



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:29 AM GMT

PDB ID : 2QZA
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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

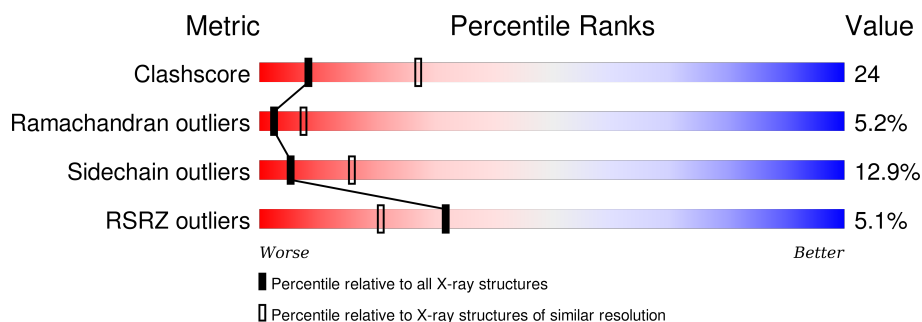
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 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	618	 3% 56% 36% 7% •
1	B	618	 7% 53% 36% 9% ••

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			

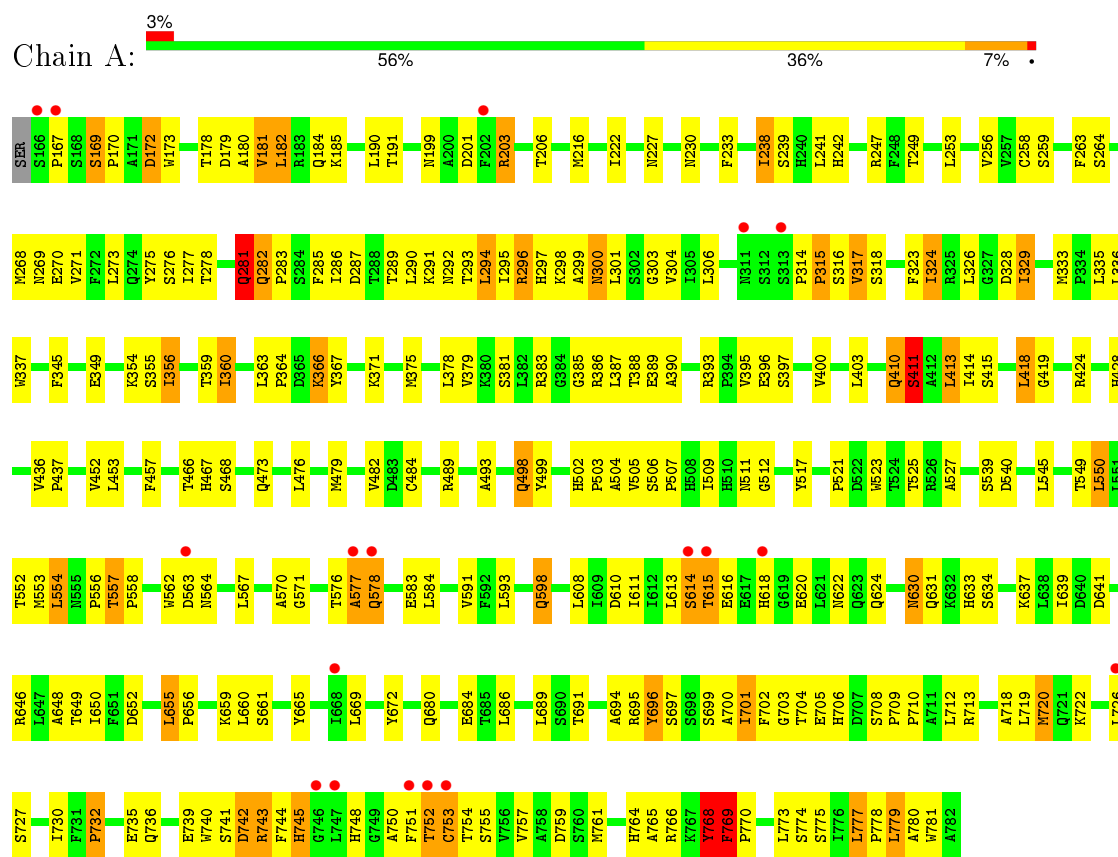
- Molecule 2 is water.

