



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 11:11 PM UTC

PDB ID : 2QZA / pdb_00002qza
Title : Crystal structure of Salmonella effector protein SopA
Authors : Diao, J.; Chen, J.
Deposited on : 2007-08-16
Resolution : 2.80 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

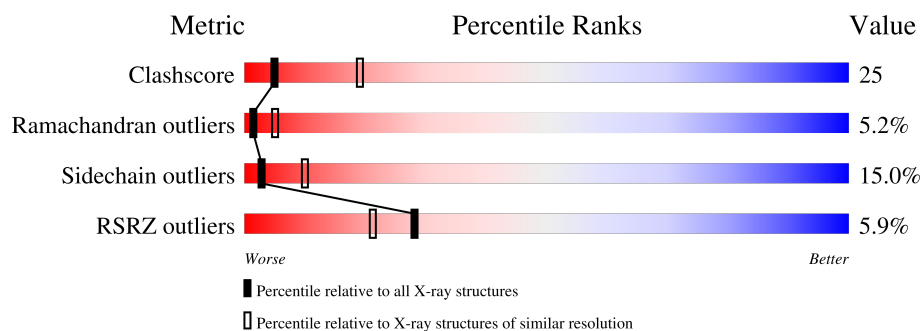
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	618	3% 55% 36% 8%
1	B	618	9% 50% 38% 10% ..

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9441 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 Secreted effector protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	617	Total	C	N	O	S	Se	0	0	0
			4747	3011	804	912	8	12			
1	B	612	Total	C	N	O	S	Se	0	0	0
			4599	2913	784	882	8	12			

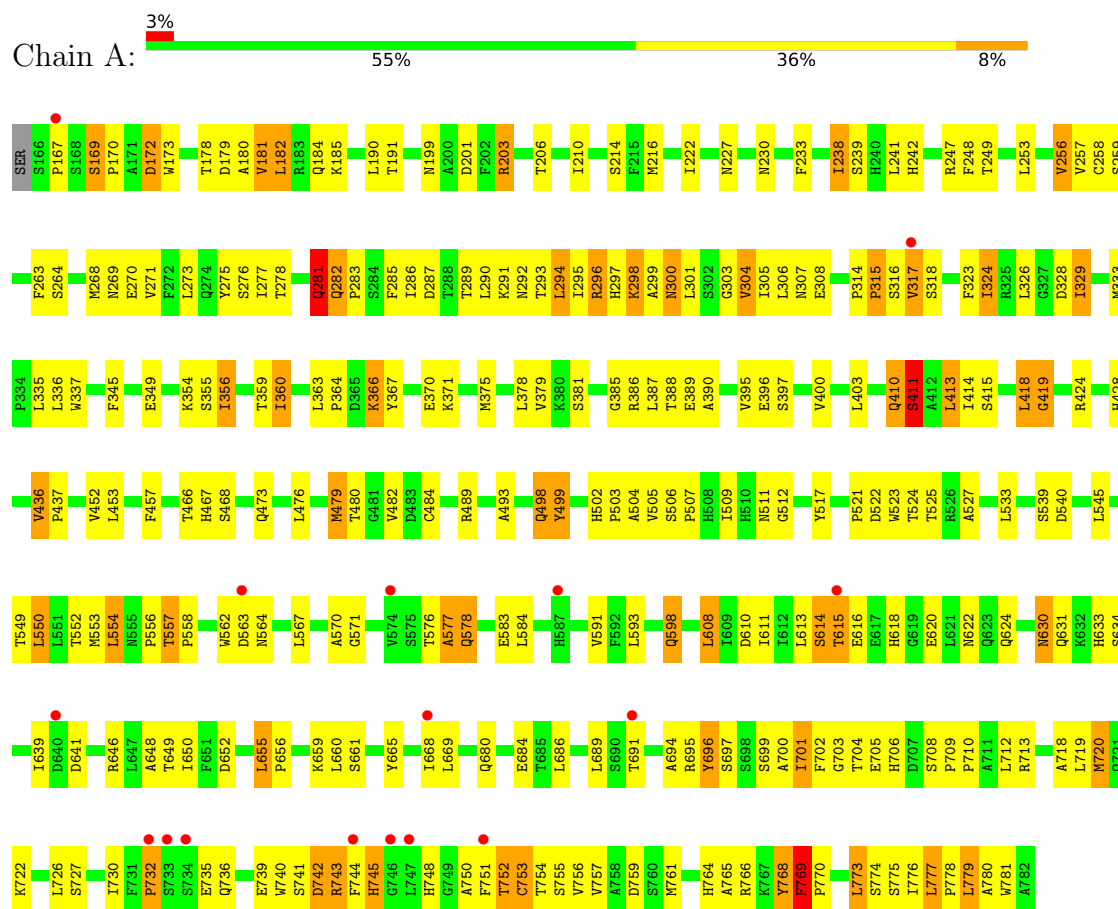
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	48	Total	O	0	0
			48	48		
2	B	47	Total	O	0	0
			47	47		

