



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:31 AM UTC

PDB ID : 1RR9 / pdb_00001rr9
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 : 2003-12-08
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

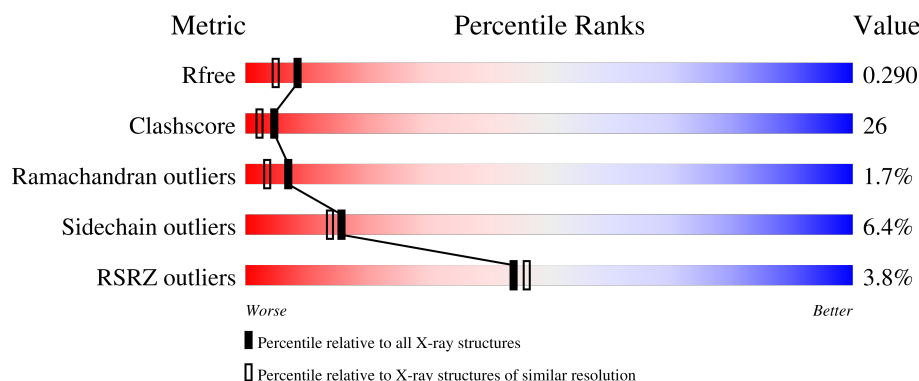
1 Overall quality at a glance

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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	2% 55% 32% • 9%
1	B	200	4% 51% 36% • 9%
1	C	200	3% 58% 30% • 9%
1	D	200	4% 52% 34% • • 9%
1	E	200	6% 52% 37% 6% •

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Mol	Chain	Length	Quality of chain
1	F	200	2% 49% 36% • • 9%

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.

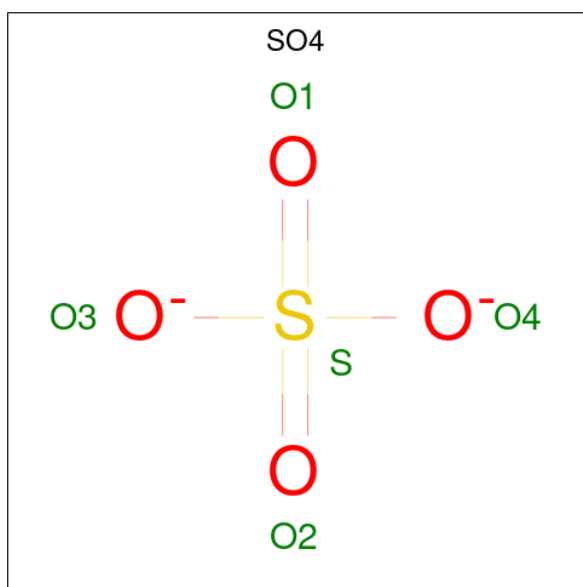
- Molecule 1 is a protein called ATP-dependent protease La.

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 mutation	UNP P0A9M0
B	679	ALA	SER	engineered mutation	UNP P0A9M0
C	679	ALA	SER	engineered mutation	UNP P0A9M0
D	679	ALA	SER	engineered mutation	UNP P0A9M0
E	679	ALA	SER	engineered mutation	UNP P0A9M0
F	679	ALA	SER	engineered mutation	UNP P0A9M0

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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		

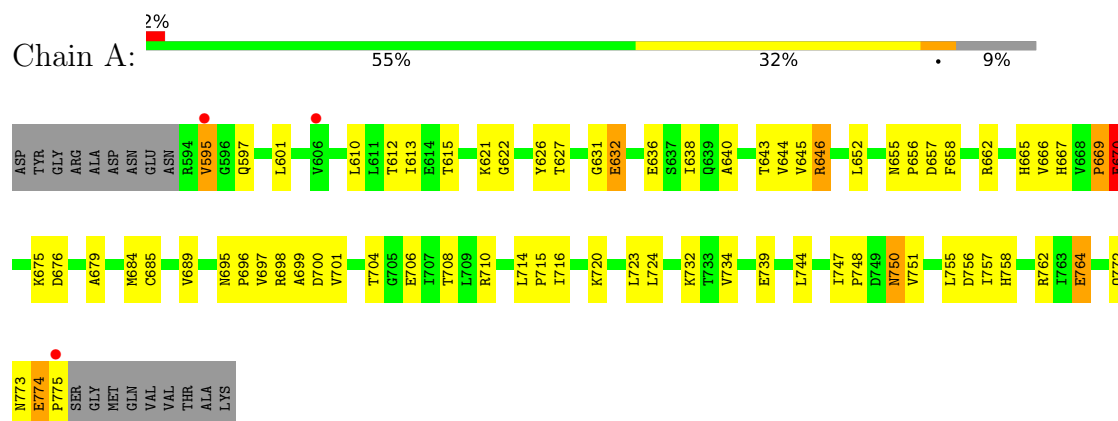
- Molecule 3 is water.

