.84
1:A:610:GLU:OE1	1:A:636:ARG:NH2	2.09	0.84
1:B:691:LYS:HG3	1:B:692:GLY:N	1.93	0.82
1:B:384:GLY:N	1:B:387:ASP:OD2	2.12	0.81
1:A:506:TYR:CE1	1:A:571:TYR:HA	2.16	0.80
1:B:333:GLY:O	1:B:371:SER:OG	1.98	0.80
1:A:284:VAL:HG22	1:A:285:LYS:H	1.47	0.80
1:B:410:LEU:HG	1:B:458:LEU:HD13	1.64	0.80
1:B:425:GLN:O	1:B:428:VAL:HG12	1.82	0.79
1:B:363:ARG:CG	1:B:363:ARG:HH11	1.89	0.79
1:A:440:HIS:NE2	1:A:442:ASP:HB3	1.97	0.79
1:A:496:PHE:O	1:A:506:TYR:HA	1.82	0.78
1:B:616:MET:SD	1:B:633:MET:HE1	2.23	0.78
1:B:113:GLU:N	1:B:116:THR:OG1	2.17	0.78
1:A:135:ASN:OD1	1:A:136:LYS:N	2.17	0.77
1:A:19:ILE:O	1:A:22:GLY:N	2.13	0.77
1:B:459:ASP:HA	1:B:462:VAL:HG12	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:LYS:NZ	1:A:382:ASP:O	2.19	0.76
1:B:292:ALA:N	1:B:395:ASP:O	2.17	0.76
1:B:204:LEU:O	1:B:204:LEU:HD23	1.84	0.76
1:A:246:GLN:O	1:A:250:ASN:ND2	2.18	0.75
1:B:656:THR:HG23	1:B:659:ARG:HH22	1.51	0.75
1:A:112:VAL:HG12	1:A:150:THR:HB	1.68	0.75
1:B:87:ASP:N	1:B:87:ASP:OD1	2.15	0.74
1:A:611:MET:N	1:A:611:MET:SD	2.60	0.74
1:A:581:PHE:O	1:A:584:ALA:N	2.21	0.74
1:B:107:ASP:OD1	1:B:139:LYS:HE3	1.86	0.74
1:B:415:LYS:NZ	1:B:474:ASN:HB3	2.02	0.74
1:B:395:ASP:OD1	1:B:395:ASP:N	2.21	0.73
1:B:662:THR:HG21	1:B:666:GLY:HA3	1.69	0.73
1:A:30:ILE:O	1:A:34:THR:OG1	2.05	0.73
1:A:8:GLU:OE1	1:A:8:GLU:N	2.20	0.73
1:A:130:ARG:HG3	1:A:130:ARG:NH1	1.96	0.73
1:A:349:ARG:O	1:A:381:LYS:NZ	2.17	0.73
1:A:390:CYS:SG	1:A:394:ASN:HB3	2.29	0.72
1:B:260:THR:HG22	1:B:265:LYS:HB2	1.71	0.72
1:A:481:SER:HB3	1:A:483:ARG:HH12	1.53	0.72
1:B:136:LYS:HB2	1:B:139:LYS:NZ	2.05	0.71
1:A:463:ASP:O	1:A:467:LYS:HG2	1.90	0.71
1:A:611:MET:HB2	1:A:612:PRO:HD2	1.73	0.71
1:B:208:GLU:CD	1:B:209:GLU:H	1.93	0.70
1:A:211:ARG:O	1:A:215:ILE:HG22	1.92	0.70
1:B:528:ILE:HD11	1:B:566:LEU:HG	1.74	0.70
1:B:34:THR:HB	1:B:70:ALA:HB1	1.72	0.70
1:A:354:ARG:NH2	1:A:365:GLU:OE1	2.17	0.70
1:B:319:ASP:HB3	1:B:322:VAL:HG22	1.74	0.70
1:B:316:VAL:HG23	1:B:433:GLU:HG2	1.74	0.70
1:B:280:SER:OG	1:B:281:PRO:HD2	1.91	0.69
1:B:487:LYS:HG3	1:B:597:ASP:O	1.92	0.69
1:A:615:TYR:OH	1:A:665:ARG:NH1	2.24	0.69
1:B:113:GLU:O	1:B:116:THR:OG1	2.08	0.69
1:B:219:ALA:HA	1:B:225:LEU:HD21	1.75	0.69
1:B:415:LYS:HZ3	1:B:474:ASN:CB	2.06	0.69
1:A:506:TYR:HE1	1:A:571:TYR:CA	2.05	0.69
1:B:85:HIS:NE2	1:B:88:LEU:HD23	2.07	0.69
1:A:506:TYR:HH	1:A:570:SER:HG	1.33	0.69
1:B:171:GLU:O	1:B:173:GLU:HG3	1.92	0.69
1:A:633:MET:HG3	1:A:634:GLU:N	2.08	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:18:HIS:ND1	1:B:19:ILE:N	2.41	0.68
1:B:381:LYS:HG3	1:B:382:ASP:H	1.57	0.68
1:A:546:LYS:O	1:A:549:MET:N	2.27	0.68
1:A:534:PRO:HD3	1:A:571:TYR:CD2	2.29	0.68
1:A:408:ILE:HG22	1:A:458:LEU:HD11	1.75	0.68
1:B:244:ILE:O	1:B:248:THR:OG1	2.04	0.68
1:B:463:ASP:OD1	1:B:464:ARG:N	2.27	0.68
1:B:656:THR:HG23	1:B:659:ARG:NH2	2.09	0.68
1:B:354:ARG:NE	1:B:365:GLU:OE1	2.26	0.68
1:A:80:ILE:HD13	1:A:98:VAL:HG12	1.75	0.68
1:A:202:ASP:OD1	1:A:202:ASP:N	2.22	0.67
1:B:136:LYS:O	1:B:139:LYS:HG2	1.95	0.67
1:B:487:LYS:NZ	1:B:677:GLU:OE2	2.15	0.67
1:A:431:GLN:N	1:A:431:GLN:OE1	2.28	0.66
1:B:208:GLU:O	1:B:211:ARG:N	2.28	0.66
