



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 2, 2017 – 08:19 PM EDT

PDB ID : 1RR9  
Title : Catalytic domain of E.coli Lon protease  
Authors : Botos, I.; Melnikov, E.E.; Cherry, S.; Tropea, J.E.; Khalatova, A.G.; Dauter, Z.; Maurizi, M.R.; Rotanova, T.V.; Wlodawer, A.; Gustchina, A.  
Deposited on : unknown  
Resolution : 2.10 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 : rb-20030345  
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) : rb-20030345

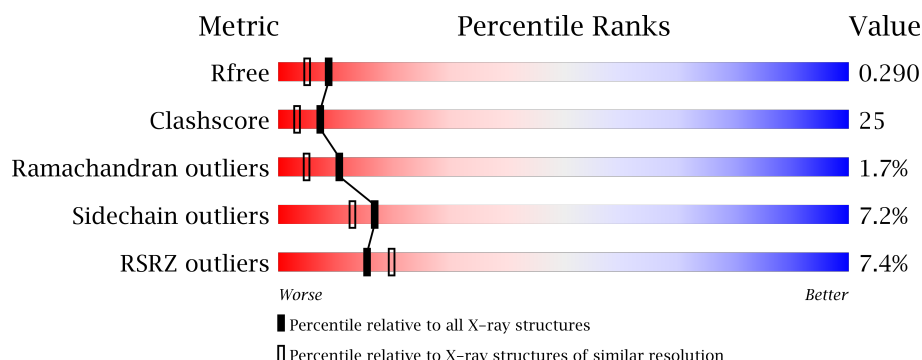
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 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	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

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	200	<div> <div>5%</div> <div>58% 28% 5% • 9%</div> </div>
1	B	200	<div> <div>5%</div> <div>52% 35% • • 9%</div> </div>
1	C	200	<div> <div>6%</div> <div>60% 28% • • 9%</div> </div>
1	D	200	<div> <div>9%</div> <div>54% 33% • • 9%</div> </div>
1	E	200	<div> <div>12%</div> <div>55% 35% 6% • 5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	200	<div><div></div><div>5%</div><div>51%</div><div>34%</div><div>6%</div><div>9%</div></div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8485 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 ATP-dependent protease La.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	182	Total	C	N	O	S	0	0	0
			1353	853	235	259	6			
1	B	182	Total	C	N	O	S	0	0	0
			1353	853	235	259	6			
1	C	182	Total	C	N	O	S	0	0	0
			1353	853	235	259	6			
1	D	182	Total	C	N	O	S	0	0	0
			1360	857	238	259	6			
1	E	191	Total	C	N	O	S	0	0	0
			1422	895	249	271	7			
1	F	182	Total	C	N	O	S	0	0	0
			1361	856	239	260	6			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	679	ALA	SER	ENGINEERED	UNP P0A9M0
B	679	ALA	SER	ENGINEERED	UNP P0A9M0
C	679	ALA	SER	ENGINEERED	UNP P0A9M0
D	679	ALA	SER	ENGINEERED	UNP P0A9M0
E	679	ALA	SER	ENGINEERED	UNP P0A9M0
F	679	ALA	SER	ENGINEERED	UNP P0A9M0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

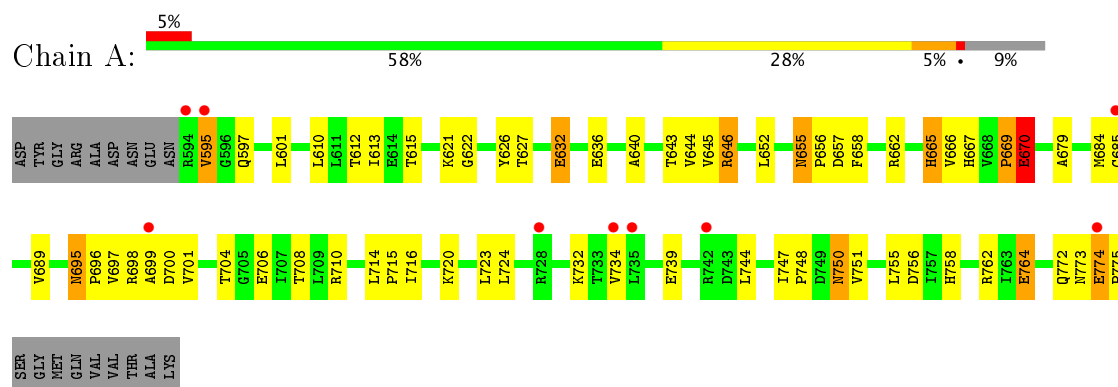
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	51	Total	O	0	0
			51	51		
3	B	45	Total	O	0	0
			45	45		
3	C	49	Total	O	0	0
			49	49		
3	D	28	Total	O	0	0
			28	28		
3	E	35	Total	O	0	0
			35	35		
3	F	50	Total	O	0	0
			50	50		

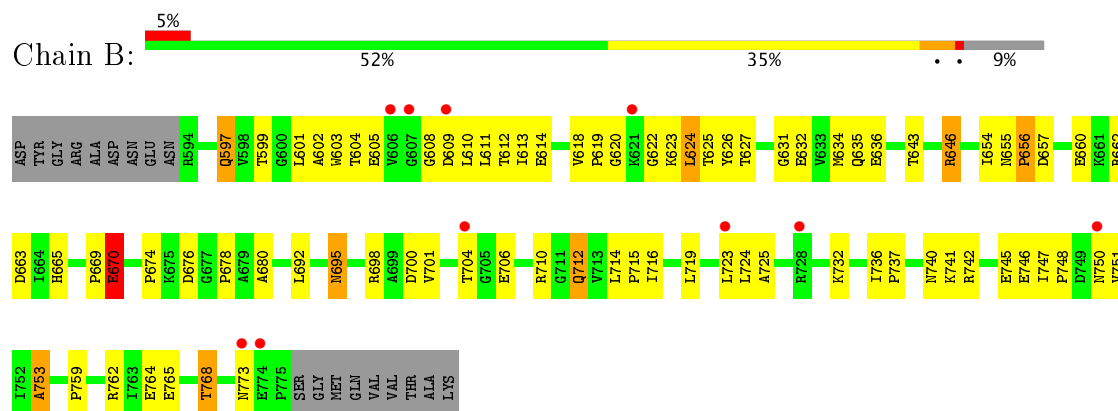
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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.