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

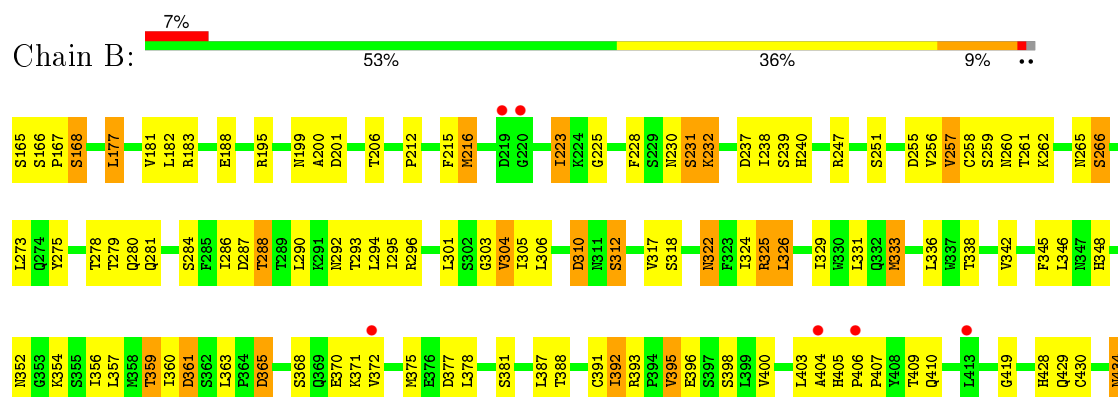
3 Residue-property plots

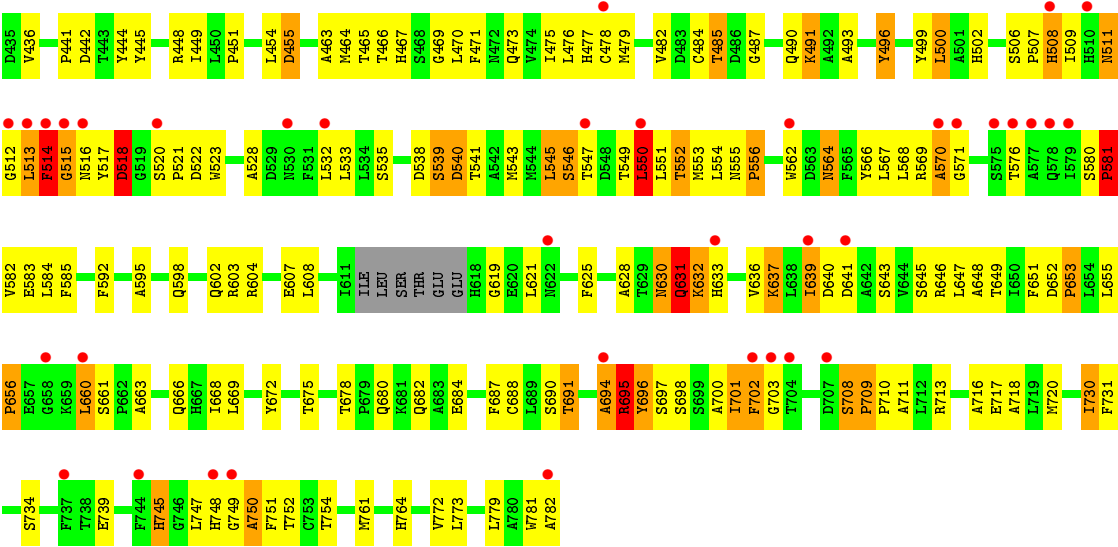
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according 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 45.99 – 2.70	Depositor EDS
% Data completeness (in resolution range)	97.0 (50.00-2.80) 94.4 (45.99-2.70)	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 0.270 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
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 , 20.0	EDS
Estimated twinning fraction	0.000 for l,k,-h 0.028 for h,-k,-l 0.020 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 38797 reflections	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, 0.375 respectively for untwinned datasets, and 0.333, 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	0.40	0/4859	0.51	1/6615 (0.0%)
1	B	0.39	0/4706	0.53	0/6410
All	All	0.40	0/9565	0.52	1/13025 (0.0%)