1:B:175:ILE:HD11	1:B:269:LEU:CD1	2.25	0.66
1:B:28:GLU:H	1:B:28:GLU:CD	1.99	0.66
1:B:24:THR:O	1:B:28:GLU:OE1	2.14	0.66
1:B:3:ARG:HB3	1:B:370:TYR:CD1	2.31	0.66
1:B:20:ASP:OD1	1:B:20:ASP:N	2.27	0.66
1:B:115:GLN:O	1:B:118:THR:OG1	2.14	0.66
1:B:354:ARG:NH2	1:B:365:GLU:OE1	2.29	0.65
1:A:186:TYR:CD2	1:A:265:LYS:HG2	2.31	0.65
1:A:350:GLU:OE2	1:A:381:LYS:HG3	1.95	0.65
1:B:211:ARG:O	1:B:215:ILE:HG13	1.97	0.65
1:A:577:SER:HB2	1:A:580:ALA:H	1.60	0.65
1:A:538:ILE:HB	1:A:539:PRO:HD3	1.79	0.65
1:B:207:ALA:N	1:B:208:GLU:OE1	2.30	0.64
1:B:245:ARG:NH1	1:B:276:ASP:O	2.29	0.64
1:B:393:LYS:O	1:B:394:ASN:HB2	1.95	0.64
1:B:337:SER:HA	1:B:352:VAL:CG2	2.28	0.64
1:B:175:ILE:HD11	1:B:269:LEU:HD12	1.79	0.64
1:B:422:LYS:HD3	1:B:470:ASN:O	1.97	0.64
1:B:659:ARG:HG3	1:B:664:GLY:HA2	1.81	0.63
1:A:622:ASP:OD1	1:A:626:ARG:NH2	2.31	0.63
1:B:221:THR:HG21	1:B:252:GLU:OE1	1.98	0.63
1:A:204:LEU:O	1:A:208:GLU:HG2	1.98	0.63
1:B:684:GLU:HG2	1:B:685:ASP:N	2.13	0.63
1:B:619:ILE:O	1:B:622:ASP:N	2.32	0.63
1:B:94:ARG:O	1:B:97:ARG:N	2.30	0.62
1:B:238:SER:O	1:B:242:GLU:OE1	2.17	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:ASP:OD1	1:B:139:LYS:CE	2.47	0.62
1:B:214:LEU:O	1:B:218:VAL:HG23	1.98	0.62
1:A:611:MET:HG3	1:A:619:ILE:HD11	1.82	0.62
1:B:648:LEU:O	1:B:651:MET:N	2.31	0.62
1:B:122:GLN:NE2	2:B:2002:HOH:O	2.14	0.62
1:B:136:LYS:HB2	1:B:139:LYS:HZ3	1.63	0.62
1:B:340:TYR:CE1	1:B:351:ARG:HD3	2.35	0.61
1:B:101:GLY:HA2	1:B:128:VAL:HG12	1.82	0.61
1:A:96:LEU:HD23	1:A:128:VAL:HG21	1.80	0.61
1:B:487:LYS:HG3	1:B:597:ASP:OD1	2.00	0.61
1:B:237:VAL:HG23	1:B:238:SER:H	1.64	0.61
1:B:208:GLU:N	1:B:208:GLU:CD	2.44	0.61
1:B:337:SER:HA	1:B:352:VAL:HG21	1.81	0.61
1:A:16:MET:HG3	1:A:104:THR:HG22	1.82	0.61
1:A:433:GLU:N	1:A:433:GLU:OE1	2.33	0.61
1:B:237:VAL:O	1:B:240:LEU:N	2.32	0.61
1:A:534:PRO:HG2	1:A:537:TYR:CD2	2.36	0.61
1:A:147:SER:O	1:A:150:THR:OG1	2.18	0.61
1:B:651:MET:CE	1:B:651:MET:HA	2.30	0.61
1:A:274:VAL:HG13	1:A:278:LEU:HD12	1.82	0.61
1:A:194:ILE:O	1:A:194:ILE:HD12	2.00	0.60
1:B:208:GLU:O	1:B:212:ALA:N	2.33	0.60
1:B:547:ASP:OD1	1:B:548:ALA:N	2.31	0.60
1:B:242:GLU:O	1:B:246:GLN:N	2.30	0.60
1:B:355:LEU:HD12	1:B:367:ASP:O	2.01	0.60
1:B:100:ASP:O	1:B:128:VAL:HG13	2.02	0.60
1:B:130:ARG:HG3	1:B:130:ARG:HH11	1.67	0.60
1:B:311:ALA:HB3	1:B:389:LEU:HB2	1.84	0.60
1:B:242:GLU:O	1:B:245:ARG:N	2.35	0.60
1:A:270:MET:HG3	1:A:271:LEU:N	2.16	0.60
1:B:474:ASN:O	1:B:474:ASN:OD1	2.20	0.59
1:B:185:LYS:HB3	1:B:195:GLU:OE2	2.01	0.59
1:B:534:PRO:HG2	1:B:537:TYR:HD2	1.68	0.59
1:A:284:VAL:HG22	1:A:285:LYS:N	2.16	0.59
1:A:354:ARG:HH21	1:A:365:GLU:CD	2.04	0.59
1:B:113:GLU:OE2	1:B:114:PRO:HD2	2.03	0.59
1:A:304:ASP:OD1	1:A:306:SER:N	2.35	0.59
1:A:691:LYS:HE3	1:A:691:LYS:HA	1.85	0.59
1:B:96:LEU:HB3	1:B:126:TYR:HD2	1.68	0.59
1:A:463:ASP:OD1	1:A:467:LYS:NZ	2.29	0.59
1:B:481:SER:OG	1:B:483:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:388:THR:HG23	1:B:398:LEU:HD12	1.84	0.58
1:B:236:SER:OG	1:B:237:VAL:N	2.36	0.58
1:A:99:LEU:HD12	1:A:99:LEU:O	2.03	0.58
1:B:337:SER:OG	1:B:353:GLY:O	2.18	0.58
1:A:467:LYS:HG3	1:A:468:GLU:H	1.69	0.58
1:A:212:ALA:O	1:A:215:ILE:HG23	2.04	0.58