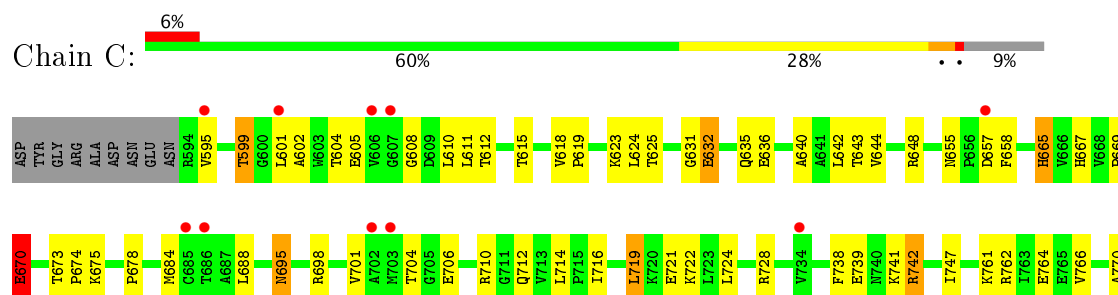
#### • Molecule 1: ATP-dependent protease La

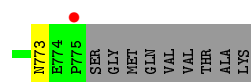


#### • Molecule 1: ATP-dependent protease La

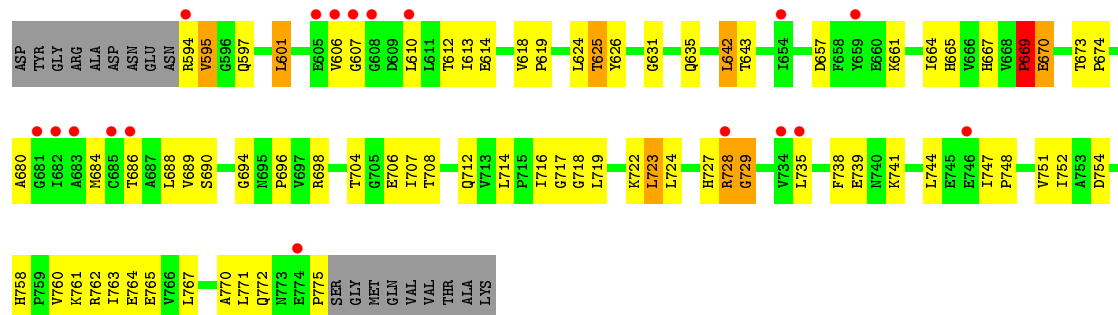


#### • Molecule 1: ATP-dependent protease La

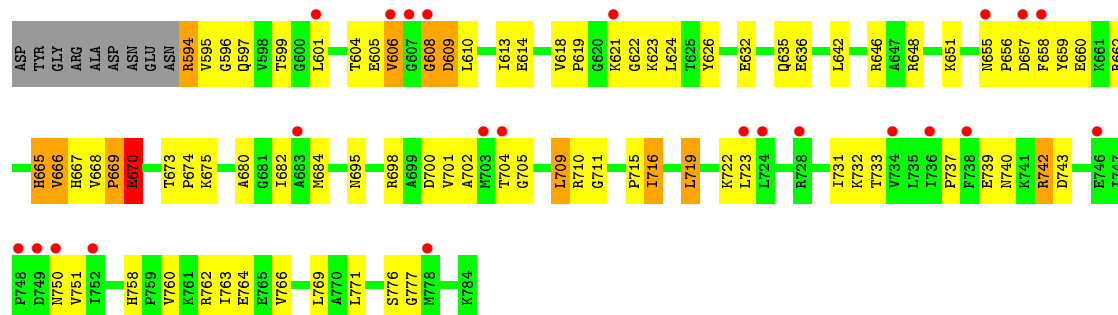




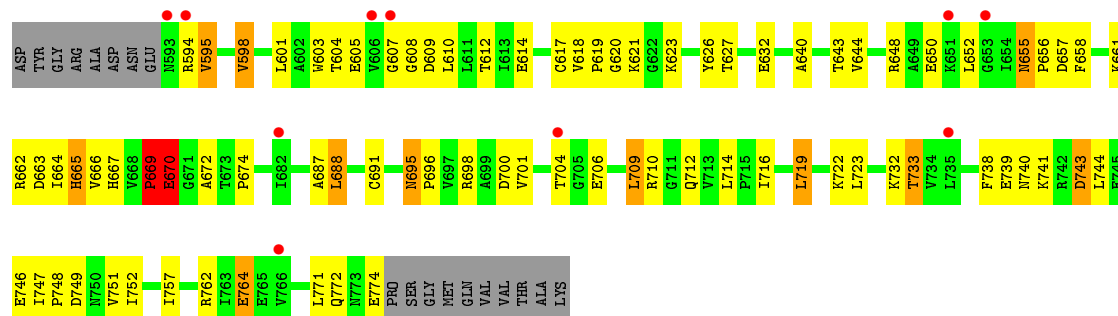
• Molecule 1: ATP-dependent protease La



• Molecule 1: ATP-dependent protease La



• Molecule 1: ATP-dependent protease La



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.21Å 86.21Å 122.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.10 19.72 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (20.00-2.10) 88.4 (19.72-2.10)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.45 (at 2.09Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.243 , 0.296 0.242 , 0.290	Depositor DCC
$R_{free}$ test set	1072 reflections (2.04%)	DCC
Wilson B-factor (Å <sup>2</sup> )	32.4	Xtriage
Anisotropy	0.597	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 63.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for -h,-k,l 0.046 for h,-h-k,-l 0.026 for -k,-h,-l	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	8485	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.55% 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: 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	0.39	0/1373	0.66	1/1866 (0.1%)
1	B	0.34	0/1373	0.63	1/1866 (0.1%)
1	C	0.34	0/1373	0.63	1/1866 (0.1%)
1	D	0.33	0/1380	0.60	0/1875
1	E	0.31	0/1442	0.63	1/1958 (0.1%)
1	F	0.36	0/1380	0.64	1/1874 (0.1%)
All	All	0.35	0/8321	0.63	5/11305 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	670	GLU	N-CA-C	-7.09	91.86	111.00
1	A	670	GLU	N-CA-C	-6.56	93.29	111.00
1	E	670	GLU	N-CA-C	-6.46	93.56	111.00
1	F	670	GLU	N-CA-C	-5.65	95.75	111.00
1	C	670	GLU	N-CA-C	-5.60	95.87	111.00

There are no chirality outliers.

There are no planarity outliers.

### 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	1353	0	1392	69	0
1	B	1353	0	1392	85	0
1	C	1353	0	1392	68	0
1	D	1360	0	1404	61	0
1	E	1422	0	1472	74	0
1	F	1361	0	1403	76	0
2	B	5	0	0	0	0
2	C	5	0	0	0	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
3	A	51	0	0	5	0
3	B	45	0	0	3	0
3	C	49	0	0	5	0
3	D	28	0	0	0	0
3	E	35	0	0	2	0
3	F	50	0	0	1	0
All	All	8485	0	8455	414	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 25.