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

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	732	PRO	N-CA-CB	5.89	110.37	103.30

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
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

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Mol	Chain	Res	Type	Group
1	B	750	ALA	Peptide

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4747	0	4484	196	0
1	B	4599	0	4257	246	0
2	A	48	0	0	6	0
2	B	47	0	0	14	0
All	All	9441	0	8741	437	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 24.

All (437) 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: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:580:SER:HA	1:B:581:PRO:C	1.84	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
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:296:ARG:HH11	1:A:296:ARG:CG	1.86	0.87
1:A:271:VAL:H	1:A:293:THR:HG22	1.38	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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: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:496:TYR:O	1:B:500:LEU:HD23	1.79	0.83
1:B:709:PRO:HB2	1:B:710:PRO:C	2.01	0.81
1:A:281:GLN:O	1:A:282:GLN:HB2	1.77	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:B:695:ARG:C	1:B:697:SER:H	1.86	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:A:769:PHE:C	1:A:769:PHE:HD1	1.88	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:B:375:MSE:CE	1:B:403:LEU:HD21	2.18	0.73
1:A:765:ALA:HA	1:A:769:PHE:CE1	2.23	0.73
1:A:646:ARG:O	1:A:650:ILE:HG12	1.87	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
1:B:223:ILE:O	1:B:223:ILE:HG13	1.87	0.72
1:B:451:PRO:HA	1:B:454:LEU:HD23	1.72	0.72
1:B:539:SER:C	1:B:541:THR:H	1.93	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:A:769:PHE:C	1:A:769:PHE:CD1	2.62	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:631:GLN:O	1:B:632:LYS:HB2	1.93	0.68
1:B:464:MSE:HE3	1:B:499:TYR:CD1	2.29	0.68
1:A:695:ARG:CD	2:A:85:HOH:O	2.41	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:B:549:THR:C	1:B:551:LEU:H	1.96	0.68
1:A:660:LEU:HD11	1:A:719:LEU:HD23	1.77	0.67
1:B:709:PRO:CB	1:B:710:PRO:HA	2.24	0.67
1:A:720:MSE:HE1	1:A:740:TRP:CE3	2.29	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:511:ASN:CG	1:B:512:GLY:H	1.98	0.66
1:B:688:CYS:SG	1:B:773:LEU:HA	2.35	0.66
1:A:525:THR:HG22	1:A:527:ALA:H	1.60	0.66
1:B:543:MSE:HA	1:B:566:TYR:O	1.96	0.65
1:A:479:MSE:HE1	1:A:493:ALA:HA	1.78	0.65
1:A:298:LYS:HE3	1:A:354:LYS:HB3	1.77	0.65
1:B:310:ASP:OD2	1:B:312:SER:HB3	1.97	0.65
1:A:400:VAL:HG11	1:A:452:VAL:HG11	1.77	0.65
1:B:695:ARG:O	1:B:697:SER:N	2.30	0.65
1:B:406:PRO:HA	1:B:409:THR:HG22	1.77	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