1:A:412:VAL:O	1:A:448:VAL:HG12	2.04	0.58
1:B:342:LYS:NZ	1:B:392:GLU:O	2.27	0.58
1:A:26:THR:O	1:A:30:ILE:HG13	2.03	0.58
1:A:424:THR:O	1:A:428:VAL:HG23	2.04	0.58
1:A:73:GLU:O	1:A:75:HIS:ND1	2.35	0.57
1:B:276:ASP:HB3	1:B:277:TYR:CE1	2.40	0.57
1:B:354:ARG:CZ	1:B:365:GLU:OE1	2.53	0.57
1:B:305:ASP:OD1	1:B:305:ASP:N	2.37	0.57
1:B:267:VAL:N	1:B:268:GLN:OE1	2.36	0.57
1:B:9:LYS:HA	1:B:75:HIS:CD2	2.39	0.57
1:B:238:SER:O	1:B:242:GLU:CD	2.43	0.57
1:B:596:CYS:O	1:B:597:ASP:OD1	2.23	0.57
1:B:18:HIS:CE1	1:B:20:ASP:OD1	2.57	0.57
1:B:390:CYS:SG	1:B:391:GLY:N	2.78	0.57
1:A:488:SER:O	1:A:515:PRO:HD3	2.05	0.57
1:B:355:LEU:HD13	1:B:369:VAL:HG23	1.85	0.57
1:B:505:GLN:N	1:B:575:ASP:HB3	2.20	0.56
1:B:270:MET:HA	1:B:273:ALA:HB3	1.88	0.56
1:A:66:ALA:HB2	1:A:315:LYS:HE2	1.86	0.56
1:B:204:LEU:O	1:B:208:GLU:OE1	2.22	0.56
1:B:146:TYR:O	1:B:149:SER:HB3	2.04	0.56
1:B:83:PRO:CB	1:B:88:LEU:HD11	2.35	0.56
1:B:423:MET:HG3	1:B:465:MET:HE1	1.86	0.56
1:A:361:ASN:N	1:A:361:ASN:OD1	2.37	0.56
1:B:681:SER:O	1:B:684:GLU:CD	2.44	0.56
1:B:276:ASP:HB3	1:B:277:TYR:CD1	2.41	0.56
1:B:266:GLY:H	1:B:268:GLN:HE22	1.54	0.56
1:A:182:LYS:HD3	1:A:196:GLU:CD	2.26	0.56
1:B:616:MET:HG2	1:B:620:MET:CE	2.36	0.55
1:B:108:ALA:HB3	1:B:139:LYS:HZ1	1.72	0.55
1:A:98:VAL:O	1:A:329:ARG:NH1	2.39	0.55
1:B:187:THR:CG2	1:B:193:GLU:O	2.54	0.55
1:B:237:VAL:HG23	1:B:238:SER:N	2.22	0.55
1:B:15:ILE:HG22	1:B:23:LYS:HG3	1.88	0.55
1:B:19:ILE:CD1	1:B:23:LYS:HD3	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:609:ILE:HD11	1:B:654:TYR:OH	2.07	0.55
1:A:19:ILE:HA	1:A:23:LYS:H	1.71	0.55
1:B:634:GLU:O	1:B:640:GLN:NE2	2.39	0.55
1:B:92:VAL:O	1:B:96:LEU:HD13	2.06	0.55
1:A:619:ILE:O	1:A:622:ASP:N	2.40	0.55
1:B:343:ASN:OD1	1:B:345:THR:HB	2.07	0.55
1:B:130:ARG:HG3	1:B:130:ARG:NH1	2.20	0.55
1:B:493:GLN:HB2	1:B:510:HIS:CE1	2.42	0.55
1:B:482:TYR:HB2	1:B:557:TYR:CD2	2.41	0.55
1:A:130:ARG:CG	1:A:130:ARG:HH11	2.11	0.55
1:B:611:MET:SD	1:B:619:ILE:HG13	2.47	0.55
1:B:350:GLU:OE2	1:B:382:ASP:N	2.40	0.55
1:B:609:ILE:CD1	1:B:654:TYR:OH	2.56	0.54
1:A:654:TYR:O	1:A:657:SER:N	2.39	0.54
1:B:88:LEU:HD22	1:B:91:GLU:HB2	1.90	0.54
1:B:544:GLY:CA	1:B:582:LYS:HG3	2.38	0.54
1:A:166:ILE:HD12	1:A:174:ALA:HB3	1.88	0.54
1:A:467:LYS:HG3	1:A:468:GLU:N	2.22	0.54
1:B:354:ARG:O	1:B:378:VAL:HG12	2.06	0.54
1:B:390:CYS:SG	1:B:394:ASN:HB3	2.48	0.54
1:B:107:ASP:OD1	1:B:139:LYS:NZ	2.41	0.54
1:B:92:VAL:HG12	1:B:93:GLU:N	2.21	0.54
1:A:612:PRO:HG2	1:A:615:TYR:CD2	2.43	0.54
1:A:663:GLN:OE1	1:A:663:GLN:N	2.41	0.54
1:A:441:THR:O	1:A:442:ASP:C	2.46	0.54
1:A:319:ASP:CG	1:A:320:PRO:HD2	2.29	0.54
1:A:99:LEU:HD13	1:A:101:GLY:O	2.08	0.53
1:A:493:GLN:NE2	1:A:508:ASP:OD1	2.39	0.53
1:A:612:PRO:HG2	1:A:615:TYR:CE2	2.42	0.53
1:A:419:ASP:OD1	1:A:420:GLN:N	2.41	0.53
1:B:106:LEU:HD13	1:B:132:VAL:HG13	1.90	0.53
1:A:335:MET:HB3	1:A:369:VAL:HG23	1.91	0.53
1:B:691:LYS:CG	1:B:692:GLY:N	2.65	0.53
1:A:186:TYR:HD2	1:A:265:LYS:HG2	1.72	0.53
1:A:201:GLU:HA	1:A:204:LEU:HB2	1.91	0.53
1:B:394:ASN:OD1	1:B:395:ASP:N	2.41	0.53
1:A:486:PHE:O	1:A:515:PRO:HB3	2.09	0.53
1:A:373:ASP:OD1	1:A:374:ILE:N	2.29	0.53