All (414) 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:E:594:ARG:HD3	1:E:595:VAL:H	1.18	1.06
1:B:716:ILE:H	1:B:740:ASN:HD21	1.03	0.99
1:C:636:GLU:HB3	3:C:33:HOH:O	1.59	0.99
1:A:715:PRO:HG3	1:A:739:GLU:HB2	1.43	0.99
1:C:615:THR:HG21	1:C:688:LEU:HD23	1.45	0.98
1:D:698:ARG:HE	1:D:772:GLN:HA	1.29	0.98
1:A:723:LEU:HD12	1:A:747:ILE:HD13	1.45	0.97
1:C:623:LYS:HZ2	1:C:624:LEU:H	1.15	0.92
1:B:695:ASN:HD21	1:B:773:ASN:H	1.13	0.91
1:A:774:GLU:HB3	1:A:775:PRO:HD3	1.53	0.88
1:D:717:GLY:O	1:D:722:LYS:HE2	1.74	0.87
1:B:764:GLU:O	1:B:768:THR:HG22	1.74	0.86
1:D:771:LEU:HD12	1:D:775:PRO:HG3	1.56	0.85
1:E:594:ARG:HD3	1:E:595:VAL:N	1.90	0.85
1:B:646:ARG:HB3	1:B:646:ARG:HH11	1.41	0.85
1:E:669:PRO:O	1:E:670:GLU:HB2	1.80	0.81
1:A:720:LYS:NZ	1:A:748:PRO:HD3	1.97	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:743:ASP:O	1:F:746:GLU:HG2	1.82	0.79
1:B:669:PRO:O	1:B:670:GLU:HB2	1.83	0.79
1:A:646:ARG:HG2	1:F:618:VAL:HG21	1.65	0.79
1:E:742:ARG:HB3	1:E:742:ARG:NH1	1.97	0.78
1:C:612:THR:O	1:C:669:PRO:HD2	1.83	0.77
1:E:655:ASN:HD21	1:E:657:ASP:HB2	1.49	0.76
1:C:741:LYS:HB2	1:C:742:ARG:NH1	2.01	0.76
1:E:626:TYR:HB3	1:E:666:VAL:HG13	1.67	0.76
1:E:604:THR:H	1:E:608:GLY:HA2	1.48	0.75
1:D:698:ARG:NE	1:D:772:GLN:HA	2.01	0.75
1:D:606:VAL:HG23	1:D:607:GLY:H	1.52	0.75
1:E:702:ALA:HB2	1:E:731:ILE:HD13	1.68	0.74
1:D:728:ARG:HG3	1:D:728:ARG:HH11	1.53	0.74
1:A:698:ARG:O	3:A:7:HOH:O	2.06	0.73
1:F:612:THR:O	1:F:669:PRO:HD2	1.91	0.71
1:C:684:MET:HG3	3:C:9:HOH:O	1.90	0.71
1:A:710:ARG:HG2	1:F:614:GLU:OE2	1.92	0.70
1:E:716:ILE:H	1:E:716:ILE:HD13	1.56	0.70
1:F:740:ASN:O	1:F:743:ASP:HB2	1.91	0.70
1:F:698:ARG:O	1:F:701:VAL:HG22	1.92	0.69
1:A:723:LEU:HD12	1:A:747:ILE:CD1	2.20	0.69
1:A:684:MET:HG3	3:A:218:HOH:O	1.91	0.69
1:C:669:PRO:O	1:C:670:GLU:HB2	1.92	0.69
1:D:686:THR:O	1:D:689:VAL:HG12	1.93	0.68
1:C:618:VAL:HB	1:C:619:PRO:HD2	1.76	0.68
1:F:723:LEU:HD12	1:F:747:ILE:HD12	1.75	0.68
1:A:696:PRO:HG2	1:A:772:GLN:HG2	1.76	0.68
1:E:698:ARG:HD2	1:E:769:LEU:O	1.94	0.68
1:D:698:ARG:HG2	1:D:770:ALA:O	1.94	0.67
1:F:603:TRP:HA	1:F:608:GLY:CA	2.24	0.66
1:A:695:ASN:ND2	1:A:773:ASN:HB2	2.09	0.66
1:B:695:ASN:ND2	1:B:773:ASN:H	1.91	0.66
1:B:655:ASN:HD21	1:B:657:ASP:HB2	1.60	0.66
1:B:750:ASN:O	1:B:753:ALA:HB3	1.95	0.66
1:C:640:ALA:O	1:C:644:VAL:HG23	1.96	0.66
1:F:701:VAL:HG12	1:F:733:THR:HG23	1.78	0.66
1:A:700:ASP:HB2	1:A:732:LYS:HB3	1.78	0.65
1:E:695:ASN:HD21	1:E:771:LEU:HB3	1.61	0.65
1:B:623:LYS:HG2	1:B:663:ASP:OD1	1.95	0.65
1:D:680:ALA:O	1:D:684:MET:HG2	1.96	0.65
1:F:710:ARG:HG3	1:F:712:GLN:HG2	1.77	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:655:ASN:HD22	1:A:656:PRO:CD	2.09	0.65
1:B:618:VAL:HG22	1:B:619:PRO:HD2	1.78	0.65
1:C:605:GLU:HB2	1:C:674:PRO:HD2	1.78	0.65
1:E:719:LEU:HD22	1:E:723:LEU:HG	1.77	0.65
1:C:704:THR:HG21	1:C:722:LYS:HD3	1.78	0.65
1:C:604:THR:HG21	1:C:611:LEU:HD21	1.79	0.65
1:A:595:VAL:HA	1:A:615:THR:O	1.97	0.65
1:C:762:ARG:HB3	1:C:764:GLU:OE2	1.95	0.65
1:B:618:VAL:CG2	1:B:619:PRO:HD2	2.27	0.64
1:A:708:THR:HG23	1:A:714:LEU:CD2	2.28	0.64
1:D:689:VAL:HG11	1:D:767:LEU:HD22	1.79	0.64
1:C:742:ARG:H	1:C:742:ARG:HH11	1.46	0.63
1:A:715:PRO:HG3	1:A:739:GLU:CB	2.23	0.63
1:E:601:LEU:HB2	1:E:704:THR:HB	1.80	0.63
1:A:643:THR:OG1	1:F:665:HIS:HD2	1.81	0.63
1:B:601:LEU:HB2	1:B:704:THR:HB	1.80	0.63
1:A:655:ASN:HD22	1:A:656:PRO:HD2	1.63	0.63
1:D:631:GLY:O	1:D:635:GLN:HG3	1.99	0.62
1:C:742:ARG:H	1:C:742:ARG:HD2	1.63	0.62
1:C:742:ARG:N	1:C:742:ARG:HH11	1.97	0.62
1:E:655:ASN:ND2	1:E:657:ASP:HB2	2.15	0.62
1:F:655:ASN:ND2	1:F:657:ASP:H	1.96	0.62
1:B:622:GLY:HA2	1:B:662:ARG:O	1.99	0.62
1:C:648:ARG:NH1	1:C:764:GLU:OE1	2.31	0.62
1:F:738:PHE:O	1:F:741:LYS:HG3	1.98	0.62
1:F:719:LEU:HD12	1:F:743:ASP:HB3	1.81	0.62
1:A:695:ASN:CG	1:A:773:ASN:HB2	2.20	0.61
1:D:718:GLY:O	1:D:722:LYS:HG3	2.00	0.61
1:E:742:ARG:HB3	1:E:742:ARG:HH11	1.64	0.61
1:F:603:TRP:HA	1:F:608:GLY:HA3	1.81	0.61
1:B:627:THR:HB	3:C:33:HOH:O	2.01	0.61
1:C:599:THR:OG1	1:C:610:LEU:HD11	2.00	0.61
1:F:695:ASN:HD22	1:F:696:PRO:HD2	1.66	0.61
1:C:655:ASN:O	1:C:658:PHE:HB3	2.00	0.61
1:F:598:VAL:CG1	1:F:687:ALA:HB2	2.31	0.61
1:B:698:ARG:O	1:B:701:VAL:HG12	2.00	0.60
1:A:714:LEU:HD22	1:A:714:LEU:N	2.16	0.60
1:D:606:VAL:HG23	1:D:607:GLY:N	2.16	0.60
1:D:708:THR:OG1	1:D:712:GLN:HG2	2.01	0.60
1:A:612:THR:O	1:A:669:PRO:HD2	2.01	0.60
1:C:632:GLU:HA	1:C:635:GLN:HE21	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:665:HIS:HD2	1:C:643:THR:OG1	1.83	0.60
1:F:605:GLU:HB2	1:F:674:PRO:HB2	1.84	0.60
1:E:667:HIS:HB3	1:F:709:LEU:HD22	1.82	0.59
1:C:741:LYS:HB2	1:C:742:ARG:HH12	1.66	0.59
1:F:719:LEU:HD13	1:F:747:ILE:HD11	1.83	0.59
1:A:756:ASP:OD2	1:A:758:HIS:HE1	1.84	0.59
1:F:594:ARG:HD2	1:F:662:ARG:HH21	1.68	0.59
1:F:664:ILE:HD13	1:F:688:LEU:HD11	1.83	0.59
1:B:706:GLU:HB3	1:B:714:LEU:HB2	1.85	0.58
1:B:614:GLU:OE2	1:C:710:ARG:HG2	2.02	0.58
1:A:695:ASN:HD22	1:A:696:PRO:HD2	1.67	0.58
1:B:624:LEU:H	1:B:624:LEU:HD22	1.69	0.58
1:F:752:ILE:HD12	1:F:757:ILE:HD12	1.83	0.58
1:C:631:GLY:O	1:C:635:GLN:HG3	2.03	0.58
1:B:631:GLY:O	1:B:635:GLN:HG3	2.04	0.58
1:B:631:GLY:HA3	1:B:676:ASP:OD2	2.04	0.58
1:A:621:LYS:HE2	1:A:621:LYS:HA	1.85	0.58
1:C:695:ASN:HD21	1:C:773:ASN:H	1.52	0.58
1:E:698:ARG:O	1:E:701:VAL:HG22	2.04	0.58
1:F:594:ARG:HH11	1:F:662:ARG:HH21	1.52	0.58
1:B:700:ASP:CG	1:B:732:LYS:HD3	2.24	0.58
1:D:719:LEU:HG	1:D:723:LEU:HD22	1.85	0.58
1:E:599:THR:HG21	1:E:731:ILE:HD11	1.86	0.57
1:E:682:ILE:HG22	1:E:763:ILE:HD13	1.86	0.57
1:D:727:HIS:HB2	1:D:751:VAL:HG23	1.87	0.57
1:E:642:LEU:O	1:E:646:ARG:HG3	2.05	0.57
1:B:719:LEU:HG	1:B:723:LEU:HD13	1.85	0.57
1:E:695:ASN:ND2	1:E:771:LEU:HB3	2.19	0.57
1:C:601:LEU:O	1:C:704:THR:HG23	2.03	0.57
1:A:695:ASN:ND2	1:A:773:ASN:HD22	2.03	0.57
1:B:646:ARG:HH11	1:B:646:ARG:CB	2.14	0.57
1:E:604:THR:N	1:E:608:GLY:HA2	2.19	0.57
1:A:669:PRO:O	1:A:670:GLU:HB2	2.04	0.57
1:C:623:LYS:NZ	1:C:624:LEU:H	1.95	0.57
1:C:724:LEU:O	1:C:728:ARG:HG3	2.05	0.57
1:A:699:ALA:O	1:A:700:ASP:OD1	2.23	0.57
1:F:601:LEU:HB2	1:F:704:THR:HB	1.87	0.57
1:C:623:LYS:HZ3	1:C:623:LYS:HA	1.70	0.56
1:A:696:PRO:HG2	1:A:772:GLN:CG	2.34	0.56
1:C:742:ARG:HG3	1:C:742:ARG:NH1	2.20	0.56