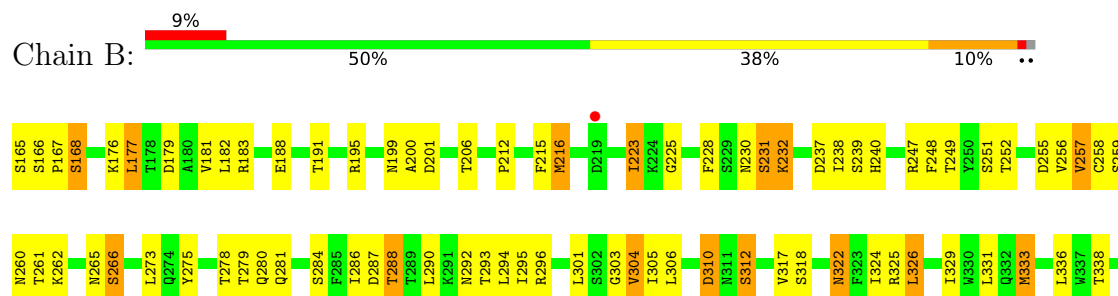
3 Residue-property plots

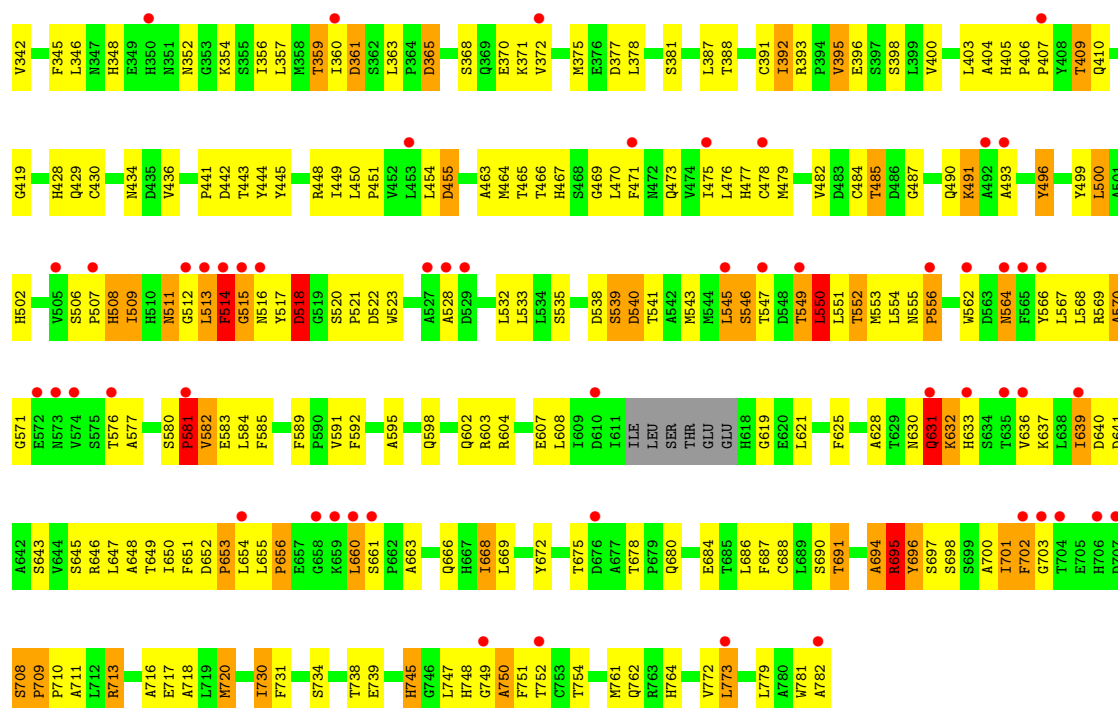
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Secreted effector protein



• Molecule 1: Secreted effector protein





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	102.73Å 68.54Å 106.61Å 90.00° 90.90° 90.00°	Depositor
Resolution (Å)	50.00 – 2.80 50.00 – 2.80	Depositor EDS
% Data completeness (in resolution range)	97.0 (50.00-2.80) 97.0 (50.00-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.270 , 0.291 0.286 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	74.3	Xtriage
Anisotropy	0.290	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 16.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.000 for l,k,-h 0.028 for h,-k,-l 0.020 for l,-k,h	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	9441	wwPDB-VP
Average B, all atoms (Å ²)	57.0	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.*

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

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	0.53	0/4859	0.79	2/6615 (0.0%)
1	B	0.52	0/4706	0.83	5/6410 (0.1%)
All	All	0.52	0/9565	0.81	7/13025 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	8
All	All	0	9

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	732	PRO	N-CA-CB	6.79	110.37	103.25
1	B	582	VAL	N-CA-C	6.56	117.35	110.72
1	B	577	ALA	N-CA-C	-5.53	106.12	112.92
1	B	654	LEU	N-CA-C	-5.49	104.16	111.24
1	A	776	ILE	N-CA-C	-5.48	107.52	112.12
1	B	589	PHE	CA-C-N	5.10	124.71	119.56
1	B	589	PHE	C-N-CA	5.10	124.71	119.56

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	630	ASN	Peptide
1	B	516	ASN	Peptide

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Mol	Chain	Res	Type	Group
1	B	518	ASP	Peptide
1	B	581	PRO	Peptide
1	B	631	GLN	Peptide
1	B	694	ALA	Peptide
1	B	748	HIS	Peptide
1	B	749	GLY	Peptide
1	B	750	ALA	Peptide