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:B:231:SER:O	1:B:232:LYS:HB2	1.98	0.64
1:B:361:ASP:HA	1:B:371:LYS:HD3	1.80	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:372:VAL:C	2:B:4:HOH:O	2.36	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:LEU:HB2	1:B:329:ILE:HG12	1.80	0.64
1:A:701:ILE:HG22	1:A:702:PHE:N	2.13	0.64
1:A:413:LEU:H	1:A:413:LEU:HD12	1.63	0.63
1:B:709:PRO:CB	1:B:710:PRO:CA	2.76	0.63
1:A:764:HIS:ND1	1:A:764:HIS:O	2.32	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:NH1	1:A:296:ARG:CG	2.54	0.62
1:A:769:PHE:O	1:A:769:PHE:HD1	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:388:THR:C	1:A:390:ALA:H	2.01	0.61
1:A:570:ALA:N	1:A:571:GLY:CA	2.53	0.61
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:A:253:LEU:O	1:A:256:VAL:HB	2.00	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:B:695:ARG:C	1:B:697:SER:N	2.55	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
1:A:285:PHE:CE1	1:A:299:ALA:HB1	2.38	0.59
1:A:269:ASN:HD21	1:A:289:THR:HB	1.68	0.59
1:B:701:ILE:O	1:B:703:GLY:N	2.36	0.58
1:A:656:PRO:CD	1:A:661:SER:HB2	2.33	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:B:625:PHE:HD2	1:B:696:TYR:CE2	2.22	0.58
1:A:648:ALA:O	1:A:652:ASP:HB2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:547:THR:C	1:B:549:THR:H	2.07	0.58
1:B:690:SER:OG	1:B:761:MSE:HE1	2.04	0.58
1:A:768:TYR:O	1:A:769:PHE:CG	2.57	0.58
1:A:552:THR:O	1:A:556:PRO:HA	2.03	0.58
1:A:273:LEU:O	1:A:295:ILE:HA	2.04	0.57
1:B:359:THR:HG22	1:B:360:ILE:H	1.69	0.57
1:A:562:TRP:O	1:A:564:ASN:N	2.37	0.57
1:B:555:ASN:CG	1:B:555:ASN:O	2.40	0.57
1:A:301:LEU:HD22	1:A:304:VAL:HG21	1.85	0.57
1:B:375:MSE:HA	1:B:375:MSE:HE3	1.86	0.57
1:B:653:PRO:CB	1:B:656:PRO:HA	2.24	0.57
1:B:637:LYS:HD3	1:B:701:ILE:O	2.03	0.57
1:B:441:PRO:HG2	1:B:477:HIS:CD2	2.39	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:B:508:HIS:CD2	1:B:508:HIS:H	2.24	0.56
1:A:598:GLN:HG3	1:A:779:LEU:HB2	1.87	0.56
1:B:406:PRO:HA	1:B:409:THR:CG2	2.36	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:B:511:ASN:CG	1:B:512:GLY:N	2.59	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:B:553:MSE:HG3	1:B:592:PHE:CE2	2.41	0.55
1:B:506:SER:N	1:B:507:PRO:HD3	2.21	0.55
1:A:620:GLU:O	1:A:624:GLN:HG3	2.06	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:386:ARG:HD2	1:A:386:ARG:N	2.22	0.55
1:B:326:LEU:HB2	1:B:331:LEU:HD12	1.89	0.55
1:B:482:VAL:HG23	2:B:73:HOH:O	2.06	0.55
1:B:346:LEU:HB2	1:B:395:VAL:HG21	1.89	0.55
1:B:580:SER:CA	1:B:581:PRO:C	2.68	0.54
1:B:690:SER:HB2	1:B:716:ALA:O	2.07	0.54
1:A:766:ARG:HA	1:A:770:PRO:HB3	1.88	0.54
1:B:363:LEU:HD12	1:B:371:LYS:HG2	1.88	0.54