1:A:655:ASN:HD22	1:A:656:PRO:N	2.04	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:708:THR:HG23	1:A:714:LEU:HD21	1.88	0.56
1:F:627:THR:OG1	1:F:665:HIS:HE1	1.89	0.56
1:C:601:LEU:HB2	1:C:704:THR:OG1	2.06	0.56
1:C:706:GLU:HB3	1:C:714:LEU:HB2	1.87	0.56
1:C:742:ARG:HH11	1:C:742:ARG:HG3	1.69	0.56
1:E:626:TYR:HB3	1:E:666:VAL:CG1	2.35	0.55
1:E:648:ARG:HH22	1:E:711:GLY:HA3	1.71	0.55
1:F:672:ALA:O	1:F:674:PRO:HD3	2.06	0.55
1:F:603:TRP:HA	1:F:608:GLY:HA2	1.87	0.55
1:E:655:ASN:OD1	1:E:656:PRO:HD2	2.06	0.55
1:A:750:ASN:HD22	1:A:750:ASN:H	1.53	0.55
1:B:627:THR:OG1	1:B:665:HIS:HE1	1.90	0.55
1:E:622:GLY:HA2	1:E:662:ARG:O	2.07	0.55
1:B:737:PRO:HD2	1:B:740:ASN:HD22	1.72	0.54
1:F:626:TYR:HA	1:F:666:VAL:O	2.07	0.54
1:D:724:LEU:O	1:D:728:ARG:HG2	2.07	0.54
1:A:774:GLU:CB	1:A:775:PRO:HD3	2.31	0.54
1:D:706:GLU:HB3	1:D:714:LEU:HB2	1.87	0.54
1:D:761:LYS:N	1:D:765:GLU:OE1	2.35	0.54
1:D:735:LEU:HD23	1:D:758:HIS:HB2	1.90	0.54
1:C:742:ARG:H	1:C:742:ARG:CD	2.20	0.54
1:A:665:HIS:HD2	1:B:643:THR:OG1	1.91	0.54
1:A:744:LEU:HD23	1:A:747:ILE:HD12	1.89	0.54
1:D:748:PRO:HG2	1:D:751:VAL:HG12	1.90	0.54
1:E:668:VAL:HG12	1:E:675:LYS:HE2	1.89	0.54
1:C:605:GLU:CB	1:C:674:PRO:HD2	2.37	0.54
1:D:601:LEU:HB2	1:D:704:THR:HB	1.90	0.54
1:A:708:THR:CG2	1:A:714:LEU:HD21	2.37	0.53
1:F:608:GLY:HA3	3:F:149:HOH:O	2.07	0.53
1:C:698:ARG:HG3	1:C:770:ALA:O	2.08	0.53
1:F:696:PRO:HG2	1:F:772:GLN:HB3	1.91	0.53
1:C:684:MET:HE3	3:C:9:HOH:O	2.07	0.53
1:E:648:ARG:NH1	1:E:764:GLU:OE2	2.42	0.53
1:A:601:LEU:HB2	1:A:704:THR:HB	1.90	0.52
1:B:624:LEU:HD13	1:B:624:LEU:N	2.24	0.52
1:E:764:GLU:HG2	3:E:80:HOH:O	2.08	0.52
1:B:719:LEU:O	1:B:723:LEU:HD13	2.10	0.52
1:D:613:ILE:N	1:D:613:ILE:HD12	2.25	0.52
1:D:748:PRO:O	1:D:751:VAL:HG12	2.09	0.52
1:F:655:ASN:HD22	1:F:656:PRO:N	2.08	0.52
1:F:762:ARG:HE	1:F:764:GLU:HG3	1.74	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:752:ILE:CD1	1:F:757:ILE:HD12	2.40	0.52
1:A:685:CYS:O	1:A:689:VAL:HG23	2.10	0.51
1:D:669:PRO:O	1:D:670:GLU:HB2	2.10	0.51
1:D:747:ILE:HB	1:D:752:ILE:HD11	1.91	0.51
1:A:669:PRO:O	1:A:670:GLU:CB	2.59	0.51
1:A:720:LYS:O	1:A:724:LEU:HG	2.10	0.51
1:A:774:GLU:HB3	1:A:775:PRO:CD	2.34	0.51
1:C:632:GLU:HA	1:C:635:GLN:NE2	2.25	0.51
1:D:618:VAL:HB	1:D:619:PRO:HD2	1.91	0.51
1:E:700:ASP:HB3	1:E:732:LYS:HB3	1.93	0.51
1:A:658:PHE:O	1:A:662:ARG:HB2	2.11	0.51
1:B:741:LYS:HE2	3:B:153:HOH:O	2.10	0.51
1:D:612:THR:O	1:D:669:PRO:HD2	2.11	0.51
1:D:669:PRO:O	1:D:670:GLU:CB	2.59	0.51
1:E:596:GLY:HA3	3:E:159:HOH:O	2.11	0.51
1:E:621:LYS:HD2	1:E:623:LYS:HE3	1.93	0.51
1:B:610:LEU:HD12	1:B:610:LEU:C	2.32	0.50
1:B:655:ASN:ND2	1:B:657:ASP:HB2	2.26	0.50
1:C:738:PHE:CD2	1:C:761:LYS:HE2	2.46	0.50
1:B:619:PRO:HD3	1:B:662:ARG:HH21	1.75	0.50
1:B:655:ASN:C	1:B:657:ASP:H	2.13	0.50
1:B:613:ILE:N	1:B:613:ILE:HD12	2.27	0.50
1:A:708:THR:HB	1:F:614:GLU:OE2	2.12	0.50
1:F:650:GLU:HB2	1:F:656:PRO:HG3	1.93	0.50
1:F:762:ARG:HG3	1:F:762:ARG:HH11	1.77	0.50
1:B:632:GLU:O	1:B:636:GLU:HG3	2.12	0.50
1:F:604:THR:H	1:F:608:GLY:HA2	1.77	0.50
1:F:623:LYS:HB2	1:F:663:ASP:OD1	2.12	0.50
1:B:715:PRO:HA	1:B:737:PRO:CB	2.42	0.50
1:D:669:PRO:HG2	1:E:710:ARG:HH12	1.77	0.50
1:B:700:ASP:HB3	1:B:732:LYS:HB2	1.92	0.49
1:C:684:MET:O	1:C:688:LEU:HG	2.12	0.49
1:B:624:LEU:HD22	1:B:624:LEU:N	2.27	0.49
1:E:605:GLU:HB2	1:E:674:PRO:HB2	1.93	0.49
1:A:708:THR:HG23	1:A:714:LEU:HD23	1.93	0.49
1:B:620:GLY:HA3	1:B:663:ASP:OD2	2.12	0.49
1:B:603:TRP:HA	1:B:608:GLY:HA2	1.94	0.49
1:E:705:GLY:HA2	1:E:716:ILE:HG23	1.93	0.49
1:B:618:VAL:HG22	1:B:619:PRO:CD	2.42	0.49
1:D:657:ASP:O	1:D:661:LYS:HG2	2.13	0.49
1:F:620:GLY:HA3	1:F:663:ASP:CG	2.33	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:720:LYS:HZ3	1:A:748:PRO:HD3	1.75	0.49
1:A:748:PRO:HB2	1:A:751:VAL:HG23	1.94	0.49
3:A:8:HOH:O	1:F:667:HIS:HE1	1.95	0.49
1:D:624:LEU:HD22	1:D:642:LEU:CD1	2.43	0.49
1:D:684:MET:O	1:D:688:LEU:HB2	2.13	0.49
1:E:655:ASN:ND2	1:E:658:PHE:H	2.10	0.49
1:B:655:ASN:O	1:B:657:ASP:N	2.44	0.48
1:B:748:PRO:HG2	1:B:751:VAL:CG2	2.43	0.48
1:E:719:LEU:O	1:E:723:LEU:HG	2.14	0.48
1:D:624:LEU:HD22	1:D:642:LEU:HD11	1.95	0.48
1:F:655:ASN:C	1:F:655:ASN:HD22	2.17	0.48
1:D:670:GLU:HA	1:D:670:GLU:OE1	2.13	0.48
1:D:727:HIS:CG	1:D:751:VAL:HG23	2.49	0.48
1:B:748:PRO:HB3	3:B:158:HOH:O	2.13	0.48
1:C:665:HIS:HD2	1:D:643:THR:OG1	1.97	0.48
1:F:706:GLU:HB3	1:F:714:LEU:HB2	1.96	0.48
1:B:605:GLU:HG2	1:B:674:PRO:HB2	1.95	0.48
1:A:597:GLN:OE1	1:B:710:ARG:HB3	2.14	0.48
1:E:606:VAL:O	1:E:606:VAL:HG13	2.14	0.48
1:F:640:ALA:O	1:F:644:VAL:HG23	2.14	0.48
1:A:610:LEU:C	1:A:610:LEU:HD23	2.34	0.47
1:C:673:THR:O	1:C:675:LYS:HG3	2.14	0.47
1:E:597:GLN:OE1	1:E:614:GLU:HG2	2.13	0.47
1:E:632:GLU:O	1:E:636:GLU:HG3	2.14	0.47
1:E:648:ARG:HH22	1:E:711:GLY:CA	2.26	0.47
1:F:594:ARG:HD2	1:F:662:ARG:NH2	2.30	0.47
1:F:700:ASP:HB2	1:F:732:LYS:HG3	1.96	0.47
1:A:723:LEU:CD1	1:A:747:ILE:HD13	2.30	0.47
1:C:719:LEU:HD13	1:C:747:ILE:HD11	1.96	0.47
1:A:701:VAL:HB	3:A:7:HOH:O	2.14	0.47
1:F:695:ASN:OD1	1:F:771:LEU:HB3	2.14	0.47
1:B:602:ALA:HB2	1:B:680:ALA:HB2	1.96	0.47
1:B:623:LYS:C	1:B:624:LEU:HD13	2.35	0.47
1:C:669:PRO:O	1:C:670:GLU:CB	2.61	0.47
1:F:723:LEU:HD12	1:F:747:ILE:CD1	2.44	0.47
1:B:723:LEU:N	1:B:723:LEU:HD12	2.30	0.47
1:D:689:VAL:HG13	1:D:690:SER:N	2.30	0.47
1:A:695:ASN:HD22	1:A:696:PRO:CD	2.28	0.47
1:C:764:GLU:CD	1:C:764:GLU:H	2.18	0.47
1:E:613:ILE:HD12	1:E:613:ILE:H	1.80	0.47
1:E:737:PRO:HB2	1:E:740:ASN:OD1	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:669:PRO:O	1:B:670:GLU:CB	2.60	0.47
1:C:704:THR:HG21	1:C:722:LYS:CD	2.45	0.47
1:D:728:ARG:NH1	1:D:728:ARG:HG3	2.24	0.47
1:F:655:ASN:HD22	1:F:656:PRO:CD	2.27	0.47
1:E:648:ARG:HH22	1:E:710:ARG:C	2.18	0.47
1:F:598:VAL:HG12	1:F:687:ALA:HB2	1.97	0.47
1:A:714:LEU:CD2	1:A:714:LEU:N	2.78	0.46
1:E:673:THR:O	1:E:675:LYS:HG3	2.14	0.46
1:E:719:LEU:HD22	1:E:723:LEU:CG	2.44	0.46
1:B:610:LEU:HD23	1:B:725:ALA:O	2.15	0.46
1:A:723:LEU:CD2	1:A:734:VAL:HG11	2.46	0.46
1:C:595:VAL:HA	1:C:615:THR:O	2.15	0.46
1:B:678:PRO:HB2	1:B:706:GLU:HG3	1.96	0.46
1:E:669:PRO:O	1:E:670:GLU:CB	2.57	0.46
1:A:697:VAL:HG12	3:A:7:HOH:O	2.15	0.46
1:E:665:HIS:HD2	1:F:643:THR:OG1	1.98	0.46
1:A:679:ALA:HA	1:A:716:ILE:HG21	1.96	0.46
1:B:605:GLU:CG	1:B:674:PRO:HB2	2.46	0.46