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	4747	0	4484	204	0
1	B	4599	0	4257	254	0
2	A	48	0	0	6	0
2	B	47	0	0	14	0
All	All	9441	0	8741	453	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 (453) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:296:ARG:HH11	1:A:296:ARG:HG2	1.11	1.15
1:B:471:PHE:O	1:B:475:ILE:HG12	1.57	1.04
1:A:570:ALA:N	1:A:571:GLY:HA3	1.73	1.03
1:B:580:SER:HA	1:B:581:PRO:C	1.84	1.02
1:A:315:PRO:CB	1:A:316:SER:HA	1.90	1.01
1:B:653:PRO:HB3	1:B:656:PRO:HA	1.38	1.01
1:A:315:PRO:HB2	1:A:316:SER:HA	1.02	1.00
1:B:375:MSE:HE2	1:B:403:LEU:HD21	1.45	0.98
1:A:570:ALA:H	1:A:571:GLY:HA3	1.26	0.97
1:B:259:SER:H	1:B:279:THR:HG23	1.28	0.97
1:B:708:SER:CB	1:B:709:PRO:HD3	1.95	0.97
1:A:360:ILE:HD11	1:A:375:MSE:SE	2.18	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:454:LEU:HD21	1:B:478:CYS:SG	2.09	0.93
1:A:315:PRO:HB2	1:A:316:SER:CA	1.96	0.93
1:A:410:GLN:O	1:A:410:GLN:HG2	1.66	0.92
1:B:633:HIS:HA	1:B:700:ALA:O	1.69	0.92
1:A:271:VAL:H	1:A:293:THR:HG22	1.38	0.87
1:A:296:ARG:HH11	1:A:296:ARG:CG	1.86	0.87
1:B:696:TYR:H	1:B:701:ILE:HD11	1.39	0.87
1:B:239:SER:HA	1:B:258:CYS:O	1.75	0.87
1:B:709:PRO:HB2	1:B:710:PRO:C	2.01	0.86
1:B:709:PRO:HB2	1:B:710:PRO:CA	2.05	0.86
1:B:540:ASP:O	1:B:569:ARG:HA	1.78	0.84
1:B:215:PHE:HB2	2:B:48:HOH:O	1.76	0.84
1:B:695:ARG:C	1:B:697:SER:H	1.86	0.83
1:B:496:TYR:O	1:B:500:LEU:HD23	1.79	0.83
1:A:281:GLN:O	1:A:282:GLN:HB2	1.77	0.81
1:A:769:PHE:HD1	1:A:769:PHE:C	1.88	0.81
1:B:541:THR:HA	1:B:568:LEU:O	1.81	0.81
1:B:368:SER:O	1:B:372:VAL:HG23	1.79	0.81
1:B:469:GLY:O	1:B:473:GLN:HG2	1.81	0.80
1:B:166:SER:HB2	1:B:167:PRO:HA	1.62	0.80
1:B:464:MSE:HE3	1:B:499:TYR:HD1	1.45	0.79
1:B:228:PHE:O	1:B:231:SER:HB2	1.83	0.79
1:B:363:LEU:HB2	1:B:371:LYS:HE2	1.64	0.79
1:B:646:ARG:HA	1:B:649:THR:HG22	1.64	0.79
1:A:545:LEU:HD11	1:A:550:LEU:HD23	1.64	0.78
1:B:720:MSE:HE2	1:B:731:PHE:HE1	1.47	0.78
1:A:296:ARG:HG2	1:A:296:ARG:NH1	1.92	0.78
1:A:720:MSE:HE3	1:A:761:MSE:SE	2.35	0.77
1:A:333:MSE:HE3	1:A:337:TRP:HZ2	1.50	0.77
1:B:709:PRO:HG2	1:B:713:ARG:HB2	1.65	0.77
1:B:539:SER:C	1:B:541:THR:H	1.93	0.76
1:A:757:VAL:HG12	1:A:761:MSE:HE2	1.67	0.76
1:A:631:GLN:HA	1:A:780:ALA:HB1	1.69	0.75
1:A:360:ILE:CD1	1:A:375:MSE:SE	2.85	0.74
1:A:769:PHE:O	1:A:769:PHE:CD1	2.41	0.74
1:A:769:PHE:C	1:A:769:PHE:CD1	2.62	0.74
1:B:375:MSE:CE	1:B:403:LEU:HD21	2.18	0.73
1:A:646:ARG:O	1:A:650:ILE:HG12	1.87	0.73
1:A:765:ALA:HA	1:A:769:PHE:CE1	2.23	0.73
1:A:400:VAL:CG1	1:A:452:VAL:HG11	2.18	0.73
1:A:742:ASP:O	1:A:745:HIS:N	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:549:THR:C	1:B:551:LEU:H	1.96	0.72
1:B:223:ILE:HG13	1:B:223:ILE:O	1.87	0.72
1:B:451:PRO:HA	1:B:454:LEU:HD23	1.72	0.72
1:B:511:ASN:CG	1:B:512:GLY:H	1.98	0.71
1:B:375:MSE:HE2	1:B:403:LEU:CD2	2.21	0.71
1:A:473:GLN:HG2	1:A:554:LEU:HD11	1.72	0.71
1:A:503:PRO:HB2	1:B:168:SER:HB2	1.73	0.71
1:A:258:CYS:SG	1:A:283:PRO:HG3	2.31	0.70
1:B:333:MSE:HE1	1:B:378:LEU:HA	1.74	0.70
1:A:618:HIS:CE1	1:A:650:ILE:HD11	2.27	0.70
1:A:618:HIS:NE2	1:A:650:ILE:HD11	2.05	0.69
1:B:655:LEU:HA	1:B:661:SER:O	1.92	0.69
1:B:640:ASP:H	1:B:643:SER:HB3	1.57	0.69
1:A:502:HIS:HD2	1:A:504:ALA:H	1.41	0.68
1:B:372:VAL:C	2:B:4:HOH:O	2.36	0.68
1:A:695:ARG:CD	2:A:85:HOH:O	2.41	0.68
1:B:464:MSE:HE3	1:B:499:TYR:CD1	2.29	0.68
1:B:631:GLN:O	1:B:632:LYS:HB2	1.93	0.68
1:A:333:MSE:HE2	1:A:381:SER:HB3	1.75	0.68
1:A:680:GLN:O	1:A:684:GLU:HG3	1.93	0.68
1:A:660:LEU:HD11	1:A:719:LEU:HD23	1.77	0.67
1:A:720:MSE:HE1	1:A:740:TRP:CE3	2.29	0.67
1:B:709:PRO:CB	1:B:710:PRO:HA	2.24	0.67
1:B:375:MSE:HB2	2:B:4:HOH:O	1.93	0.67
1:B:709:PRO:HB2	1:B:710:PRO:HA	1.76	0.67
1:A:285:PHE:HE1	1:A:299:ALA:HB1	1.59	0.67
1:B:580:SER:HA	1:B:582:VAL:N	2.10	0.67
1:B:333:MSE:CE	1:B:378:LEU:HA	2.25	0.67
1:A:695:ARG:HD2	2:A:85:HOH:O	1.94	0.66
1:B:688:CYS:SG	1:B:773:LEU:HA	2.35	0.66
1:A:388:THR:C	1:A:390:ALA:H	2.01	0.66
1:A:525:THR:HG22	1:A:527:ALA:H	1.60	0.66
1:A:298:LYS:HE3	1:A:354:LYS:HB3	1.77	0.65
1:A:479:MSE:HE1	1:A:493:ALA:HA	1.78	0.65
1:B:310:ASP:OD2	1:B:312:SER:HB3	1.97	0.65
1:B:543:MSE:HA	1:B:566:TYR:O	1.96	0.65
1:A:400:VAL:HG11	1:A:452:VAL:HG11	1.77	0.65
1:B:406:PRO:HA	1:B:409:THR:HG22	1.77	0.65
1:B:695:ARG:O	1:B:697:SER:N	2.30	0.65
1:A:479:MSE:HE3	1:A:523:TRP:CZ2	2.32	0.65
1:B:265:ASN:HA	1:B:287:ASP:O	1.97	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:695:ARG:C	1:B:697:SER:N	2.55	0.64
1:B:539:SER:O	1:B:541:THR:N	2.31	0.64
1:B:345:PHE:O	1:B:356:ILE:HG22	1.98	0.64
1:A:298:LYS:HA	1:A:359:THR:OG1	1.97	0.64
1:A:290:LEU:HB2	1:A:329:ILE:HD13	1.79	0.64
1:A:665:TYR:O	1:A:669:LEU:HG	1.98	0.64
1:B:361:ASP:HA	1:B:371:LYS:HD3	1.80	0.64
1:A:701:ILE:HG22	1:A:702:PHE:N	2.13	0.64
1:B:290:LEU:HB2	1:B:329:ILE:HG12	1.80	0.64
1:A:413:LEU:HD12	1:A:413:LEU:H	1.63	0.63
1:B:709:PRO:CB	1:B:710:PRO:CA	2.76	0.63
1:B:547:THR:C	1:B:549:THR:H	2.07	0.63
1:A:764:HIS:O	1:A:764:HIS:ND1	2.32	0.62
1:B:231:SER:O	1:B:232:LYS:HB2	1.98	0.62
1:B:555:ASN:CG	1:B:555:ASN:O	2.40	0.62