1:B:258:CYS:SG	1:B:275:TYR:CD2	3.01	0.54
1:A:410:GLN:O	1:A:410:GLN:CG	2.49	0.54
1:B:539:SER:C	1:B:541:THR:N	2.61	0.54
1:B:709:PRO:CD	1:B:710:PRO:HA	2.37	0.54
1:B:475:ILE:O	1:B:479:MSE:HG2	2.08	0.54
1:B:375:MSE:HE1	1:B:378:LEU:HD13	1.89	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:434:ASN:HD22	1:B:434:ASN:C	2.11	0.53
1:B:535:SER:HB3	1:B:538:ASP:O	2.08	0.53
1:B:604:ARG:HD3	1:B:672:TYR:HA	1.91	0.53
1:A:222:ILE:HD12	1:A:242:HIS:ND1	2.24	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:B:696:TYR:N	1:B:701:ILE:HD11	2.19	0.52
1:A:708:SER:OG	1:A:713:ARG:HD3	2.09	0.52
1:A:505:VAL:HG12	1:A:509:ILE:HD13	1.91	0.52
1:B:653:PRO:HB3	1:B:656:PRO:CA	2.27	0.52
1:B:359:THR:HG23	1:B:360:ILE:N	2.24	0.52
1:A:742:ASP:O	1:A:744:PHE:N	2.43	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:B:549:THR:C	1:B:551:LEU:N	2.63	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
1:A:634:SER:HB3	1:A:701:ILE:HA	1.92	0.51
1:B:322:ASN:ND2	1:B:322:ASN:H	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:B:317:VAL:HG12	1:B:318:SER:N	2.26	0.51
1:B:479:MSE:HE2	1:B:523:TRP:CD1	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:506:SER:N	1:B:507:PRO:CD	2.74	0.51
1:A:722:LYS:O	1:A:722:LYS:HG3	2.11	0.51
1:B:621:LEU:O	1:B:625:PHE:HD1	1.93	0.51
1:B:266:SER:O	1:B:288:THR:HB	2.11	0.51
1:A:751:PHE:HD2	1:A:752:THR:H	1.55	0.51
1:B:750:ALA:HB1	1:B:752:THR:HG23	1.92	0.50
1:B:663:ALA:O	1:B:666:GLN:N	2.44	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:513:LEU:O	1:B:514:PHE:CD1	2.63	0.50
1:B:465:THR:HG21	1:B:502:HIS:CD2	2.47	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:B:375:MSE:N	2:B:4:HOH:O	2.44	0.50
1:A:239:SER:HB3	1:A:259:SER:HB2	1.93	0.50
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:633:HIS:HB2	2:A:86:HOH:O	2.12	0.49
1:A:379:VAL:HG21	1:A:414:ILE:HG12	1.95	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:639:ILE:O	1:B:639:ILE:HG23	2.12	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: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:286:ILE:HA	1:B:303:GLY:HA3	1.95	0.49
1:A:170:PRO:HA	1:A:173:TRP:HD1	1.78	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:B:709:PRO:CG	1:B:710:PRO:HA	2.43	0.48
1:A:696:TYR:O	1:A:702:PHE:HB2	2.14	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:B:508:HIS:HD2	1:B:508:HIS:H	1.61	0.48
1:B:471:PHE:HE1	1:B:496:TYR:HD1	1.62	0.48
1:B:310:ASP:OD2	1:B:312:SER:N	2.45	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:262:LYS:HG2	1:B:284:SER:OG	2.13	0.48
1:A:768:TYR:O	1:A:769:PHE:CD1	2.67	0.48
1:A:631:GLN:HA	1:A:780:ALA:CB	2.41	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:A:317:VAL:HG13	1:A:318:SER:N	2.29	0.48