1:E:606:VAL:O	1:E:606:VAL:HG22	2.16	0.46
1:D:667:HIS:HB3	1:E:709:LEU:HD22	1.98	0.46
1:A:655:ASN:ND2	1:A:657:ASP:H	2.14	0.46
1:B:665:HIS:CD2	1:C:643:THR:OG1	2.65	0.46
1:D:707:ILE:HD12	1:D:763:ILE:HD13	1.98	0.46
1:D:738:PHE:O	1:D:741:LYS:HG3	2.15	0.46
1:E:613:ILE:HD12	1:E:613:ILE:N	2.30	0.46
1:F:609:ASP:HB2	1:F:610:LEU:H	1.51	0.45
1:D:762:ARG:O	1:D:765:GLU:HG2	2.16	0.45
1:E:660:GLU:OE1	1:E:660:GLU:HA	2.16	0.45
1:E:626:TYR:HA	1:E:666:VAL:O	2.16	0.45
1:B:747:ILE:HG23	1:B:748:PRO:HD2	1.98	0.45
1:D:610:LEU:HD11	1:D:729:GLY:HA3	1.97	0.45
1:E:742:ARG:HB3	1:E:742:ARG:CZ	2.47	0.45
1:F:595:VAL:HA	1:F:691:CYS:SG	2.57	0.45
1:C:648:ARG:HH12	1:C:764:GLU:CD	2.17	0.45
1:F:748:PRO:O	1:F:751:VAL:HG22	2.17	0.45
1:F:771:LEU:HB2	1:F:774:GLU:HB3	1.98	0.45
1:E:700:ASP:O	1:E:731:ILE:HG23	2.16	0.45
1:B:736:ILE:O	1:B:759:PRO:HA	2.16	0.45
1:E:658:PHE:O	1:E:662:ARG:HG2	2.16	0.45
1:E:715:PRO:HB3	1:E:739:GLU:HB2	1.99	0.45
1:F:618:VAL:HB	1:F:619:PRO:HD2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:654:ILE:O	1:B:656:PRO:HD3	2.16	0.45
1:F:751:VAL:HG23	1:F:752:ILE:N	2.32	0.45
1:C:615:THR:CG2	1:C:688:LEU:HD23	2.32	0.45
1:C:608:GLY:N	1:C:721:GLU:OE1	2.49	0.45
1:D:760:VAL:HB	1:D:765:GLU:HG3	1.99	0.45
1:E:651:LYS:NZ	1:E:776:SER:HB3	2.31	0.45
1:F:621:LYS:HB3	1:F:623:LYS:NZ	2.32	0.44
1:C:678:PRO:HB2	1:C:706:GLU:HG3	1.98	0.44
1:C:742:ARG:CG	1:C:742:ARG:HH11	2.31	0.44
1:F:594:ARG:HH11	1:F:662:ARG:NH2	2.13	0.44
1:C:623:LYS:HZ2	1:C:624:LEU:N	1.98	0.44
1:F:658:PHE:O	1:F:662:ARG:HB2	2.17	0.44
1:A:706:GLU:OE2	1:F:670:GLU:HA	2.18	0.44
1:B:614:GLU:OE2	1:C:710:ARG:NH1	2.50	0.44
1:F:655:ASN:ND2	1:F:655:ASN:C	2.70	0.44
1:F:655:ASN:O	1:F:658:PHE:HB3	2.18	0.44
1:A:667:HIS:HE1	3:B:18:HOH:O	2.00	0.44
1:B:748:PRO:HG2	1:B:751:VAL:HB	1.99	0.44
1:D:626:TYR:CE1	1:D:635:GLN:HB3	2.52	0.44
1:D:664:ILE:HG21	1:D:688:LEU:HD11	1.99	0.44
1:D:716:ILE:C	1:D:716:ILE:HD12	2.38	0.44
1:F:594:ARG:HD3	1:F:617:CYS:O	2.17	0.44
1:F:648:ARG:O	1:F:652:LEU:HG	2.17	0.44
1:D:762:ARG:HB3	1:D:764:GLU:OE1	2.18	0.44
1:F:618:VAL:HB	1:F:619:PRO:CD	2.48	0.44
1:F:701:VAL:HG12	1:F:733:THR:CG2	2.48	0.44
1:B:695:ASN:HD22	1:B:695:ASN:C	2.21	0.44
1:D:669:PRO:O	1:D:670:GLU:HG2	2.17	0.44
1:B:646:ARG:HH11	1:B:646:ARG:CG	2.31	0.43
1:B:716:ILE:C	1:B:716:ILE:HD12	2.39	0.43
1:C:710:ARG:HE	1:C:712:GLN:HG3	1.83	0.43
1:E:719:LEU:HD12	1:E:743:ASP:HB2	2.00	0.43
1:E:733:THR:HG23	1:E:758:HIS:HD2	1.83	0.43
1:E:760:VAL:HG21	1:E:766:VAL:HG22	1.99	0.43
1:B:634:MET:HB2	1:B:676:ASP:HA	2.00	0.43
1:B:625:THR:C	1:B:626:TYR:CD2	2.92	0.43
1:B:773:ASN:N	1:B:773:ASN:HD22	2.16	0.43
1:D:751:VAL:O	1:D:754:ASP:HB3	2.18	0.43
1:C:624:LEU:HD13	1:C:642:LEU:HD22	2.01	0.43
1:D:739:GLU:HG3	1:D:739:GLU:O	2.19	0.43
1:E:626:TYR:HE1	1:E:635:GLN:HE21	1.64	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:610:LEU:CD1	1:D:729:GLY:HA3	2.48	0.43
1:D:744:LEU:HD12	1:D:744:LEU:N	2.33	0.43
1:B:737:PRO:CD	1:B:740:ASN:HD22	2.32	0.43
1:C:602:ALA:O	1:C:608:GLY:HA2	2.18	0.43
1:A:762:ARG:HB3	1:A:764:GLU:OE2	2.19	0.43
1:C:599:THR:HG23	1:C:701:VAL:O	2.18	0.43
1:A:627:THR:OG1	1:A:667:HIS:HD2	2.02	0.43
1:C:632:GLU:O	1:C:636:GLU:HG3	2.18	0.43
1:B:773:ASN:N	1:B:773:ASN:ND2	2.67	0.42
1:F:648:ARG:HH12	1:F:764:GLU:CD	2.22	0.42
1:A:613:ILE:N	1:A:613:ILE:HD12	2.34	0.42
1:E:626:TYR:CB	1:E:666:VAL:HG13	2.45	0.42
1:A:640:ALA:O	1:A:644:VAL:HG23	2.18	0.42
1:C:625:THR:O	1:C:665:HIS:HA	2.19	0.42
1:C:704:THR:HG22	1:C:716:ILE:HG12	2.02	0.42
1:B:631:GLY:HA3	1:B:676:ASP:CG	2.40	0.42
1:C:602:ALA:HB1	3:C:102:HOH:O	2.19	0.42
1:D:673:THR:HA	1:D:674:PRO:HD3	1.86	0.42
1:E:762:ARG:HB3	1:E:764:GLU:OE1	2.20	0.42
1:A:632:GLU:O	1:A:636:GLU:HG3	2.20	0.42
1:D:594:ARG:HG2	1:D:594:ARG:HH11	1.84	0.42
1:E:609:ASP:HB2	1:E:610:LEU:H	1.62	0.42
1:B:712:GLN:OE1	1:B:762:ARG:HD2	2.19	0.42
1:B:765:GLU:O	1:B:768:THR:HG23	2.20	0.42
1:E:750:ASN:CG	1:E:751:VAL:H	2.23	0.42
1:A:622:GLY:HA2	1:A:662:ARG:O	2.20	0.42
1:A:627:THR:OG1	1:A:665:HIS:HE1	2.03	0.42
1:A:696:PRO:HD2	1:A:773:ASN:HD22	1.85	0.42
1:A:626:TYR:HA	1:A:666:VAL:O	2.20	0.41
1:A:744:LEU:HA	1:A:747:ILE:HD12	2.01	0.41
1:B:750:ASN:OD1	1:B:751:VAL:N	2.53	0.41
1:B:704:THR:O	1:B:737:PRO:HD3	2.21	0.41
1:E:704:THR:O	1:E:737:PRO:HD3	2.20	0.41
1:B:716:ILE:HG13	1:B:737:PRO:HG2	2.01	0.41
1:B:716:ILE:N	1:B:740:ASN:HD21	1.88	0.41
1:E:750:ASN:CG	1:E:751:VAL:N	2.73	0.41
1:F:698:ARG:HG2	1:F:772:GLN:HE22	1.86	0.41
1:B:604:THR:CG2	1:B:611:LEU:HD21	2.50	0.41
1:C:605:GLU:HB2	1:C:674:PRO:CD	2.48	0.41
1:F:744:LEU:HA	1:F:747:ILE:HG12	2.03	0.41
1:B:700:ASP:HB3	1:B:732:LYS:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:657:ASP:N	1:C:657:ASP:OD2	2.54	0.41
1:D:597:GLN:OE1	1:D:614:GLU:HG2	2.21	0.41
1:D:595:VAL:HG12	1:D:696:PRO:HA	2.02	0.41
1:B:597:GLN:OE1	1:C:710:ARG:HB3	2.21	0.41
1:B:746:GLU:N	1:B:746:GLU:OE2	2.54	0.41
1:D:694:GLY:O	1:D:696:PRO:HD3	2.20	0.41
1:E:680:ALA:O	1:E:684:MET:HG2	2.20	0.41
1:F:695:ASN:HD22	1:F:696:PRO:CD	2.31	0.41
1:E:659:TYR:CD1	1:E:659:TYR:C	2.93	0.41
1:E:667:HIS:O	1:E:669:PRO:HD3	2.20	0.41
1:D:614:GLU:OE2	1:E:710:ARG:HG2	2.21	0.41
1:B:612:THR:HG23	1:B:612:THR:O	2.20	0.41
1:E:618:VAL:HB	1:E:619:PRO:HD2	2.02	0.41
1:F:595:VAL:HG22	1:F:595:VAL:O	2.20	0.41
1:F:748:PRO:HB2	1:F:751:VAL:HG22	2.01	0.41
1:C:667:HIS:O	1:C:669:PRO:HD3	2.21	0.40
1:D:625:THR:O	1:D:665:HIS:HA	2.20	0.40
1:A:695:ASN:OD1	1:A:773:ASN:HB2	2.22	0.40
1:B:599:THR:HG23	1:B:610:LEU:HD13	2.03	0.40
1:B:700:ASP:CB	1:B:732:LYS:HD3	2.51	0.40
1:C:605:GLU:HB2	1:C:674:PRO:HB2	2.03	0.40
1:F:601:LEU:HD13	1:F:722:LYS:O	2.21	0.40
1:F:594:ARG:CD	1:F:662:ARG:HH21	2.34	0.40
1:F:716:ILE:O	1:F:716:ILE:HD12	2.21	0.40
1:B:762:ARG:HB3	1:B:762:ARG:HE	1.73	0.40
1:E:601:LEU:HD13	1:E:722:LYS:O	2.22	0.40
1:A:621:LYS:HD2	1:B:660:GLU:OE1	2.21	0.40
1:B:604:THR:HG21	1:B:611:LEU:HD21	2.03	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	180/200 (90%)	169 (94%)	7 (4%)	4 (2%)	8	3
1	B	180/200 (90%)	162 (90%)	14 (8%)	4 (2%)	8	3
1	C	180/200 (90%)	170 (94%)	9 (5%)	1 (1%)	28	24
1	D	180/200 (90%)	166 (92%)	11 (6%)	3 (2%)	11	5
1	E	189/200 (94%)	173 (92%)	12 (6%)	4 (2%)	8	3
1	F	180/200 (90%)	169 (94%)	9 (5%)	2 (1%)	17	11
All	All	1089/1200 (91%)	1009 (93%)	62 (6%)	18 (2%)	11	5