1:B:626:ARG:HD3	1:B:651:MET:CE	2.38	0.53
1:A:350:GLU:HG3	1:A:381:LYS:HE2	1.91	0.52
1:A:163:GLN:HA	1:A:176:ILE:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:THR:O	1:A:436:THR:HG22	2.09	0.52
1:A:18:HIS:ND1	1:A:19:ILE:N	2.57	0.52
1:A:186:TYR:CE2	1:A:265:LYS:HA	2.44	0.52
1:A:149:SER:O	1:A:152:HIS:HB2	2.10	0.52
1:A:509:VAL:HG22	1:A:584:ALA:HB1	1.91	0.52
1:A:577:SER:HB2	1:A:579:MET:H	1.74	0.52
1:A:288:ILE:HD11	1:A:298:GLU:HG3	1.92	0.52
1:B:233:GLU:O	1:B:234:GLU:HB2	2.09	0.52
1:A:337:SER:OG	1:A:353:GLY:O	2.21	0.52
1:A:619:ILE:O	1:A:622:ASP:HB3	2.11	0.51
1:A:689:LYS:O	1:A:691:LYS:HD2	2.10	0.51
1:B:538:ILE:HB	1:B:539:PRO:HD3	1.92	0.51
1:A:162:ILE:HG22	1:A:214:LEU:HD21	1.91	0.51
1:B:269:LEU:O	1:B:272:ASP:HB2	2.10	0.51
1:A:413:GLU:O	1:A:413:GLU:HG3	2.11	0.51
1:A:159:ALA:HB2	1:A:254:TYR:HB2	1.93	0.51
1:A:537:TYR:HB3	1:A:581:PHE:CE2	2.45	0.51
1:B:605:MET:HG3	1:B:648:LEU:HD13	1.92	0.51
1:B:605:MET:HE3	1:B:670:MET:HG2	1.92	0.51
1:B:285:LYS:HG3	1:B:285:LYS:O	2.10	0.51
1:A:559:LEU:HD21	1:A:562:VAL:HG21	1.91	0.51
1:A:611:MET:HG3	1:A:619:ILE:CD1	2.40	0.51
1:B:159:ALA:HB2	1:B:254:TYR:HB2	1.93	0.51
1:B:85:HIS:HB2	1:B:87:ASP:OD1	2.11	0.51
1:B:459:ASP:HA	1:B:462:VAL:CG1	2.40	0.51
1:B:120:TRP:HZ2	1:B:254:TYR:CE2	2.29	0.51
1:A:488:SER:HB2	1:A:596:CYS:HA	1.92	0.51
1:B:90:VAL:O	1:B:93:GLU:HG2	2.10	0.50
1:A:610:GLU:CD	1:A:636:ARG:HH21	2.09	0.50
1:A:414:PRO:HB2	1:A:419:ASP:OD1	2.12	0.50
1:B:134:VAL:HG23	1:B:257:LEU:O	2.11	0.50
1:B:381:LYS:HG3	1:B:382:ASP:N	2.25	0.50
1:B:187:THR:HG21	1:B:193:GLU:O	2.11	0.50
1:A:510:HIS:HB3	1:A:567:TYR:CZ	2.46	0.50
1:A:223:ASP:HA	1:A:226:MET:HB2	1.93	0.50
1:B:491:GLN:HG2	1:B:512:GLU:HB2	1.93	0.50
1:B:174:ALA:HB1	1:B:184:PHE:O	2.11	0.50
1:B:135:ASN:OD1	1:B:136:LYS:N	2.45	0.50
1:B:136:LYS:HB2	1:B:139:LYS:HZ2	1.77	0.50
1:A:399:GLU:CG	1:A:400:SER:N	2.74	0.50
1:B:113:GLU:CD	1:B:114:PRO:HD2	2.32	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:328:PHE:O	1:A:374:ILE:HG23	2.12	0.50
1:B:251:VAL:O	1:B:251:VAL:HG12	2.12	0.50
1:B:268:GLN:HG2	1:B:269:LEU:N	2.27	0.50
1:B:19:ILE:HD13	1:B:23:LYS:HB3	1.93	0.50
1:A:615:TYR:O	1:A:618:ASP:N	2.43	0.50
1:B:36:ARG:HG3	1:B:36:ARG:O	2.11	0.50
1:B:289:GLY:C	1:B:299:VAL:HG12	2.33	0.50
1:B:343:ASN:O	1:B:347:GLY:N	2.45	0.49
1:A:66:ALA:HB2	1:A:315:LYS:NZ	2.27	0.49
1:B:658:LEU:O	1:B:662:THR:HG22	2.11	0.49
1:A:293:SER:O	1:A:295:PRO:HD3	2.13	0.49
1:A:330:VAL:O	1:A:330:VAL:HG13	2.11	0.49
1:A:527:ALA:HB3	1:A:566:LEU:O	2.13	0.49
1:A:463:ASP:O	1:A:467:LYS:NZ	2.45	0.49
1:A:89:THR:O	1:A:93:GLU:HG3	2.13	0.49
1:A:392:GLU:N	2:A:2008:HOH:O	2.43	0.49
1:A:399:GLU:CG	1:A:400:SER:H	2.26	0.49
1:B:477:ALA:O	1:B:479:MET:HG3	2.12	0.49
1:B:528:ILE:HD12	1:B:566:LEU:O	2.12	0.49
1:A:537:TYR:HB3	1:A:581:PHE:CD2	2.47	0.49
1:A:257:LEU:HD12	1:A:257:LEU:N	2.27	0.49
1:A:214:LEU:O	1:A:218:VAL:HG23	2.13	0.49
1:B:268:GLN:CG	1:B:269:LEU:N	2.76	0.48
1:B:456:LEU:HD12	1:B:456:LEU:HA	1.62	0.48
1:B:164:LEU:HD21	1:B:206:ARG:HG2	1.94	0.48
1:B:308:GLU:HG3	1:B:309:PHE:H	1.78	0.48
1:B:554:LEU:CD2	1:B:600:ILE:HG13	2.43	0.48
1:A:462:VAL:HG13	1:A:463:ASP:N	2.29	0.48