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		

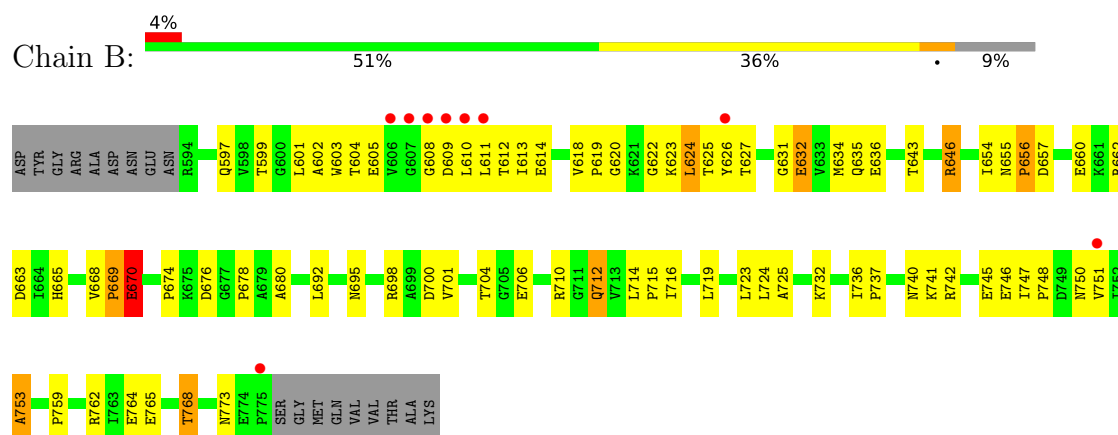
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