1:B:182:LEU:HD21	1:B:212:PRO:HG3	1.82	0.62
1:B:709:PRO:HD2	1:B:710:PRO:HA	1.81	0.62
1:A:502:HIS:CD2	1:A:504:ALA:H	2.17	0.62
1:A:296:ARG:CG	1:A:296:ARG:NH1	2.54	0.62
1:A:769:PHE:HD1	1:A:769:PHE:O	1.81	0.62
1:B:708:SER:CB	1:B:709:PRO:CD	2.74	0.61
1:A:317:VAL:HG22	1:A:318:SER:H	1.64	0.61
1:A:699:SER:HA	1:A:703:GLY:O	2.00	0.61
1:B:359:THR:CG2	1:B:360:ILE:N	2.62	0.61
1:A:570:ALA:N	1:A:571:GLY:CA	2.53	0.61
1:A:253:LEU:O	1:A:256:VAL:HB	2.00	0.60
1:B:442:ASP:HB2	2:B:5:HOH:O	2.01	0.60
1:B:556:PRO:HG3	1:B:562:TRP:HH2	1.66	0.60
1:B:647:LEU:N	2:B:12:HOH:O	2.33	0.60
1:B:672:TYR:HB2	2:B:7:HOH:O	2.01	0.60
1:B:324:ILE:HG22	1:B:377:ASP:HB3	1.83	0.60
1:A:256:VAL:O	1:A:275:TYR:HB2	2.01	0.60
1:A:466:THR:HG22	1:B:201:ASP:HB2	1.84	0.60
1:A:375:MSE:HE2	1:A:403:LEU:HD21	1.84	0.60
1:B:514:PHE:CZ	1:B:528:ALA:HA	2.35	0.60
1:A:271:VAL:N	1:A:293:THR:HG22	2.15	0.59
1:B:508:HIS:N	1:B:508:HIS:CD2	2.68	0.59
1:B:359:THR:CG2	1:B:360:ILE:H	2.15	0.59
1:B:660:LEU:HB2	1:B:718:ALA:HB1	1.83	0.59
1:B:333:MSE:HE2	1:B:381:SER:HB3	1.84	0.59
1:B:360:ILE:O	1:B:361:ASP:CB	2.50	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:269:ASN:HD21	1:A:289:THR:HB	1.68	0.59
1:A:285:PHE:CE1	1:A:299:ALA:HB1	2.38	0.59
1:A:656:PRO:CD	1:A:661:SER:HB2	2.33	0.58
1:B:539:SER:C	1:B:541:THR:N	2.61	0.58
1:B:701:ILE:O	1:B:703:GLY:N	2.36	0.58
1:A:755:SER:O	1:A:759:ASP:HB2	2.04	0.58
1:A:333:MSE:HE3	1:A:337:TRP:CZ2	2.34	0.58
1:A:648:ALA:O	1:A:652:ASP:HB2	2.03	0.58
1:B:625:PHE:HD2	1:B:696:TYR:CE2	2.22	0.58
1:B:690:SER:OG	1:B:761:MSE:HE1	2.04	0.58
1:A:552:THR:O	1:A:556:PRO:HA	2.03	0.58
1:A:768:TYR:O	1:A:769:PHE:CG	2.57	0.58
1:B:511:ASN:CG	1:B:512:GLY:N	2.59	0.58
1:A:273:LEU:O	1:A:295:ILE:HA	2.04	0.57
1:A:562:TRP:O	1:A:564:ASN:N	2.37	0.57
1:B:359:THR:HG22	1:B:360:ILE:H	1.69	0.57
1:B:434:ASN:C	1:B:434:ASN:HD22	2.11	0.57
1:A:301:LEU:HD22	1:A:304:VAL:HG21	1.85	0.57
1:B:375:MSE:HE3	1:B:375:MSE:HA	1.86	0.57
1:B:441:PRO:HG2	1:B:477:HIS:CD2	2.39	0.57
1:B:637:LYS:HD3	1:B:701:ILE:O	2.03	0.57
1:B:653:PRO:CB	1:B:656:PRO:HA	2.24	0.57
1:A:773:LEU:O	1:A:777:LEU:HB2	2.05	0.57
1:A:388:THR:O	1:A:390:ALA:N	2.37	0.57
1:B:239:SER:OG	1:B:259:SER:HB3	2.04	0.57
1:A:570:ALA:H	1:A:571:GLY:CA	2.10	0.57
1:B:476:LEU:HD23	1:B:550:LEU:HD13	1.87	0.57
1:B:688:CYS:HA	1:B:691:THR:HG23	1.86	0.57
1:A:363:LEU:HB2	1:A:371:LYS:HD3	1.86	0.56
1:A:264:SER:HA	1:A:286:ILE:O	2.05	0.56
1:B:487:GLY:HA2	1:B:490:GLN:CG	2.35	0.56
1:A:479:MSE:HE3	1:A:523:TRP:CE2	2.39	0.56
1:A:598:GLN:HG3	1:A:779:LEU:HB2	1.87	0.56
1:B:508:HIS:CD2	1:B:508:HIS:H	2.24	0.56
1:B:406:PRO:HA	1:B:409:THR:CG2	2.36	0.56
1:B:549:THR:C	1:B:551:LEU:N	2.63	0.56
1:B:651:PHE:N	2:B:59:HOH:O	2.39	0.56
1:B:720:MSE:HE2	1:B:731:PHE:CE1	2.37	0.56
1:A:201:ASP:OD2	1:A:203:ARG:HD3	2.05	0.56
1:B:360:ILE:O	1:B:361:ASP:HB3	2.07	0.55
1:A:620:GLU:O	1:A:624:GLN:HG3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:506:SER:N	1:B:507:PRO:HD3	2.21	0.55
1:B:553:MSE:HG3	1:B:592:PHE:CE2	2.41	0.55
1:A:656:PRO:HD2	1:A:661:SER:HB2	1.87	0.55
1:A:287:ASP:N	1:A:303:GLY:O	2.39	0.55
1:A:268:MSE:O	1:A:293:THR:HG21	2.07	0.55
1:A:766:ARG:HD3	2:A:87:HOH:O	2.05	0.55
1:A:695:ARG:HD3	2:A:85:HOH:O	2.05	0.55
1:B:260:ASN:HB2	1:B:281:GLN:HB2	1.88	0.55
1:A:414:ILE:O	1:A:418:LEU:HB2	2.07	0.55
1:A:386:ARG:N	1:A:386:ARG:HD2	2.22	0.55
1:B:326:LEU:HB2	1:B:331:LEU:HD12	1.89	0.55
1:B:346:LEU:HB2	1:B:395:VAL:HG21	1.89	0.55
1:B:482:VAL:HG23	2:B:73:HOH:O	2.06	0.55
1:A:766:ARG:HA	1:A:770:PRO:HB3	1.88	0.54
1:B:690:SER:HB2	1:B:716:ALA:O	2.07	0.54
1:B:363:LEU:HD12	1:B:371:LYS:HG2	1.88	0.54
1:A:410:GLN:O	1:A:410:GLN:CG	2.49	0.54
1:B:258:CYS:SG	1:B:275:TYR:CD2	3.01	0.54
1:B:709:PRO:CD	1:B:710:PRO:HA	2.37	0.54
1:B:375:MSE:HE1	1:B:378:LEU:HD13	1.89	0.54
1:B:475:ILE:O	1:B:479:MSE:HG2	2.08	0.54
1:B:687:PHE:O	1:B:691:THR:HG22	2.09	0.53
1:A:630:ASN:O	1:A:631:GLN:HB3	2.07	0.53
1:B:514:PHE:HZ	1:B:528:ALA:HA	1.72	0.53
1:B:535:SER:HB3	1:B:538:ASP:O	2.08	0.53
1:A:222:ILE:HD12	1:A:242:HIS:ND1	2.24	0.53
1:B:604:ARG:HD3	1:B:672:TYR:HA	1.91	0.53
1:B:580:SER:CA	1:B:581:PRO:C	2.68	0.53
1:B:582:VAL:O	1:B:585:PHE:HB2	2.09	0.53
1:B:608:LEU:HD11	1:B:668:ILE:HD13	1.91	0.52
1:A:577:ALA:O	1:A:578:GLN:HG3	2.08	0.52
1:A:708:SER:OG	1:A:713:ARG:HD3	2.09	0.52
1:B:696:TYR:N	1:B:701:ILE:HD11	2.19	0.52
1:A:505:VAL:HG12	1:A:509:ILE:HD13	1.91	0.52
1:A:742:ASP:O	1:A:744:PHE:N	2.43	0.52
1:B:359:THR:HG23	1:B:360:ILE:N	2.24	0.52
1:B:653:PRO:HB3	1:B:656:PRO:CA	2.27	0.52
1:B:533:LEU:HD11	1:B:545:LEU:HD11	1.92	0.52
1:B:434:ASN:ND2	1:B:469:GLY:HA3	2.24	0.52
1:A:778:PRO:HG2	1:A:781:TRP:CD2	2.45	0.52
1:B:709:PRO:HG2	1:B:713:ARG:CB	2.38	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:634:SER:HB3	1:A:701:ILE:HA	1.92	0.51
1:B:322:ASN:H	1:B:322:ASN:ND2	2.08	0.51
1:A:249:THR:HA	1:A:269:ASN:O	2.10	0.51
1:A:297:HIS:HB2	1:A:356:ILE:HG12	1.92	0.51
1:A:751:PHE:C	1:A:753:CYS:N	2.67	0.51
1:B:317:VAL:HG12	1:B:318:SER:N	2.26	0.51
1:A:557:THR:O	1:A:558:PRO:C	2.52	0.51
1:A:722:LYS:O	1:A:722:LYS:HG3	2.11	0.51