1:A:227:ASN:OD1	1:A:247:ARG:HB3	2.13	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:751:PHE:C	1:A:753:CYS:N	2.67	0.48
1:B:200:ALA:O	1:B:231:SER:O	2.31	0.47
1:A:466:THR:CG2	1:B:201:ASP:HB2	2.43	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: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:333:MSE:HE1	1:B:378:LEU:HG	1.96	0.47
1:B:691:THR:HA	1:B:694:ALA:HB2	1.96	0.47
1:B:649:THR:HA	1:B:652:ASP:HB2	1.97	0.47
1:A:521:PRO:HG2	1:A:523:TRP:CZ2	2.50	0.47
1:B:388:THR:O	1:B:392:ILE:HG22	2.14	0.47
1:A:709:PRO:HA	1:A:710:PRO:HD2	1.82	0.46
1:A:557:THR:O	1:A:558:PRO:C	2.52	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:514:PHE:CG	1:B:515:GLY:N	2.82	0.46
1:A:751:PHE:C	1:A:753:CYS:H	2.18	0.46
1:A:424:ARG:HD2	2:A:6:HOH:O	2.16	0.46
1:B:585:PHE:CD2	1:B:585:PHE:N	2.82	0.46
1:B:436:VAL:HG13	1:B:779:LEU:HD21	1.97	0.46
1:B:387:LEU:HD22	1:B:391:CYS:SG	2.56	0.46
1:A:506:SER:N	1:A:507:PRO:HD2	2.31	0.46
1:A:199:ASN:HA	1:A:230:ASN:O	2.15	0.46
1:A:304:VAL:HG12	1:A:306:LEU:HD12	1.99	0.45
1:A:276:SER:OG	1:A:278:THR:HG22	2.15	0.45
1:B:709:PRO:HB2	1:B:711:ALA:N	2.30	0.45
1:B:691:THR:HA	1:B:694:ALA:CB	2.46	0.45
1:B:564:ASN:HA	1:B:564:ASN:HD22	1.56	0.45
1:A:411:SER:HB2	1:A:414:ILE:HB	1.99	0.45
1:A:238:ILE:HG12	1:A:238:ILE:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:669:LEU:HD22	1:B:675:THR:HA	1.98	0.45
1:A:479:MSE:CE	1:A:493:ALA:HA	2.44	0.45
1:B:405:HIS:C	1:B:407:PRO:HD2	2.37	0.45
1:A:424:ARG:O	1:A:428:HIS:CD2	2.69	0.45
1:B:552:THR:C	1:B:554:LEU:H	2.18	0.45
1:B:206:THR:HA	1:B:237:ASP:HB3	1.99	0.45
1:A:502:HIS:CD2	1:A:504:ALA:HB3	2.52	0.45
1:A:238:ILE:HB	1:A:241:LEU:HD12	1.98	0.45
1:B:567:LEU:HD21	1:B:584:LEU:HD21	1.98	0.45
1:B:696:TYR:HD1	1:B:701:ILE:CD1	2.29	0.45
1:A:502:HIS:HD2	1:A:504:ALA:HB3	1.82	0.45
1:B:237:ASP:HA	1:B:257:VAL:HG13	1.98	0.45
1:A:614:SER:O	1:A:616:GLU:N	2.50	0.45
1:A:660:LEU:HG	1:A:718:ALA:HB1	1.98	0.44
1:B:697:SER:HB2	1:B:754:THR:HG21	2.00	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:A:476:LEU:HD22	1:A:550:LEU:CD1	2.48	0.44
1:B:476:LEU:HD12	1:B:476:LEU:C	2.37	0.44
1:B:648:ALA:C	2:B:59:HOH:O	2.56	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:N	1:B:410:GLN:OE1	2.47	0.44
1:B:464:MSE:CE	1:B:499:TYR:HD1	2.22	0.44
1:A:764:HIS:CG	1:A:764:HIS:O	2.67	0.44
1:B:231:SER:HB2	1:B:251:SER:OG	2.17	0.44
1:A:388:THR:C	1:A:390:ALA:N	2.69	0.44
1:B:469:GLY:O	1:B:473:GLN:CG	2.61	0.44
1:B:393:ARG:C	1:B:395:VAL:H	2.21	0.44
1:A:180:ALA:O	1:A:190:LEU:HD11	2.18	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:314:PRO:O	1:A:315:PRO:C	2.56	0.43
1:B:569:ARG:O	1:B:570:ALA:HB2	2.17	0.43
1:A:453:LEU:O	1:A:457:PHE:HD1	2.01	0.43
1:B:166:SER:CB	1:B:167:PRO:HA	2.40	0.43
1:A:512:GLY:HA2	1:A:517:TYR:HD1	1.83	0.43