1:B:534:PRO:HG2	1:B:537:TYR:CD2	2.48	0.48
1:B:223:ASP:HA	1:B:226:MET:HB3	1.94	0.48
1:B:88:LEU:HD13	1:B:91:GLU:HB3	1.95	0.48
1:A:397:ILE:N	1:A:397:ILE:HD12	2.28	0.48
1:B:221:THR:O	1:B:221:THR:HG22	2.13	0.48
1:B:223:ASP:HA	1:B:226:MET:CB	2.43	0.48
1:B:291:ARG:HB3	1:B:395:ASP:HB2	1.94	0.48
1:A:133:PHE:HE2	1:A:135:ASN:HD22	1.60	0.48
1:A:66:ALA:HB2	1:A:315:LYS:CE	2.43	0.48
1:B:120:TRP:HZ2	1:B:254:TYR:CD2	2.31	0.48
1:B:662:THR:HG21	1:B:666:GLY:CA	2.40	0.48
1:B:19:ILE:HD11	1:B:23:LYS:HD3	1.95	0.48
1:B:177:ASP:OD2	1:B:180:GLU:HB2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:THR:O	1:A:668:TYR:HA	2.14	0.48
1:A:605:MET:HE3	1:A:670:MET:HG2	1.96	0.48
1:B:312:LEU:HD12	1:B:387:ASP:O	2.14	0.48
1:B:651:MET:HE3	1:B:651:MET:HA	1.96	0.48
1:B:630:VAL:HA	1:B:644:ALA:HA	1.95	0.48
1:A:34:THR:HG22	1:A:72:TRP:HB2	1.95	0.47
1:A:534:PRO:HD3	1:A:571:TYR:CE2	2.48	0.47
1:B:544:GLY:O	1:B:547:ASP:OD1	2.33	0.47
1:B:28:GLU:O	1:B:31:LEU:CA	2.62	0.47
1:B:605:MET:CE	1:B:670:MET:HG2	2.44	0.47
1:A:72:TRP:HH2	1:A:268:GLN:HG2	1.79	0.47
1:A:178:LEU:O	1:A:211:ARG:HD2	2.15	0.47
1:B:174:ALA:CB	1:B:185:LYS:HA	2.45	0.47
1:A:186:TYR:HE2	1:A:265:LYS:HA	1.79	0.47
1:A:493:GLN:HG2	1:A:494:GLY:N	2.29	0.47
1:A:667:THR:CG2	1:A:668:TYR:N	2.77	0.47
1:A:88:LEU:O	1:A:92:VAL:HG23	2.15	0.47
1:B:420:GLN:O	1:B:424:THR:HG22	2.14	0.47
1:B:25:THR:O	1:B:29:ARG:HG2	2.14	0.47
1:A:390:CYS:SG	1:A:391:GLY:N	2.87	0.47
1:B:113:GLU:HG3	1:B:114:PRO:HD2	1.96	0.47
1:A:181:MET:HG2	1:A:211:ARG:HH11	1.79	0.47
1:A:253:PHE:CD1	1:A:254:TYR:N	2.82	0.47
1:A:330:VAL:HG13	1:A:371:SER:HA	1.96	0.47
1:B:411:SER:HA	1:B:449:ILE:HD13	1.96	0.47
1:B:426:ALA:HB2	1:B:469:PHE:CD2	2.50	0.47
1:A:577:SER:HB2	1:A:579:MET:N	2.30	0.47
1:A:412:VAL:HG22	1:A:448:VAL:CG1	2.45	0.47
1:B:423:MET:HG3	1:B:465:MET:CE	2.44	0.47
1:B:222:SER:CB	1:B:225:LEU:HD23	2.30	0.47
1:A:635:PRO:HB3	1:A:640:GLN:OE1	2.16	0.46
1:B:113:GLU:CG	1:B:114:PRO:HD2	2.45	0.46
1:B:28:GLU:O	1:B:31:LEU:HB2	2.16	0.46
1:B:88:LEU:HD13	1:B:92:VAL:H	1.80	0.46
1:B:349:ARG:CZ	1:B:392:GLU:OE1	2.63	0.46
1:A:428:VAL:O	1:A:431:GLN:CD	2.51	0.46
1:B:612:PRO:O	1:B:615:TYR:HD2	1.99	0.46
1:B:340:TYR:CD2	1:B:349:ARG:NH2	2.81	0.46
1:A:480:VAL:N	2:A:2011:HOH:O	2.33	0.46
1:B:429:LYS:O	1:B:432:GLU:HB2	2.15	0.46
1:B:130:ARG:CG	1:B:130:ARG:HH11	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:619:ILE:O	1:B:622:ASP:HB3	2.15	0.46
1:A:350:GLU:OE2	1:A:382:ASP:N	2.45	0.46
1:A:567:TYR:CD1	1:A:567:TYR:C	2.89	0.46
1:A:29:ARG:NH1	1:A:264:ASN:OD1	2.49	0.46
1:A:350:GLU:HG2	1:A:380:LEU:HD22	1.97	0.46
1:A:291:ARG:NH1	1:A:395:ASP:OD1	2.48	0.46
1:A:236:SER:OG	1:A:239:GLU:HB2	2.15	0.46
1:B:204:LEU:HD23	1:B:208:GLU:HG3	1.98	0.46
1:B:330:VAL:O	1:B:330:VAL:HG23	2.16	0.46
1:B:101:GLY:HA2	1:B:128:VAL:CG1	2.45	0.46
1:B:28:GLU:O	1:B:29:ARG:C	2.54	0.46
1:B:308:GLU:O	1:B:332:SER:OG	2.34	0.46
1:A:144:PHE:O	1:A:148:VAL:HG23	2.15	0.46
1:B:415:LYS:HZ3	1:B:474:ASN:N	2.13	0.46
1:B:413:GLU:OE1	1:B:474:ASN:CG	2.54	0.46
1:B:195:GLU:HG2	1:B:197:ILE:HG23	1.97	0.46
1:B:132:VAL:HB	1:B:256:VAL:HG22	1.98	0.46
1:B:154:ARG:HG3	1:B:636:ARG:HD2	1.98	0.46