1:B:479:MSE:HE2	1:B:523:TRP:CD1	2.46	0.51
1:B:506:SER:N	1:B:507:PRO:CD	2.74	0.51
1:A:751:PHE:C	1:A:753:CYS:H	2.18	0.51
1:B:266:SER:O	1:B:288:THR:HB	2.11	0.51
1:B:621:LEU:O	1:B:625:PHE:HD1	1.93	0.51
1:A:751:PHE:HD2	1:A:752:THR:H	1.55	0.51
1:B:663:ALA:O	1:B:666:GLN:N	2.44	0.50
1:B:750:ALA:HB1	1:B:752:THR:HG23	1.92	0.50
1:B:701:ILE:HG13	1:B:702:PHE:N	2.25	0.50
1:B:183:ARG:O	1:B:188:GLU:HB3	2.11	0.50
1:A:360:ILE:O	1:A:371:LYS:HD2	2.12	0.50
1:B:465:THR:HG21	1:B:502:HIS:CD2	2.47	0.50
1:B:513:LEU:O	1:B:514:PHE:CD1	2.63	0.50
1:B:216:MSE:SE	2:B:48:HOH:O	2.79	0.50
1:B:680:GLN:HG3	1:B:730:ILE:HD11	1.93	0.50
1:A:239:SER:HB3	1:A:259:SER:HB2	1.93	0.50
1:B:375:MSE:N	2:B:4:HOH:O	2.44	0.50
1:B:405:HIS:C	1:B:407:PRO:HD2	2.37	0.49
1:B:513:LEU:O	1:B:514:PHE:HD1	1.95	0.49
1:B:195:ARG:HD2	1:B:225:GLY:O	2.11	0.49
1:A:379:VAL:HG21	1:A:414:ILE:HG12	1.95	0.49
1:A:633:HIS:HB2	2:A:86:HOH:O	2.12	0.49
1:A:686:LEU:HA	1:A:689:LEU:HD12	1.93	0.49
1:A:484:CYS:O	1:A:489:ARG:NH2	2.45	0.49
1:B:552:THR:C	1:B:554:LEU:H	2.18	0.49
1:A:388:THR:C	1:A:390:ALA:N	2.69	0.49
1:B:639:ILE:O	1:B:639:ILE:HG23	2.12	0.49
1:B:476:LEU:HD12	1:B:476:LEU:C	2.37	0.49
1:B:701:ILE:HG13	1:B:702:PHE:H	1.77	0.49
1:B:781:TRP:O	1:B:782:ALA:HB3	2.13	0.49
1:A:633:HIS:HA	1:A:700:ALA:O	2.13	0.49
1:B:556:PRO:HG3	1:B:562:TRP:CH2	2.47	0.49
1:B:648:ALA:C	2:B:59:HOH:O	2.56	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:170:PRO:HA	1:A:173:TRP:HD1	1.78	0.49
1:B:286:ILE:HA	1:B:303:GLY:HA3	1.95	0.49
1:B:357:LEU:O	1:B:360:ILE:O	2.30	0.49
1:B:553:MSE:HG3	1:B:592:PHE:HE2	1.76	0.49
1:B:445:TYR:CE1	1:B:449:ILE:HG21	2.47	0.48
1:A:169:SER:O	1:A:172:ASP:HB2	2.13	0.48
1:A:727:SER:O	1:A:730:ILE:HG12	2.12	0.48
1:A:269:ASN:N	1:A:269:ASN:HD22	2.10	0.48
1:A:613:LEU:HB2	1:A:622:ASN:HD22	1.77	0.48
1:A:696:TYR:O	1:A:702:PHE:HB2	2.14	0.48
1:B:393:ARG:C	1:B:395:VAL:H	2.21	0.48
1:B:709:PRO:CG	1:B:710:PRO:HA	2.43	0.48
1:B:508:HIS:H	1:B:508:HIS:HD2	1.61	0.48
1:B:262:LYS:HG2	1:B:284:SER:OG	2.13	0.48
1:B:310:ASP:OD2	1:B:312:SER:N	2.45	0.48
1:B:471:PHE:HE1	1:B:496:TYR:HD1	1.62	0.48
1:A:314:PRO:O	1:A:315:PRO:C	2.56	0.48
1:A:631:GLN:HA	1:A:780:ALA:CB	2.41	0.48
1:A:768:TYR:O	1:A:769:PHE:CD1	2.67	0.48
1:B:338:THR:O	1:B:342:VAL:HG23	2.13	0.48
1:A:324:ILE:HD12	1:A:333:MSE:SE	2.63	0.48
1:B:547:THR:C	1:B:549:THR:N	2.72	0.48
1:A:227:ASN:OD1	1:A:247:ARG:HB3	2.13	0.48
1:A:317:VAL:HG13	1:A:318:SER:N	2.29	0.48
1:A:317:VAL:HG22	1:A:318:SER:N	2.29	0.48
1:B:645:SER:N	2:B:12:HOH:O	2.47	0.48
1:A:466:THR:CG2	1:B:201:ASP:HB2	2.43	0.47
1:B:200:ALA:O	1:B:231:SER:O	2.31	0.47
1:A:395:VAL:O	1:A:396:GLU:C	2.57	0.47
1:B:396:GLU:OE1	1:B:428:HIS:HD2	1.97	0.47
1:A:178:THR:O	1:A:182:LEU:HB2	2.14	0.47
1:A:385:GLY:C	1:A:386:ARG:HD2	2.39	0.47
1:A:618:HIS:NE2	1:A:650:ILE:CD1	2.75	0.47
1:B:292:ASN:OD1	1:B:325:ARG:NH2	2.37	0.47
1:B:628:ALA:C	1:B:630:ASN:H	2.22	0.47
1:A:742:ASP:O	1:A:743:ARG:C	2.57	0.47
1:B:333:MSE:HE1	1:B:378:LEU:HG	1.96	0.47
1:A:521:PRO:HG2	1:A:523:TRP:CZ2	2.50	0.47
1:B:649:THR:HA	1:B:652:ASP:HB2	1.97	0.47
1:B:691:THR:HA	1:B:694:ALA:HB2	1.96	0.47
1:B:388:THR:O	1:B:392:ILE:HG22	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:709:PRO:HA	1:A:710:PRO:HD2	1.82	0.46
1:A:270:GLU:OE2	1:A:292:ASN:HB2	2.15	0.46
1:B:518:ASP:CB	1:B:522:ASP:HB2	2.45	0.46
1:A:281:GLN:O	1:A:282:GLN:CB	2.56	0.46
1:B:641:ASP:C	1:B:643:SER:H	2.24	0.46
1:B:694:ALA:C	1:B:695:ARG:O	2.58	0.46
1:B:514:PHE:CG	1:B:515:GLY:N	2.82	0.46
1:A:424:ARG:HD2	2:A:6:HOH:O	2.16	0.46
1:B:436:VAL:HG13	1:B:779:LEU:HD21	1.97	0.46
1:B:585:PHE:N	1:B:585:PHE:CD2	2.82	0.46
1:B:764:HIS:C	1:B:764:HIS:CD2	2.94	0.46
1:A:199:ASN:HA	1:A:230:ASN:O	2.15	0.46
1:A:300:ASN:C	1:A:300:ASN:ND2	2.72	0.46
1:A:506:SER:N	1:A:507:PRO:HD2	2.31	0.46
1:B:387:LEU:HD22	1:B:391:CYS:SG	2.56	0.46
1:A:649:THR:C	1:A:650:ILE:HD13	2.40	0.45
1:B:698:SER:C	1:B:700:ALA:H	2.24	0.45
1:A:276:SER:OG	1:A:278:THR:HG22	2.15	0.45
1:A:304:VAL:HG12	1:A:306:LEU:HD12	1.99	0.45
1:B:691:THR:HA	1:B:694:ALA:CB	2.46	0.45
1:B:709:PRO:HB2	1:B:711:ALA:N	2.30	0.45
1:B:564:ASN:HD22	1:B:564:ASN:HA	1.56	0.45
1:A:411:SER:HB2	1:A:414:ILE:HB	1.99	0.45
1:B:404:ALA:C	1:B:405:HIS:ND1	2.75	0.45
1:B:698:SER:C	1:B:700:ALA:N	2.74	0.45
1:A:238:ILE:O	1:A:238:ILE:HG12	2.16	0.45
1:B:669:LEU:HD22	1:B:675:THR:HA	1.98	0.45
1:A:300:ASN:C	1:A:300:ASN:HD22	2.24	0.45
1:A:424:ARG:O	1:A:428:HIS:CD2	2.69	0.45
1:A:479:MSE:CE	1:A:493:ALA:HA	2.44	0.45
1:A:614:SER:O	1:A:615:THR:C	2.60	0.45
1:B:650:ILE:C	1:B:652:ASP:H	2.24	0.45
1:B:206:THR:HA	1:B:237:ASP:HB3	1.99	0.45
1:A:238:ILE:HB	1:A:241:LEU:HD12	1.98	0.45
1:A:502:HIS:CD2	1:A:504:ALA:HB3	2.52	0.45
1:B:567:LEU:HD21	1:B:584:LEU:HD21	1.98	0.45
1:A:502:HIS:HD2	1:A:504:ALA:HB3	1.82	0.45
1:A:614:SER:O	1:A:616:GLU:N	2.50	0.45
1:B:237:ASP:HA	1:B:257:VAL:HG13	1.98	0.45
1:B:696:TYR:HD1	1:B:701:ILE:CD1	2.29	0.45
1:A:660:LEU:HG	1:A:718:ALA:HB1	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:697:SER:HB2	1:B:754:THR:HG21	2.00	0.44