1:B:333:MSE:HE2	1:B:378:LEU:HA	2.01	0.43
1:B:273:LEU:HB3	1:B:295:ILE:HG22	2.00	0.43
1:B:632:LYS:O	1:B:633:HIS:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:598:GLN:HE21	1:B:602:GLN:HB2	1.84	0.43
1:B:490:GLN:HA	1:B:493:ALA:HB3	2.01	0.43
1:B:430:CYS:HB3	1:B:467:HIS:CD2	2.53	0.43
1:A:466:THR:HG21	1:B:199:ASN:O	2.19	0.43
1:A:201:ASP:OD2	1:A:203:ARG:CD	2.67	0.43
1:B:595:ALA:O	1:B:598:GLN:HB3	2.18	0.43
1:A:181:VAL:HA	1:A:184:GLN:HB3	2.01	0.43
1:B:455:ASP:HB2	2:B:46:HOH:O	2.18	0.43
1:A:395:VAL:O	1:A:396:GLU:C	2.57	0.43
1:B:365:ASP:OD2	1:B:365:ASP:N	2.47	0.43
1:B:301:LEU:HB3	1:B:304:VAL:HG21	2.01	0.43
1:B:547:THR:C	1:B:549:THR:N	2.72	0.43
1:A:553:MSE:HE3	1:A:562:TRP:HE3	1.84	0.43
1:A:385:GLY:C	1:A:386:ARG:HD2	2.39	0.43
1:A:735:GLU:O	1:A:739:GLU:HB2	2.19	0.43
1:A:345:PHE:O	1:A:355:SER:HB2	2.18	0.43
1:B:628:ALA:C	1:B:630:ASN:H	2.22	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
1:A:364:PRO:HG2	1:A:367:TYR:CD1	2.54	0.42
1:A:720:MSE:CE	1:A:761:MSE:SE	3.13	0.42
1:A:324:ILE:H	1:A:324:ILE:HD13	1.85	0.42
1:B:695:ARG:HA	1:B:698:SER:CB	2.50	0.42
1:A:656:PRO:HD3	1:A:661:SER:HB2	2.01	0.42
1:A:610:ASP:HA	1:A:622:ASN:HD21	1.84	0.42
1:B:463:ALA:HA	1:B:466:THR:OG1	2.20	0.42
1:A:511:ASN:H	1:A:511:ASN:ND2	2.17	0.42
1:A:375:MSE:HE2	1:A:403:LEU:CD2	2.48	0.42
1:B:608:LEU:CD1	1:B:668:ILE:HD13	2.49	0.42
1:B:603:ARG:O	1:B:607:GLU:HG3	2.18	0.42
1:B:356:ILE:O	1:B:359:THR:HG22	2.17	0.42
1:A:742:ASP:O	1:A:743:ARG:C	2.57	0.42
1:A:502:HIS:HD2	1:A:504:ALA:CB	2.33	0.42
1:B:266:SER:H	1:B:288:THR:HB	1.84	0.42
1:B:500:LEU:HD13	1:B:509:ILE:HG13	2.01	0.42
1:B:199:ASN:ND2	1:B:230:ASN:HD22	2.17	0.42
1:B:490:GLN:HG2	1:B:490:GLN:H	1.55	0.42
1:B:444:TYR:CE2	1:B:448:ARG:HD2	2.55	0.42
1:A:479:MSE:HE1	1:A:493:ALA:CA	2.49	0.42
1:A:233:PHE:HB2	1:A:253:LEU:HD23	2.02	0.42
1:B:165:SER:HB2	2:B:14:HOH:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:523:TRP:HA	1:B:523:TRP:CE3	2.53	0.42
1:B:256:VAL:O	1:B:275:TYR:HB2	2.19	0.42
1:B:698:SER:HA	1:B:754:THR:HG22	2.01	0.42
1:A:333:MSE:CE	1:A:381:SER:HB3	2.47	0.42
1:A:285:PHE:HB2	1:A:304:VAL:HG23	2.02	0.41
1:B:543:MSE:HE2	1:B:545:LEU:HD23	2.02	0.41
1:A:300:ASN:C	1:A:300:ASN:HD22	2.24	0.41
1:A:300:ASN:C	1:A:300:ASN:ND2	2.72	0.41
1:A:608:LEU:HA	1:A:611:ILE:HD12	2.02	0.41
1:B:239:SER:CB	1:B:259:SER:HB3	2.50	0.41
1:B:528:ALA:O	1:B:546:SER:HA	2.20	0.41
1:A:655:LEU:CB	1:A:659:LYS:O	2.68	0.41
1:A:294:LEU:HD21	1:A:323:PHE:CE2	2.55	0.41
1:B:520:SER:HA	1:B:521:PRO:HA	1.79	0.41
1:B:641:ASP:C	1:B:643:SER:H	2.24	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:349:GLU:OE1	1:A:397:SER:OG	2.37	0.41
1:B:630:ASN:O	1:B:631:GLN:CB	2.68	0.41
1:B:694:ALA:C	1:B:695:ARG:O	2.58	0.41