All (18) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	670	GLU
1	C	670	GLU
1	D	670	GLU
1	E	670	GLU
1	A	670	GLU
1	B	609	ASP
1	E	777	GLY
1	A	669	PRO
1	F	669	PRO
1	A	595	VAL
1	B	753	ALA
1	E	608	GLY
1	F	607	GLY
1	A	774	GLU
1	D	669	PRO
1	E	606	VAL
1	B	656	PRO
1	D	729	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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	145/160 (91%)	135 (93%)	10 (7%)	18	14
1	B	145/160 (91%)	135 (93%)	10 (7%)	18	14
1	C	145/160 (91%)	137 (94%)	8 (6%)	25	22
1	D	146/160 (91%)	139 (95%)	7 (5%)	30	27
1	E	153/160 (96%)	142 (93%)	11 (7%)	17	13
1	F	146/160 (91%)	129 (88%)	17 (12%)	6	3
All	All	880/960 (92%)	817 (93%)	63 (7%)	17	13

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	632	GLU
1	A	645	VAL
1	A	646	ARG
1	A	652	LEU
1	A	655	ASN
1	A	665	HIS
1	A	695	ASN
1	A	750	ASN
1	A	755	LEU
1	A	764	GLU
1	B	597	GLN
1	B	624	LEU
1	B	646	ARG
1	B	692	LEU
1	B	695	ASN
1	B	712	GLN
1	B	724	LEU
1	B	742	ARG
1	B	745	GLU
1	B	768	THR
1	C	599	THR
1	C	632	GLU
1	C	665	HIS
1	C	695	ASN
1	C	719	LEU
1	C	739	GLU
1	C	742	ARG