1:A:476:LEU:HD22	1:A:550:LEU:CD1	2.48	0.44
1:A:540:ASP:O	1:A:570:ALA:HB2	2.17	0.44
1:B:216:MSE:HE2	1:B:216:MSE:HB3	1.84	0.44
1:B:216:MSE:HA	1:B:240:HIS:O	2.17	0.44
1:B:552:THR:C	1:B:554:LEU:N	2.75	0.44
1:B:781:TRP:CD1	1:B:781:TRP:N	2.85	0.44
1:A:424:ARG:O	1:A:428:HIS:HD2	2.01	0.44
1:B:410:GLN:OE1	1:B:410:GLN:N	2.47	0.44
1:A:418:LEU:O	1:A:419:GLY:C	2.61	0.44
1:A:764:HIS:O	1:A:764:HIS:CG	2.67	0.44
1:B:464:MSE:CE	1:B:499:TYR:HD1	2.22	0.44
1:A:248:PHE:O	1:A:249:THR:C	2.60	0.44
1:B:231:SER:HB2	1:B:251:SER:OG	2.17	0.44
1:A:180:ALA:O	1:A:190:LEU:HD11	2.18	0.44
1:B:469:GLY:O	1:B:473:GLN:CG	2.61	0.44
1:A:271:VAL:HG22	1:A:293:THR:HG21	1.99	0.43
1:B:287:ASP:HA	1:B:305:ILE:HD11	1.99	0.43
1:A:453:LEU:O	1:A:457:PHE:HD1	2.01	0.43
1:B:569:ARG:O	1:B:570:ALA:HB2	2.17	0.43
1:A:512:GLY:HA2	1:A:517:TYR:HD1	1.83	0.43
1:B:166:SER:CB	1:B:167:PRO:HA	2.40	0.43
1:B:652:ASP:O	1:B:653:PRO:C	2.61	0.43
1:B:273:LEU:HB3	1:B:295:ILE:HG22	2.00	0.43
1:B:333:MSE:HE2	1:B:378:LEU:HA	2.01	0.43
1:B:598:GLN:HE21	1:B:602:GLN:HB2	1.84	0.43
1:B:430:CYS:HB3	1:B:467:HIS:CD2	2.53	0.43
1:B:490:GLN:HA	1:B:493:ALA:HB3	2.01	0.43
1:A:181:VAL:HA	1:A:184:GLN:HB3	2.01	0.43
1:A:201:ASP:OD2	1:A:203:ARG:CD	2.67	0.43
1:A:466:THR:HG21	1:B:199:ASN:O	2.19	0.43
1:B:301:LEU:HB3	1:B:304:VAL:HG21	2.01	0.43
1:B:365:ASP:OD2	1:B:365:ASP:N	2.47	0.43
1:B:455:ASP:HB2	2:B:46:HOH:O	2.18	0.43
1:B:595:ALA:O	1:B:598:GLN:HB3	2.18	0.43
1:A:345:PHE:O	1:A:355:SER:HB2	2.18	0.43
1:A:553:MSE:HE3	1:A:562:TRP:HE3	1.84	0.43
1:A:735:GLU:O	1:A:739:GLU:HB2	2.19	0.43
1:A:364:PRO:HG2	1:A:367:TYR:CD1	2.54	0.42
1:A:467:HIS:NE2	1:B:230:ASN:ND2	2.66	0.42
1:B:301:LEU:HB3	1:B:304:VAL:CG2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:ILE:HD13	1:A:324:ILE:H	1.85	0.42
1:A:349:GLU:OE1	1:A:397:SER:OG	2.37	0.42
1:A:613:LEU:O	1:A:614:SER:C	2.62	0.42
1:A:720:MSE:CE	1:A:761:MSE:SE	3.13	0.42
1:A:511:ASN:H	1:A:511:ASN:ND2	2.17	0.42
1:A:610:ASP:HA	1:A:622:ASN:HD21	1.84	0.42
1:A:656:PRO:HD3	1:A:661:SER:HB2	2.01	0.42
1:B:442:ASP:O	1:B:443:THR:C	2.63	0.42
1:B:463:ALA:HA	1:B:466:THR:OG1	2.20	0.42
1:B:695:ARG:HA	1:B:698:SER:CB	2.50	0.42
1:A:375:MSE:HE2	1:A:403:LEU:CD2	2.48	0.42
1:B:603:ARG:O	1:B:607:GLU:HG3	2.18	0.42
1:B:608:LEU:CD1	1:B:668:ILE:HD13	2.49	0.42
1:A:502:HIS:HD2	1:A:504:ALA:CB	2.33	0.42
1:B:248:PHE:O	1:B:249:THR:C	2.61	0.42
1:B:266:SER:H	1:B:288:THR:HB	1.84	0.42
1:B:356:ILE:O	1:B:359:THR:HG22	2.17	0.42
1:B:449:ILE:O	1:B:450:LEU:C	2.62	0.42
1:B:199:ASN:ND2	1:B:230:ASN:HD22	2.17	0.42
1:B:444:TYR:CE2	1:B:448:ARG:HD2	2.55	0.42
1:B:490:GLN:H	1:B:490:GLN:HG2	1.55	0.42
1:B:500:LEU:HD13	1:B:509:ILE:HG13	2.01	0.42
1:A:233:PHE:HB2	1:A:253:LEU:HD23	2.02	0.42
1:A:479:MSE:HE1	1:A:493:ALA:CA	2.49	0.42
1:B:165:SER:HB2	2:B:14:HOH:O	2.19	0.42
1:B:632:LYS:O	1:B:633:HIS:HB2	2.19	0.42
1:A:333:MSE:CE	1:A:381:SER:HB3	2.47	0.42
1:B:256:VAL:O	1:B:275:TYR:HB2	2.19	0.42
1:B:523:TRP:CE3	1:B:523:TRP:HA	2.53	0.42
1:B:698:SER:HA	1:B:754:THR:HG22	2.01	0.42
1:A:285:PHE:HB2	1:A:304:VAL:HG23	2.02	0.41
1:A:608:LEU:HA	1:A:611:ILE:HD12	2.02	0.41
1:B:543:MSE:HE2	1:B:545:LEU:HD23	2.02	0.41
1:A:294:LEU:HD21	1:A:323:PHE:CE2	2.55	0.41
1:A:655:LEU:CB	1:A:659:LYS:O	2.68	0.41
1:B:239:SER:CB	1:B:259:SER:HB3	2.50	0.41
1:B:520:SER:HA	1:B:521:PRO:HA	1.79	0.41
1:B:528:ALA:O	1:B:546:SER:HA	2.20	0.41
1:A:297:HIS:HB2	1:A:356:ILE:CG1	2.50	0.41
1:B:177:LEU:O	1:B:181:VAL:HG22	2.21	0.41
1:A:263:PHE:CG	1:A:268:MSE:SE	3.23	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:VAL:HA	1:A:437:PRO:HD3	1.87	0.41
1:B:487:GLY:O	1:B:491:LYS:HB2	2.20	0.41
1:B:630:ASN:O	1:B:631:GLN:CB	2.68	0.41
1:B:555:ASN:O	1:B:556:PRO:C	2.63	0.41
1:A:268:MSE:CE	1:A:273:LEU:HD11	2.50	0.41
1:A:697:SER:HB3	1:A:712:LEU:HB3	2.02	0.41
1:B:216:MSE:H	1:B:216:MSE:HG2	1.60	0.41
1:A:268:MSE:C	1:A:269:ASN:HD22	2.28	0.41
1:A:694:ALA:HB2	1:A:761:MSE:HE1	2.03	0.41
1:B:406:PRO:N	1:B:407:PRO:CD	2.83	0.41
1:B:549:THR:OG1	1:B:550:LEU:N	2.54	0.41
1:A:307:ASN:O	1:A:308:GLU:C	2.63	0.41
1:A:522:ASP:C	1:A:524:THR:H	2.29	0.41
1:A:741:SER:O	1:A:745:HIS:CD2	2.74	0.41
1:B:275:TYR:O	1:B:296:ARG:NH2	2.53	0.41
1:B:322:ASN:O	1:B:333:MSE:HB2	2.21	0.41
1:B:549:THR:O	1:B:553:MSE:HG2	2.20	0.41
1:B:684:GLU:OE2	1:B:772:VAL:HG21	2.21	0.41
1:A:704:THR:O	1:A:706:HIS:N	2.55	0.40
1:B:465:THR:HG21	1:B:502:HIS:NE2	2.37	0.40
1:B:471:PHE:HE1	1:B:496:TYR:CD1	2.39	0.40
1:B:761:MSE:HE2	1:B:761:MSE:HB3	2.01	0.40
1:A:291:LYS:HG2	1:A:328:ASP:HB2	2.02	0.40
1:A:498:GLN:O	1:A:499:TYR:C	2.64	0.40
1:A:686:LEU:HA	1:A:689:LEU:HB2	2.04	0.40
1:A:699:SER:O	1:A:700:ALA:HB3	2.21	0.40
1:B:375:MSE:HE3	1:B:375:MSE:CA	2.50	0.40
1:B:260:ASN:N	1:B:281:GLN:O	2.49	0.40
1:B:348:HIS:HE1	1:B:398:SER:O	2.03	0.40
1:A:660:LEU:O	1:A:661:SER:C	2.64	0.40
1:B:568:LEU:C	1:B:570:ALA:H	2.30	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	615/618 (100%)	494 (80%)	90 (15%)	31 (5%)	1	5
1	B	608/618 (98%)	484 (80%)	92 (15%)	32 (5%)	1	5
All	All	1223/1236 (99%)	978 (80%)	182 (15%)	63 (5%)	1	5