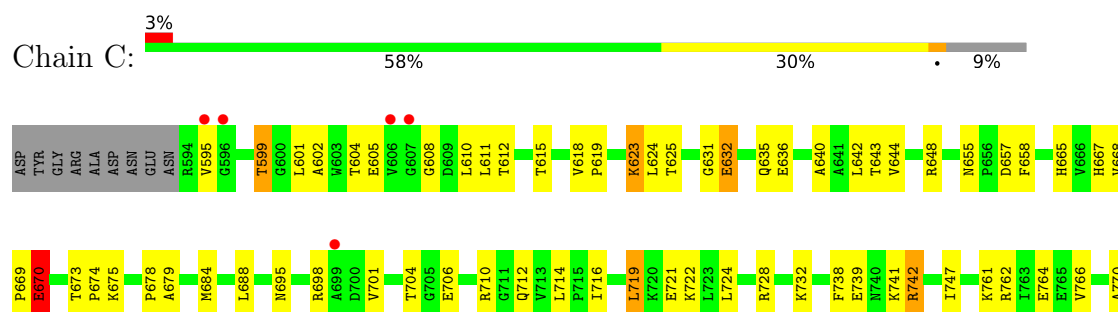
• Molecule 1: ATP-dependent protease La

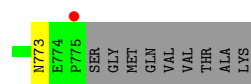


• Molecule 1: ATP-dependent protease La

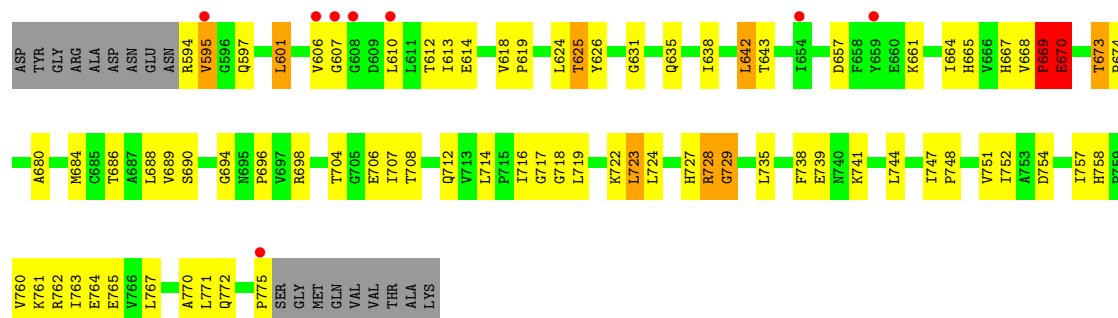


• Molecule 1: ATP-dependent protease La

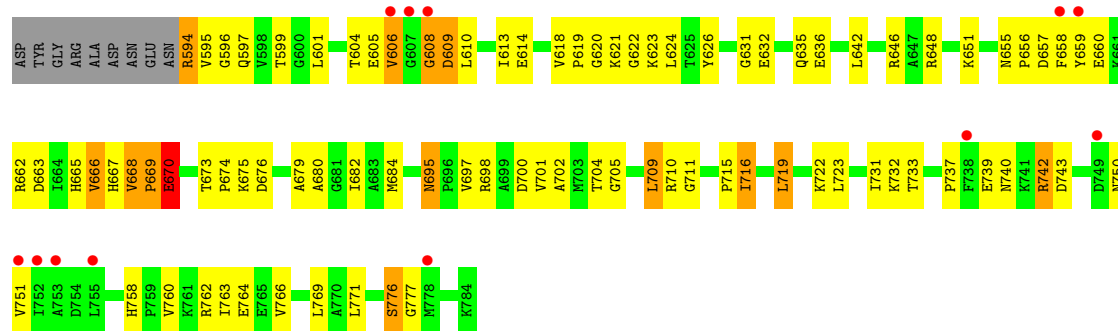




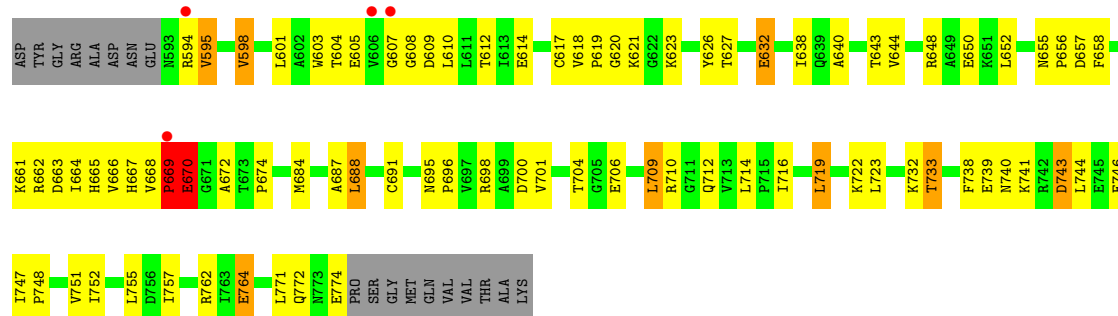
• Molecule 1: ATP-dependent protease La



• 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, α , β , γ	86.21Å 86.21Å 122.68Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.10 20.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	98.0 (20.00-2.10) 88.4 (20.00-2.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	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	1158 reflections (1.99%)	wwPDB-VP
Wilson B-factor (Å ²)	32.4	Xtriage
Anisotropy	0.597	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	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 ²)	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.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.51	0/1373	0.98	4/1866 (0.2%)
1	B	0.46	0/1373	0.93	1/1866 (0.1%)
1	C	0.47	0/1373	0.97	4/1866 (0.2%)
1	D	0.44	0/1380	0.92	6/1875 (0.3%)
1	E	0.42	0/1442	0.98	7/1958 (0.4%)
1	F	0.48	0/1380	0.97	5/1874 (0.3%)
All	All	0.46	0/8321	0.96	27/11305 (0.2%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	670	GLU	N-CA-C	-8.89	91.86	110.80