1:B:138:ASP:HA	1:B:169:GLU:O	2.16	0.46
1:B:90:VAL:HA	1:B:93:GLU:OE2	2.16	0.45
1:B:616:MET:O	1:B:618:ASP:N	2.49	0.45
1:B:480:VAL:HG23	1:B:482:TYR:CE2	2.51	0.45
1:B:257:LEU:HD12	1:B:257:LEU:N	2.31	0.45
1:A:406:PRO:HG3	1:A:438:HIS:CD2	2.52	0.45
1:B:85:HIS:NE2	1:B:88:LEU:CD2	2.77	0.45
1:B:260:THR:O	1:B:260:THR:HG23	2.17	0.45
1:A:572:HIS:CD2	1:A:573:ASP:H	2.34	0.45
1:A:537:TYR:CB	1:A:581:PHE:HE2	2.29	0.45
1:A:136:LYS:O	1:A:139:LYS:HG2	2.16	0.45
1:A:96:LEU:CD2	1:A:128:VAL:HG21	2.46	0.45
1:A:634:GLU:HG2	1:A:635:PRO:O	2.16	0.45
1:A:419:ASP:O	1:A:422:LYS:N	2.49	0.45
1:B:554:LEU:HD23	1:B:600:ILE:HG13	1.97	0.45
1:A:480:VAL:HG22	2:A:2011:HOH:O	2.15	0.45
1:B:440:HIS:O	1:B:448:VAL:HG23	2.15	0.45
1:B:631:ASP:C	1:B:631:ASP:OD1	2.55	0.45
1:B:268:GLN:CG	1:B:269:LEU:H	2.30	0.45
1:B:605:MET:SD	1:B:672:PHE:HA	2.56	0.45
1:A:270:MET:O	1:A:273:ALA:N	2.49	0.45
1:B:228:LYS:HA	1:B:233:GLU:OE2	2.17	0.45
1:B:450:ILE:HD11	1:B:461:LEU:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:215:ILE:H	1:B:215:ILE:HG13	1.62	0.45
1:A:270:MET:HG3	1:A:271:LEU:H	1.80	0.45
1:B:225:LEU:HG	1:B:226:MET:N	2.31	0.45
1:A:412:VAL:HG22	1:A:448:VAL:HG11	1.99	0.45
1:B:200:PRO:HG2	1:B:203:HIS:NE2	2.32	0.45
1:A:109:GLN:HG3	1:A:110:SER:N	2.31	0.45
1:A:269:LEU:O	1:A:272:ASP:HB2	2.16	0.45
1:B:85:HIS:CD2	1:B:88:LEU:HG	2.51	0.45
1:A:194:ILE:HG13	2:A:2006:HOH:O	2.17	0.45
1:B:88:LEU:CD1	1:B:91:GLU:HB3	2.47	0.45
1:A:633:MET:CG	1:A:634:GLU:N	2.79	0.45
1:B:597:ASP:OD1	1:B:597:ASP:O	2.35	0.45
1:B:164:LEU:HB3	1:B:176:ILE:HG13	1.99	0.45
1:B:545:LEU:O	1:B:549:MET:HG3	2.17	0.45
1:A:338:GLY:HA2	1:A:351:ARG:HH12	1.82	0.45
1:B:162:ILE:HG13	1:B:163:GLN:HG3	1.99	0.44
1:A:633:MET:SD	1:A:640:GLN:HG3	2.57	0.44
1:A:19:ILE:HD13	1:A:24:THR:H	1.83	0.44
1:A:291:ARG:HD2	1:A:297:GLU:OE1	2.18	0.44
1:B:341:VAL:HG23	1:B:350:GLU:HB2	2.00	0.44
1:A:132:VAL:HB	1:A:256:VAL:HG13	1.99	0.44
1:B:287:ILE:HD12	1:B:398:LEU:HD22	2.00	0.44
1:B:19:ILE:O	1:B:19:ILE:HG22	2.17	0.44
1:A:605:MET:HA	1:A:671:TYR:O	2.17	0.44
1:B:411:SER:HA	1:B:449:ILE:CD1	2.48	0.44
1:A:325:LEU:HA	1:A:325:LEU:HD12	1.89	0.44
1:B:209:GLU:HA	1:B:212:ALA:HB3	2.00	0.44
1:B:89:THR:O	1:B:93:GLU:HB3	2.18	0.44
1:A:493:GLN:HB2	1:A:510:HIS:CE1	2.53	0.44
1:A:177:ASP:OD2	1:A:180:GLU:HB2	2.17	0.44
1:A:354:ARG:HB3	1:A:365:GLU:OE2	2.18	0.44
1:A:298:GLU:HA	1:A:298:GLU:OE1	2.18	0.44
1:B:291:ARG:HD3	1:B:395:ASP:OD2	2.17	0.43
1:B:34:THR:CB	1:B:70:ALA:HB1	2.47	0.43
1:B:418:ALA:O	1:B:422:LYS:HG3	2.18	0.43
1:B:419:ASP:OD2	1:B:472:GLU:HG3	2.18	0.43
1:B:485:THR:HG22	1:B:601:LEU:HD11	1.99	0.43
1:B:35:GLY:O	1:B:36:ARG:C	2.57	0.43
1:A:415:LYS:NZ	1:A:474:ASN:OD1	2.50	0.43
1:A:381:LYS:HG3	1:A:382:ASP:H	1.82	0.43
1:B:136:LYS:CB	1:B:139:LYS:HZ3	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:292:ALA:H	1:B:395:ASP:HB2	1.83	0.43
1:B:354:ARG:HB2	1:B:378:VAL:HG11	1.99	0.43
1:B:339:SER:O	1:B:352:VAL:HG13	2.18	0.43
1:B:69:THR:HG22	1:B:76:ARG:NH1	2.33	0.43
1:B:616:MET:O	1:B:619:ILE:N	2.44	0.43
1:A:135:ASN:HD21	1:A:261:ALA:HB2	1.82	0.43
1:B:208:GLU:CD	1:B:209:GLU:N	2.67	0.43
1:A:633:MET:HG2	1:B:633:MET:HB3	2.01	0.43