All (63) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	282	GLN
1	A	315	PRO
1	A	317	VAL
1	A	389	GLU
1	A	563	ASP
1	A	578	GLN
1	A	615	THR
1	A	742	ASP
1	A	743	ARG
1	A	750	ALA
1	A	752	THR
1	B	515	GLY
1	B	539	SER
1	B	540	ASP
1	B	570	ALA
1	B	581	PRO
1	B	653	PRO
1	B	656	PRO
1	B	695	ARG
1	B	702	PHE
1	B	708	SER
1	B	709	PRO
1	A	366	LYS
1	A	419	GLY
1	A	498	GLN
1	A	576	THR
1	A	769	PHE
1	A	775	SER
1	B	168	SER
1	B	485	THR
1	B	550	LEU
1	B	576	THR
1	B	619	GLY

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Mol	Chain	Res	Type
1	B	631	GLN
1	B	639	ILE
1	B	696	TYR
1	B	701	ILE
1	B	751	PHE
1	A	336	LEU
1	A	413	LEU
1	A	499	TYR
1	A	577	ALA
1	A	614	SER
1	B	556	PRO
1	B	571	GLY
1	A	167	PRO
1	A	281	GLN
1	A	411	SER
1	A	705	GLU
1	B	511	ASN
1	B	517	TYR
1	A	768	TYR
1	B	232	LYS
1	B	280	GLN
1	B	310	ASP
1	B	419	GLY
1	B	514	PHE
1	B	745	HIS
1	A	387	LEU
1	A	701	ILE
1	A	726	LEU
1	B	361	ASP
1	A	732	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	508/527 (96%)	436 (86%)	72 (14%)	3 12