1	A	670	GLU	N-CA-C	-8.22	93.29	110.80
1	E	670	GLU	N-CA-C	-8.09	93.56	110.80
1	F	668	VAL	CA-C-N	7.62	129.36	119.84
1	F	668	VAL	C-N-CA	7.62	129.36	119.84
1	A	638	ILE	N-CA-C	-7.18	103.78	110.53
1	F	670	GLU	N-CA-C	-7.07	95.75	110.80
1	C	670	GLU	N-CA-C	-7.01	95.87	110.80
1	E	679	ALA	N-CA-C	6.55	120.85	112.34
1	A	757	ILE	N-CA-C	6.34	117.71	108.58
1	C	668	VAL	CA-C-N	5.99	127.32	119.84
1	C	668	VAL	C-N-CA	5.99	127.32	119.84
1	D	670	GLU	N-CA-C	-5.99	98.05	110.80
1	D	668	VAL	CA-C-N	5.89	127.20	119.84
1	D	668	VAL	C-N-CA	5.89	127.20	119.84
1	E	668	VAL	CA-C-N	5.81	127.10	119.84
1	E	668	VAL	C-N-CA	5.81	127.10	119.84
1	E	776	SER	N-CA-C	5.61	117.66	108.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	679	ALA	N-CA-C	5.51	119.11	112.38
1	E	695	ASN	CA-C-N	5.48	125.48	119.89
1	E	695	ASN	C-N-CA	5.48	125.48	119.89
1	D	757	ILE	N-CA-C	5.40	115.97	108.84
1	F	755	LEU	N-CA-C	5.35	118.78	110.17
1	A	646	ARG	N-CA-C	-5.12	105.61	111.14
1	D	673	THR	CA-C-N	5.09	124.85	119.76
1	D	673	THR	C-N-CA	5.09	124.85	119.76
1	F	632	GLU	N-CA-C	5.04	116.77	111.28

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	76	0
1	B	1353	0	1392	85	0
1	C	1353	0	1392	67	0
1	D	1360	0	1404	63	0
1	E	1422	0	1472	78	0
1	F	1361	0	1403	78	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	6	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	428	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 26.