1:B:547:ASP:OD1	1:B:547:ASP:N	2.51	0.43
1:A:292:ALA:HB2	1:A:397:ILE:HD11	2.00	0.43
1:A:631:ASP:OD1	1:A:631:ASP:C	2.57	0.43
1:B:541:VAL:HG13	1:B:585:ALA:HB2	2.01	0.43
1:A:496:PHE:CZ	1:A:583:ILE:HD12	2.54	0.43
1:A:5:PHE:CD2	1:A:76:ARG:HB2	2.53	0.43
1:B:88:LEU:HD13	1:B:91:GLU:CB	2.48	0.43
1:A:441:THR:HG22	1:A:441:THR:O	2.18	0.43
1:A:421:ASP:O	1:A:424:THR:OG1	2.35	0.42
1:A:414:PRO:HG3	1:A:423:MET:HE2	2.00	0.42
1:B:174:ALA:HB2	1:B:185:LYS:HA	2.00	0.42
1:A:32:TYR:CD1	1:A:32:TYR:C	2.93	0.42
1:B:268:GLN:CD	1:B:269:LEU:H	2.23	0.42
1:B:356:LEU:HD23	1:B:365:GLU:HA	2.01	0.42
1:B:484:GLU:CD	1:B:554:LEU:HB3	2.39	0.42
1:A:358:MET:CE	1:A:363:ARG:HH11	2.32	0.42
1:B:689:LYS:HB3	1:B:689:LYS:HE2	1.85	0.42
1:A:581:PHE:O	1:A:582:LYS:C	2.58	0.42
1:B:616:MET:HG2	1:B:620:MET:HE2	2.00	0.42
1:A:458:LEU:O	1:A:462:VAL:HG12	2.20	0.42
1:A:181:MET:HE3	1:A:211:ARG:HD3	2.01	0.42
1:A:638:ASN:C	1:A:638:ASN:OD1	2.56	0.42
1:B:410:LEU:HD23	1:B:478:PRO:HA	2.01	0.42
1:B:622:ASP:O	1:B:626:ARG:HG3	2.20	0.42
1:B:3:ARG:HB3	1:B:370:TYR:CE1	2.54	0.42
1:B:338:GLY:H	1:B:352:VAL:HG22	1.84	0.42
1:A:415:LYS:HB2	1:A:472:GLU:OE1	2.19	0.42
1:B:270:MET:HG3	1:B:271:LEU:N	2.34	0.42
1:A:399:GLU:HG2	1:A:400:SER:N	2.35	0.42
1:B:442:ASP:OD1	1:B:447:GLN:O	2.37	0.42
1:A:354:ARG:HG3	1:A:354:ARG:H	1.35	0.42
1:A:510:HIS:HB3	1:A:567:TYR:CE1	2.54	0.42
1:A:529:VAL:HG23	1:A:530:GLY:H	1.84	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:THR:HG21	1:A:453:MET:SD	2.60	0.42
1:B:31:LEU:HD22	1:B:68:THR:HG21	2.01	0.42
1:B:146:TYR:CD1	1:B:146:TYR:C	2.92	0.42
1:A:89:THR:HG22	1:A:93:GLU:OE2	2.20	0.42
1:B:678:VAL:HG13	1:B:679:PRO:HD2	2.00	0.42
1:A:536:GLU:HG3	1:A:537:TYR:CD1	2.55	0.42
1:B:622:ASP:OD2	1:B:654:TYR:HE1	2.02	0.42
1:A:157:ALA:HB1	1:A:254:TYR:CD2	2.54	0.42
1:A:117:GLU:HG3	1:A:155:LEU:HD11	2.02	0.42
1:A:346:LYS:O	1:A:348:LYS:HG3	2.20	0.41
1:A:112:VAL:CG1	1:A:150:THR:HB	2.46	0.41
1:A:188:ASN:ND2	1:A:192:THR:OG1	2.53	0.41
1:B:646:VAL:HG13	1:B:647:PRO:HD2	2.02	0.41
1:A:199:ILE:H	1:A:199:ILE:HG13	1.52	0.41
1:B:83:PRO:CG	1:B:88:LEU:HD11	2.50	0.41
1:B:88:LEU:CD1	1:B:92:VAL:H	2.32	0.41
1:B:466:LYS:O	1:B:470:ASN:HA	2.20	0.41
1:A:493:GLN:HB2	1:A:510:HIS:ND1	2.35	0.41
1:B:413:GLU:OE1	1:B:474:ASN:ND2	2.53	0.41
1:A:250:ASN:C	1:A:251:VAL:HG23	2.40	0.41
1:B:304:ASP:OD1	1:B:306:SER:N	2.51	0.41
1:B:144:PHE:CD2	1:B:165:PRO:HG3	2.55	0.41
1:A:160:ALA:HA	1:A:161:PRO:HD3	1.97	0.41
1:B:319:ASP:CB	1:B:322:VAL:HG22	2.48	0.41
1:A:436:THR:HG21	1:A:453:MET:CE	2.50	0.41
1:A:546:LYS:HG3	1:A:547:ASP:N	2.36	0.41
1:B:345:THR:OG1	1:B:388:THR:N	2.46	0.41
1:A:269:LEU:HD13	1:A:269:LEU:HA	1.80	0.41
1:A:484:GLU:OE2	1:A:555:ALA:N	2.49	0.41
1:A:381:LYS:HE3	1:A:382:ASP:OD2	2.21	0.41
1:B:29:ARG:HE	1:B:29:ARG:HA	1.86	0.41
1:B:456:LEU:O	1:B:459:ASP:N	2.54	0.41
1:A:304:ASP:O	1:A:333:GLY:N	2.50	0.41
1:A:338:GLY:HA2	1:A:351:ARG:NH1	2.35	0.41
1:B:511:ILE:HG23	1:B:565:LYS:O	2.21	0.41
1:B:230:LEU:H	1:B:230:LEU:HD12	1.85	0.41
1:A:203:HIS:HA	1:A:206:ARG:HD3	2.03	0.41
1:A:413:GLU:HA	1:A:414:PRO:HD2	1.79	0.41
1:A:120:TRP:HZ2	1:A:254:TYR:CE2	2.38	0.40
1:B:434:ASP:HA	1:B:435:PRO:HD2	1.91	0.40