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	473/527 (90%)	398 (84%)	75 (16%)	2 9
All	All	981/1054 (93%)	834 (85%)	147 (15%)	3 10

All (147) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	169	SER
1	A	172	ASP
1	A	179	ASP
1	A	181	VAL
1	A	182	LEU
1	A	185	LYS
1	A	191	THR
1	A	203	ARG
1	A	206	THR
1	A	210	ILE
1	A	214	SER
1	A	216	MSE
1	A	238	ILE
1	A	256	VAL
1	A	257	VAL
1	A	277	ILE
1	A	281	GLN
1	A	294	LEU
1	A	296	ARG
1	A	298	LYS
1	A	300	ASN
1	A	304	VAL
1	A	305	ILE
1	A	324	ILE
1	A	326	LEU
1	A	329	ILE
1	A	335	LEU
1	A	356	ILE
1	A	360	ILE
1	A	366	LYS
1	A	370	GLU
1	A	378	LEU
1	A	410	GLN
1	A	411	SER
1	A	415	SER
1	A	418	LEU

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Mol	Chain	Res	Type
1	A	436	VAL
1	A	468	SER
1	A	479	MSE
1	A	480	THR
1	A	482	VAL
1	A	533	LEU
1	A	539	SER
1	A	549	THR
1	A	550	LEU
1	A	554	LEU
1	A	557	THR
1	A	567	LEU
1	A	583	GLU
1	A	584	LEU
1	A	591	VAL
1	A	593	LEU
1	A	598	GLN
1	A	608	LEU
1	A	639	ILE
1	A	641	ASP
1	A	655	LEU
1	A	668	ILE
1	A	691	THR
1	A	696	TYR
1	A	720	MSE
1	A	736	GLN
1	A	745	HIS
1	A	748	HIS
1	A	753	CYS
1	A	754	THR
1	A	756	VAL
1	A	769	PHE
1	A	773	LEU
1	A	774	SER
1	A	777	LEU
1	A	779	LEU
1	B	176	LYS
1	B	177	LEU
1	B	179	ASP
1	B	191	THR
1	B	216	MSE
1	B	223	ILE

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Mol	Chain	Res	Type
1	B	231	SER
1	B	238	ILE
1	B	247	ARG
1	B	252	THR
1	B	255	ASP
1	B	257	VAL
1	B	261	THR
1	B	266	SER
1	B	278	THR
1	B	288	THR
1	B	293	THR
1	B	294	LEU
1	B	304	VAL
1	B	306	LEU
1	B	312	SER
1	B	322	ASN
1	B	326	LEU
1	B	333	MSE
1	B	336	LEU
1	B	352	ASN
1	B	354	LYS
1	B	359	THR
1	B	365	ASP
1	B	370	GLU
1	B	392	ILE
1	B	395	VAL
1	B	400	VAL
1	B	409	THR
1	B	429	GLN
1	B	455	ASP
1	B	470	LEU
1	B	484	CYS
1	B	485	THR
1	B	491	LYS
1	B	496	TYR
1	B	500	LEU
1	B	508	HIS
1	B	509	ILE
1	B	513	LEU
1	B	514	PHE
1	B	518	ASP
1	B	532	LEU

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Mol	Chain	Res	Type
1	B	545	LEU
1	B	546	SER
1	B	549	THR
1	B	550	LEU
1	B	552	THR
1	B	564	ASN
1	B	583	GLU
1	B	591	VAL
1	B	632	LYS
1	B	636	VAL
1	B	660	LEU
1	B	668	ILE
1	B	678	THR
1	B	686	LEU
1	B	691	THR
1	B	695	ARG
1	B	713	ARG
1	B	717	GLU
1	B	720	MSE
1	B	730	ILE
1	B	734	SER
1	B	738	THR
1	B	739	GLU
1	B	745	HIS
1	B	747	LEU
1	B	762	GLN
1	B	773	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	269	ASN
1	A	281	GLN
1	A	300	ASN
1	A	350	HIS
1	A	490	GLN
1	A	502	HIS
1	A	511	ASN
1	A	587	HIS
1	A	598	GLN
1	A	622	ASN
1	A	631	GLN

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Mol	Chain	Res	Type
1	A	682	GLN
1	A	736	GLN
1	B	199	ASN
1	B	282	GLN
1	B	300	ASN
1	B	322	ASN
1	B	340	ASN
1	B	428	HIS
1	B	446	GLN
1	B	498	GLN
1	B	555	ASN
1	B	564	ASN
1	B	622	ASN
1	B	673	HIS
1	B	748	HIS
1	B	764	HIS

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 oligosaccharides 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

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	605/618 (97%)	0.32	16 (2%)	57 47	34, 47, 85, 97	0
1	B	600/618 (97%)	0.77	55 (9%)	14 10	41, 58, 94, 116	0
All	All	1205/1236 (97%)	0.54	71 (5%)	28 21	34, 54, 89, 116	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	513	LEU	5.4
1	B	565	PHE	4.6
1	B	478	CYS	4.2
1	B	707	ASP	4.0
1	A	733	SER	3.5
1	B	654	LEU	3.4
1	A	563	ASP	3.4
1	A	746	GLY	3.4
1	A	732	PRO	3.0
1	B	660	LEU	3.0
1	B	547	THR	3.0
1	B	676	ASP	3.0
1	B	219	ASP	2.9
1	B	782	ALA	2.8
1	B	562	TRP	2.7
1	B	407	PRO	2.7
1	B	573	ASN	2.7
1	A	734	SER	2.7
1	B	572	GLU	2.6
1	B	610	ASP	2.6
1	B	507	PRO	2.6
1	B	475	ILE	2.6
1	A	668	ILE	2.6
1	B	493	ALA	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	453	LEU	2.6
1	B	661	SER	2.5
1	B	566	TYR	2.5
1	B	639	ILE	2.5
1	A	167	PRO	2.5
1	B	581	PRO	2.4
1	B	633	HIS	2.4
1	A	317	VAL	2.4
1	A	751	PHE	2.4
1	B	514	PHE	2.4
1	B	703	GLY	2.4
1	A	744	PHE	2.4
1	B	505	VAL	2.3
1	B	512	GLY	2.3
1	B	706	HIS	2.3
1	B	659	LYS	2.3
1	B	631	GLN	2.3
1	B	702	PHE	2.2
1	B	574	VAL	2.2
1	B	749	GLY	2.2
1	B	516	ASN	2.2
1	B	360	ILE	2.2
1	B	350	HIS	2.2
1	B	636	VAL	2.2
1	B	549	THR	2.2
1	B	635	THR	2.2
1	B	515	GLY	2.2
1	B	527	ALA	2.2
1	B	564	ASN	2.2
1	A	640	ASP	2.2
1	B	529	ASP	2.2
1	B	752	THR	2.2
1	B	658	GLY	2.1
1	B	545	LEU	2.1
1	B	372	VAL	2.1
1	B	773	LEU	2.1
1	A	615	THR	2.1
1	B	576	THR	2.1
1	A	574	VAL	2.0
1	B	471	PHE	2.0
1	B	704	THR	2.0
1	B	528	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	587	HIS	2.0
1	B	556	PRO	2.0
1	A	747	LEU	2.0
1	A	691	THR	2.0
1	B	492	ALA	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.