All (428) 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:C:623:LYS:HZ2	1:C:624:LEU:H	1.07	1.00
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: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
1:F:743:ASP:O	1:F:746:GLU:HG2	1.82	0.79
1:A:646:ARG:HG2	1:F:618:VAL:HG21	1.65	0.79
1:B:669:PRO:O	1:B:670:GLU:HB2	1.83	0.79
1:E:742:ARG:NH1	1:E:742:ARG:HB3	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:HD13	1:E:716:ILE:H	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:695:ASN:CG	1:A:773:ASN:HB2	2.20	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
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:C:623:LYS:HZ2	1:C:624:LEU:N	1.87	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:B:700:ASP:CG	1:B:732:LYS:HD3	2.24	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:742:ARG:H	1:C:742:ARG:HD2	1.63	0.62
1:C:742:ARG:HH11	1:C:742:ARG:N	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:719:LEU:HD12	1:F:743:ASP:HB3	1.81	0.62
1:F:738:PHE:O	1:F:741:LYS:HG3	1.98	0.62
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:N	1:A:714:LEU:HD22	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
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:614:GLU:OE2	1:C:710:ARG:HG2	2.02	0.58
1:B:706:GLU:HB3	1:B:714:LEU:HB2	1.85	0.58
1:A:695:ASN:HD22	1:A:696:PRO:HD2	1.67	0.58
1:B:624:LEU:HD22	1:B:624:LEU:H	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:HA3	1:B:676:ASP:OD2	2.04	0.58
1:B:631:GLY:O	1:B:635:GLN:HG3	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:594:ARG:HH11	1:F:662:ARG:HH21	1.52	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: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:A:696:PRO:HG2	1:A:772:GLN:CG	2.34	0.56
1:C:742:ARG:NH1	1:C:742:ARG:HG3	2.20	0.56
1:A:655:ASN:HD22	1:A:656:PRO:N	2.04	0.56
1:A:708:THR:HG23	1:A:714:LEU:HD21	1.88	0.56
1:D:638:ILE:CG1	1:D:684:MET:HE3	2.35	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:B:610:LEU:HD12	1:B:610:LEU:C	2.32	0.55
1:E:648:ARG:HH22	1:E:711:GLY:HA3	1.71	0.55
1:B:655:ASN:C	1:B:657:ASP:H	2.13	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:F:620:GLY:HA3	1:F:663:ASP:CG	2.33	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:F:655:ASN:C	1:F:655:ASN:HD22	2.17	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:A:610:LEU:C	1:A:610:LEU:HD23	2.34	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
1:B:623:LYS:C	1:B:624:LEU:HD13	2.35	0.52
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:C:764:GLU:CD	1:C:764:GLU:H	2.18	0.51
1:D:747:ILE:HB	1:D:752:ILE:HD11	1.91	0.51
1:E:648:ARG:HH22	1:E:710:ARG:C	2.18	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:669:PRO:O	1:D:670:GLU:HB2	2.10	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:A:708:THR:HB	1:F:614:GLU:OE2	2.12	0.50
1:B:613:ILE:N	1:B:613:ILE:HD12	2.27	0.50
1:F:650:GLU:HB2	1:F:656:PRO:HG3	1.93	0.50
1:F:762:ARG:HH11	1:F:762:ARG:HG3	1.77	0.50
1:B:632:GLU:O	1:B:636:GLU:HG3	2.12	0.50
1:C:648:ARG:HH12	1:C:764:GLU:CD	2.17	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:A:720:LYS:HZ3	1:A:748:PRO:HD3	1.74	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:E:651:LYS:HZ3	1:E:776:SER:HB3	1.77	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: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:D:716:ILE:C	1:D:716:ILE:HD12	2.38	0.49
1:F:655:ASN:ND2	1:F:655:ASN:C	2.70	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:B:695:ASN:C	1:B:695:ASN:HD22	2.21	0.48
1:B:716:ILE:C	1:B:716:ILE:HD12	2.39	0.48
1:D:624:LEU:HD22	1:D:642:LEU:HD11	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:670:GLU:OE1	1:D:670:GLU:HA	2.13	0.48
1:D:727:HIS:CG	1:D:751:VAL:HG23	2.49	0.48
1:B:625:THR:C	1:B:626:TYR:CD2	2.92	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:A:597:GLN:OE1	1:B:710:ARG:HB3	2.14	0.48
1:B:605:GLU:HG2	1:B:674:PRO:HB2	1.95	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: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:F:648:ARG:HH12	1:F:764:GLU:CD	2.22	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:HD12	1:B:723:LEU:N	2.30	0.47
1:D:689:VAL:HG13	1:D:690:SER:N	2.30	0.47
1:E:750:ASN:CG	1:E:751:VAL:H	2.23	0.47