1:A:335:MET:HG3	1:A:336:THR:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:643:ASN:OD1	1:A:643:ASN:C	2.60	0.40
1:B:686:ILE:HG22	1:B:690:ASN:ND2	2.36	0.40
1:B:635:PRO:HA	1:B:640:GLN:OE1	2.21	0.40
1:B:213:SER:O	1:B:216:GLU:OE1	2.39	0.40
1:A:426:ALA:O	1:A:430:LEU:HG	2.22	0.40
1:A:528:ILE:HG13	1:A:533:VAL:HB	2.03	0.40
1:A:260:THR:HG23	1:A:263:LYS:HB2	2.04	0.40
1:B:178:LEU:HD11	1:B:210:ALA:HB1	2.03	0.40
1:A:300:ILE:CG2	1:A:302:LYS:HG2	2.51	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:GLU:OE2	1:A:340:TYR:OH[1_455]	2.18	0.02

## 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	639/693 (92%)	592 (93%)	46 (7%)	1 (0%)	52	86
1	B	639/693 (92%)	583 (91%)	53 (8%)	3 (0%)	34	74
All	All	1278/1386 (92%)	1175 (92%)	99 (8%)	4 (0%)	46	81

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	691	LYS
1	B	394	ASN
1	B	251	VAL
1	A	251	VAL

### 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	543/579 (94%)	511 (94%)	32 (6%)	24	61
1	B	543/579 (94%)	500 (92%)	43 (8%)	15	46
All	All	1086/1158 (94%)	1011 (93%)	75 (7%)	19	54

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

Mol	Chain	Res	Type
1	A	18	HIS
1	A	34	THR
1	A	96	LEU
1	A	109	GLN
1	A	113	GLU
1	A	118	THR
1	A	150	THR
1	A	202	ASP
1	A	204	LEU
1	A	213	SER
1	A	215	ILE
1	A	234	GLU
1	A	269	LEU
1	A	288	ILE
1	A	298	GLU
1	A	317	MET
1	A	329	ARG
1	A	336	THR
1	A	350	GLU
1	A	354	ARG
1	A	361	ASN
1	A	369	VAL
1	A	396	ILE
1	A	416	SER
1	A	529	VAL
1	A	532	VAL
1	A	559	LEU

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Mol	Chain	Res	Type
1	A	567	TYR
1	A	577	SER
1	A	611	MET
1	A	631	ASP
1	A	633	MET
1	B	8	GLU
1	B	20	ASP
1	B	29	ARG
1	B	86	VAL
1	B	87	ASP
1	B	109	GLN
1	B	112	VAL
1	B	116	THR
1	B	176	ILE
1	B	187	THR
1	B	192	THR
1	B	203	HIS
1	B	208	GLU
1	B	220	GLU
1	B	225	LEU
1	B	226	MET
1	B	233	GLU
1	B	235	ILE
1	B	268	GLN
1	B	293	SER
1	B	294	ASN
1	B	305	ASP
1	B	306	SER
1	B	325	LEU
1	B	332	SER
1	B	352	VAL
1	B	361	ASN
1	B	363	ARG
1	B	393	LYS
1	B	395	ASP
1	B	463	ASP
1	B	475	VAL
1	B	487	LYS
1	B	492	VAL
1	B	573	ASP
1	B	574	VAL
1	B	579	MET

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Mol	Chain	Res	Type
1	B	611	MET
1	B	624	THR
1	B	630	VAL
1	B	649	SER
1	B	662	THR
1	B	684	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	572	HIS
1	B	75	HIS
1	B	640	GLN

### 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](#)

There are no ligands in this entry.

### 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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

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	649/693 (93%)	-0.12	7 (1%) 82 65	41, 81, 128, 172	0
1	B	649/693 (93%)	-0.03	6 (0%) 85 70	43, 97, 157, 227	0
All	All	1298/1386 (93%)	-0.08	13 (1%) 84 67	41, 89, 145, 227	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	398	LEU	2.8
1	A	389	LEU	2.7
1	A	284	VAL	2.7
1	B	641	VAL	2.6
1	B	127	GLY	2.5
1	B	85	HIS	2.4
1	B	310	ALA	2.3
1	B	235	ILE	2.2
1	A	285	LYS	2.1
1	A	341	VAL	2.1
1	B	442	ASP	2.0
1	A	2	ALA	2.0
1	A	115	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](#)

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.