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Mol	Chain	Res	Type
1	C	766	VAL
1	D	595	VAL
1	D	601	LEU
1	D	625	THR
1	D	642	LEU
1	D	669	PRO
1	D	723	LEU
1	D	728	ARG
1	E	594	ARG
1	E	609	ASP
1	E	624	LEU
1	E	665	HIS
1	E	666	VAL
1	E	669	PRO
1	E	670	GLU
1	E	709	LEU
1	E	716	ILE
1	E	719	LEU
1	E	742	ARG
1	F	595	VAL
1	F	598	VAL
1	F	632	GLU
1	F	655	ASN
1	F	661	LYS
1	F	665	HIS
1	F	669	PRO
1	F	670	GLU
1	F	688	LEU
1	F	695	ASN
1	F	709	LEU
1	F	719	LEU
1	F	733	THR
1	F	739	GLU
1	F	743	ASP
1	F	749	ASP
1	F	764	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (35) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	655	ASN
1	A	665	HIS

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Mol	Chain	Res	Type
1	A	667	HIS
1	A	695	ASN
1	A	750	ASN
1	A	758	HIS
1	A	773	ASN
1	B	597	GLN
1	B	655	ASN
1	B	665	HIS
1	B	695	ASN
1	B	740	ASN
1	B	758	HIS
1	B	773	ASN
1	C	635	GLN
1	C	655	ASN
1	C	665	HIS
1	C	695	ASN
1	C	712	GLN
1	D	635	GLN
1	D	655	ASN
1	D	712	GLN
1	D	727	HIS
1	D	773	ASN
1	E	655	ASN
1	E	665	HIS
1	E	758	HIS
1	E	772	GLN
1	E	773	ASN
1	F	655	ASN
1	F	665	HIS
1	F	667	HIS
1	F	695	ASN
1	F	772	GLN
1	F	773	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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



## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	B	1201	-	4,4,4	0.30	0	6,6,6	0.07	0
2	SO4	C	1301	-	4,4,4	0.35	0	6,6,6	0.13	0
2	SO4	D	1401	-	4,4,4	0.27	0	6,6,6	0.16	0
2	SO4	E	1501	-	4,4,4	0.35	0	6,6,6	0.15	0
2	SO4	F	1601	-	4,4,4	0.33	0	6,6,6	0.16	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	B	1201	-	-	0/0/0/0	0/0/0/0
2	SO4	C	1301	-	-	0/0/0/0	0/0/0/0
2	SO4	D	1401	-	-	0/0/0/0	0/0/0/0
2	SO4	E	1501	-	-	0/0/0/0	0/0/0/0
2	SO4	F	1601	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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	182/200 (91%)	0.33	9 (4%) 30 37	20, 37, 57, 77	0
1	B	182/200 (91%)	0.64	10 (5%) 26 32	27, 46, 70, 84	1 (0%)
1	C	182/200 (91%)	0.52	11 (6%) 23 28	26, 41, 69, 78	0
1	D	182/200 (91%)	0.80	18 (9%) 8 10	33, 49, 73, 85	0
1	E	191/200 (95%)	0.84	23 (12%) 5 6	32, 53, 79, 91	0
1	F	182/200 (91%)	0.63	10 (5%) 26 32	29, 45, 63, 72	0
All	All	1101/1200 (91%)	0.63	81 (7%) 15 20	20, 45, 71, 91	1 (0%)

All (81) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	607	GLY	9.0
1	D	606	VAL	6.2
1	B	607	GLY	5.7
1	F	607	GLY	5.2
1	D	659	TYR	4.7
1	D	607	GLY	4.6
1	F	593	ASN	4.5
1	C	595	VAL	4.4
1	A	595	VAL	4.1
1	C	606	VAL	4.1
1	E	658	PHE	3.8
1	D	682	ILE	3.8
1	E	608	GLY	3.7
1	E	606	VAL	3.7
1	B	606	VAL	3.6
1	C	657	ASP	3.5
1	B	774	GLU	3.4
1	B	750	ASN	3.4
1	E	752	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	742	ARG	3.3
1	E	601	LEU	3.3
1	E	748	PRO	3.3
1	C	685	CYS	3.2
1	A	594	ARG	3.2
1	B	728	ARG	3.1
1	A	685	CYS	3.1
1	F	704	THR	3.1
1	D	683	ALA	3.1
1	F	651	LYS	3.1
1	E	738	PHE	3.1
1	D	594	ARG	3.0
1	E	704	THR	3.0
1	C	607	GLY	3.0
1	D	685	CYS	2.9
1	D	608	GLY	2.9
1	E	655	ASN	2.8
1	E	749	ASP	2.8
1	D	686	THR	2.8
1	D	746	GLU	2.8
1	E	734	VAL	2.7
1	A	699	ALA	2.7
1	E	778	MET	2.7
1	B	621	LYS	2.7
1	F	606	VAL	2.6
1	D	654	ILE	2.6
1	A	734	VAL	2.6
1	E	723	LEU	2.6
1	F	653	GLY	2.6
1	A	735	LEU	2.5
1	F	735	LEU	2.4
1	E	750	ASN	2.4
1	E	746	GLU	2.4
1	E	683	ALA	2.4
1	F	594	ARG	2.4
1	E	621	LYS	2.3
1	F	682	ILE	2.3
1	E	736	ILE	2.3
1	B	609	ASP	2.3
1	C	703	MET	2.2
1	E	657	ASP	2.2
1	C	734	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	773	ASN	2.2
1	C	775	PRO	2.2
1	A	728	ARG	2.2
1	D	774	GLU	2.2
1	A	774	GLU	2.2
1	D	605	GLU	2.2
1	B	704	THR	2.2
1	D	610	LEU	2.1
1	E	724	LEU	2.1
1	D	681	GLY	2.1
1	F	766	VAL	2.1
1	B	723	LEU	2.1
1	E	728	ARG	2.1
1	D	734	VAL	2.1
1	E	703	MET	2.1
1	C	702	ALA	2.1
1	D	735	LEU	2.0
1	C	686	THR	2.0
1	D	728	ARG	2.0
1	C	601	LEU	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
2	SO4	D	1401	5/5	0.98	0.16	0.86	52,52,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	SO4	E	1501	5/5	0.94	0.13	0.00	69,70,71,71	0
2	SO4	F	1601	5/5	0.96	0.13	-0.20	70,70,72,73	0
2	SO4	C	1301	5/5	0.95	0.11	-0.43	56,58,59,60	0
2	SO4	B	1201	5/5	0.99	0.11	-0.71	52,52,54,54	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.