1:A:695:ASN:HD22	1:A:696:PRO:CD	2.28	0.47
1:E:613:ILE:H	1:E:613:ILE:HD12	1.80	0.47
1:E:737:PRO:HB2	1:E:740:ASN:OD1	2.15	0.47
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:HG3	1:D:728:ARG:NH1	2.24	0.47
1:F:655:ASN:HD22	1:F:656:PRO:CD	2.27	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:B:631:GLY:HA3	1:B:676:ASP:CG	2.40	0.46
1:A:723:LEU:CD2	1:A:734:VAL:HG11	2.46	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:750:ASN:CG	1:E:751:VAL:N	2.73	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:D:667:HIS:HB3	1:E:709:LEU:HD22	1.98	0.46
1:E:606:VAL:O	1:E:606:VAL:HG22	2.16	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:E:659:TYR:CD1	1:E:659:TYR:C	2.93	0.45
1:D:762:ARG:O	1:D:765:GLU:HG2	2.16	0.45
1:E:626:TYR:HA	1:E:666:VAL:O	2.16	0.45
1:E:660:GLU:HA	1:E:660:GLU:OE1	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: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:A:684:MET:HE3	3:A:218:HOH:O	2.15	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
1:B:654:ILE:O	1:B:656:PRO:HD3	2.16	0.45
1:C:615:THR:CG2	1:C:688:LEU:HD23	2.32	0.45
1:E:620:GLY:HA3	1:E:663:ASP:CG	2.42	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: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:HH11	1:C:742:ARG:CG	2.31	0.44
1:A:670:GLU:O	1:A:675:LYS:NZ	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:594:ARG:HH11	1:F:662:ARG:NH2	2.13	0.44
1:A:706:GLU:OE2	1:F:670:GLU:HA	2.18	0.44
1:F:658:PHE:O	1:F:662:ARG:HB2	2.17	0.44
1:B:614:GLU:OE2	1:C:710:ARG:NH1	2.50	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: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:E:651:LYS:NZ	1:E:776:SER:HB3	2.31	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:D:669:PRO:O	1:D:670:GLU:HG2	2.17	0.44
1:F:751:VAL:HG23	1:F:752:ILE:N	2.32	0.44
1:B:646:ARG:HH11	1:B:646:ARG:CG	2.31	0.43
1:C:710:ARG:HE	1:C:712:GLN:HG3	1.83	0.43
1:E:697:VAL:O	1:E:698:ARG:C	2.60	0.43
1:F:638:ILE:HG12	1:F:684:MET:HE2	2.00	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: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:O	1:D:739:GLU:HG3	2.19	0.43
1:E:626:TYR:HE1	1:E:635:GLN:HE21	1.64	0.43
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:D:638:ILE:HG12	1:D:684:MET:HE3	2.00	0.43
1:A:699:ALA:O	1:A:700:ASP:CG	2.61	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:613:ILE:HD12	1:A:613:ILE:N	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:A:696:PRO:HG2	1:A:772:GLN:CD	2.44	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:C:655:ASN:ND2	1:C:655:ASN:C	2.77	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: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:A:655:ASN:HD22	1:A:655:ASN:C	2.26	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: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
1:D:595:VAL:HG12	1:D:696:PRO:HA	2.02	0.41
1:D:597:GLN:OE1	1:D:614:GLU:HG2	2.21	0.41
1:B:597:GLN:OE1	1:C:710:ARG:HB3	2.21	0.41
1:B:746:GLU:OE2	1:B:746:GLU:N	2.54	0.41
1:D:694:GLY:O	1:D:696:PRO:HD3	2.20	0.41
1:E:631:GLY:HA3	1:E:676:ASP:CG	2.45	0.41
1:E:680:ALA:O	1:E:684:MET:HG2	2.20	0.41
1:D:614:GLU:OE2	1:E:710:ARG:HG2	2.21	0.41
1:E:667:HIS:O	1:E:669:PRO:HD3	2.20	0.41
1:F:695:ASN:HD22	1:F:696:PRO:CD	2.31	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:O	1:F:595:VAL:HG22	2.20	0.41
1:F:658:PHE:CD1	1:F:658:PHE:C	2.99	0.41
1:F:748:PRO:HB2	1:F:751:VAL:HG22	2.01	0.41
1:A:631:GLY:HA3	1:A:676:ASP:CG	2.46	0.40
1:A:655:ASN:ND2	1:A:655:ASN:C	2.76	0.40
1:C:667:HIS:O	1:C:669:PRO:HD3	2.21	0.40
1:C:716:ILE:HD12	1:C:716:ILE:C	2.46	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:594:ARG:CD	1:F:662:ARG:HH21	2.34	0.40
1:F:601:LEU:HD13	1:F:722:LYS:O	2.21	0.40
1:F:716:ILE:O	1:F:716:ILE:HD12	2.21	0.40
1:B:762:ARG:HE	1:B:762:ARG:HB3	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%)	5 2
1	B	180/200 (90%)	162 (90%)	14 (8%)	4 (2%)	5 2
1	C	180/200 (90%)	170 (94%)	9 (5%)	1 (1%)	21 18
1	D	180/200 (90%)	166 (92%)	11 (6%)	3 (2%)	7 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	189/200 (94%)	173 (92%)	12 (6%)	4 (2%)	5	2
1	F	180/200 (90%)	169 (94%)	9 (5%)	2 (1%)	11	8
All	All	1089/1200 (91%)	1009 (93%)	62 (6%)	18 (2%)	7	3

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.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	145/160 (91%)	139 (96%)	6 (4%)	27	29
1	B	145/160 (91%)	134 (92%)	11 (8%)	12	9
1	C	145/160 (91%)	136 (94%)	9 (6%)	16	14
1	D	146/160 (91%)	139 (95%)	7 (5%)	23	23

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	153/160 (96%)	143 (94%)	10 (6%)	15	13
1	F	146/160 (91%)	133 (91%)	13 (9%)	9	6
All	All	880/960 (92%)	824 (94%)	56 (6%)	16	14

All (56) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	632	GLU
1	A	645	VAL
1	A	652	LEU
1	A	750	ASN
1	A	755	LEU
1	A	764	GLU
1	B	624	LEU
1	B	632	GLU
1	B	646	ARG
1	B	668	VAL
1	B	669	PRO
1	B	692	LEU
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	623	LYS
1	C	632	GLU
1	C	657	ASP
1	C	719	LEU
1	C	732	LYS
1	C	739	GLU
1	C	742	ARG
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

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Mol	Chain	Res	Type
1	E	609	ASP
1	E	624	LEU
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	661	LYS
1	F	669	PRO
1	F	670	GLU
1	F	688	LEU
1	F	709	LEU
1	F	719	LEU
1	F	733	THR
1	F	739	GLU
1	F	743	ASP
1	F	764	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

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

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Mol	Chain	Res	Type
1	C	665	HIS
1	C	695	ASN
1	C	712	GLN
1	C	750	ASN
1	C	772	GLN
1	C	773	ASN
1	D	635	GLN
1	D	639	GLN
1	D	712	GLN
1	D	727	HIS
1	D	758	HIS
1	D	773	ASN
1	E	655	ASN
1	E	665	HIS
1	E	695	ASN
1	E	758	HIS
1	E	772	GLN
1	E	773	ASN
1	F	597	GLN
1	F	635	GLN
1	F	639	GLN
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 ⓘ

There are no oligosaccharides 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	F	1601	-	4,4,4	0.36	0	6,6,6	0.18	0
2	SO4	C	1301	-	4,4,4	0.38	0	6,6,6	0.14	0
2	SO4	B	1201	-	4,4,4	0.34	0	6,6,6	0.10	0
2	SO4	E	1501	-	4,4,4	0.38	0	6,6,6	0.18	0
2	SO4	D	1401	-	4,4,4	0.31	0	6,6,6	0.18	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	182/200 (91%)	0.14	3 (1%) 70 73	20, 37, 57, 77	0
1	B	182/200 (91%)	0.50	9 (4%) 35 37	27, 46, 70, 84	1 (0%)
1	C	182/200 (91%)	0.36	6 (3%) 49 51	26, 41, 69, 78	0
1	D	182/200 (91%)	0.57	8 (4%) 39 41	33, 49, 73, 85	0
1	E	191/200 (95%)	0.73	12 (6%) 26 27	31, 53, 79, 91	0
1	F	182/200 (91%)	0.47	4 (2%) 62 65	29, 45, 63, 72	0
All	All	1101/1200 (91%)	0.46	42 (3%) 44 46	20, 45, 71, 91	1 (0%)

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	607	GLY	4.3
1	E	658	PHE	3.8
1	F	606	VAL	3.7
1	E	606	VAL	3.7
1	B	607	GLY	3.6
1	E	752	ILE	3.5
1	F	607	GLY	3.4
1	C	595	VAL	3.4
1	E	608	GLY	3.3
1	C	606	VAL	3.1
1	D	608	GLY	3.1
1	B	626	TYR	2.9
1	E	753	ALA	2.9
1	B	610	LEU	2.8
1	C	607	GLY	2.7
1	E	751	VAL	2.6
1	B	606	VAL	2.6
1	C	699	ALA	2.6
1	A	606	VAL	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	659	TYR	2.5
1	D	659	TYR	2.5
1	E	738	PHE	2.5
1	A	775	PRO	2.5
1	B	775	PRO	2.4
1	B	608	GLY	2.4
1	B	609	ASP	2.4
1	B	751	VAL	2.4
1	D	606	VAL	2.4
1	A	595	VAL	2.3
1	B	611	LEU	2.3
1	D	607	GLY	2.3
1	D	775	PRO	2.2
1	D	610	LEU	2.2
1	E	755	LEU	2.2
1	D	595	VAL	2.2
1	F	594	ARG	2.1
1	E	778	MET	2.1
1	F	669	PRO	2.1
1	D	654	ILE	2.1
1	C	775	PRO	2.1
1	E	749	ASP	2.0
1	C	596	GLY	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 oligosaccharides 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. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	E	1501	5/5	0.83	0.12	69,70,71,71	0
2	SO4	F	1601	5/5	0.86	0.12	70,70,72,73	0
2	SO4	C	1301	5/5	0.92	0.09	56,58,59,60	0
2	SO4	D	1401	5/5	0.95	0.10	52,52,55,55	0
2	SO4	B	1201	5/5	0.96	0.08	52,52,54,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.