1:A:263:PHE:CG	1:A:268:MSE:SE	3.23	0.41
1:B:487:GLY:O	1:B:491:LYS:HB2	2.20	0.41
1:A:436:VAL:HA	1:A:437:PRO:HD3	1.87	0.41
1:B:764:HIS:CD2	1:B:764:HIS:C	2.94	0.41
1:A:268:MSE:CE	1:A:273:LEU:HD11	2.50	0.41
1:B:216:MSE:H	1:B:216:MSE:HG2	1.60	0.41
1:A:649:THR:C	1:A:650:ILE:HD13	2.40	0.41
1:A:697:SER:HB3	1:A:712:LEU:HB3	2.02	0.41
1:A:694:ALA:HB2	1:A:761:MSE:HE1	2.03	0.41
1:B:549:THR:OG1	1:B:550:LEU:N	2.54	0.41
1:B:406:PRO:N	1:B:407:PRO:CD	2.83	0.41
1:B:322:ASN:O	1:B:333:MSE:HB2	2.21	0.41
1:B:275:TYR:O	1:B:296:ARG:NH2	2.53	0.41
1:B:698:SER:C	1:B:700:ALA:H	2.24	0.41
1:A:741:SER:O	1:A:745:HIS:CD2	2.74	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:B:471:PHE:HE1	1:B:496:TYR:CD1	2.39	0.40
1:B:761:MSE:HB3	1:B:761:MSE:HE2	2.01	0.40
1:B:465:THR:HG21	1:B:502:HIS:NE2	2.37	0.40
1:A:704:THR:O	1:A:706:HIS:N	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:375:MSE:CA	1:B:375:MSE:HE3	2.50	0.40
1:B:698:SER:C	1:B:700:ALA:N	2.74	0.40
1:B:404:ALA:C	1:B:405:HIS:ND1	2.75	0.40
1:A:699:SER:O	1:A:700:ALA:HB3	2.21	0.40
1:A:686:LEU:HA	1:A:689:LEU:HB2	2.04	0.40
1:A:291:LYS:HG2	1:A:328:ASP:HB2	2.02	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:614:SER:O	1:A:615:THR:C	2.60	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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%)	3	8
1	B	608/618 (98%)	484 (80%)	92 (15%)	32 (5%)	2	7
All	All	1223/1236 (99%)	978 (80%)	182 (15%)	63 (5%)	2	7

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

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Mol	Chain	Res	Type
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
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

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Mol	Chain	Res	Type
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%)	446 (88%)	62 (12%)	6	18
1	B	473/527 (90%)	408 (86%)	65 (14%)	4	13
All	All	981/1054 (93%)	854 (87%)	127 (13%)	5	16

All (127) 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	216	MSE
1	A	238	ILE

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Mol	Chain	Res	Type
1	A	277	ILE
1	A	281	GLN
1	A	294	LEU
1	A	296	ARG
1	A	300	ASN
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	378	LEU
1	A	383	ARG
1	A	393	ARG
1	A	410	GLN
1	A	411	SER
1	A	415	SER
1	A	418	LEU
1	A	468	SER
1	A	482	VAL
1	A	498	GLN
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	637	LYS
1	A	639	ILE
1	A	641	ASP
1	A	655	LEU
1	A	672	TYR
1	A	691	THR
1	A	696	TYR
1	A	720	MSE
1	A	736	GLN

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Mol	Chain	Res	Type
1	A	745	HIS
1	A	748	HIS
1	A	753	CYS
1	A	754	THR
1	A	768	TYR
1	A	769	PHE
1	A	774	SER
1	A	777	LEU
1	A	779	LEU
1	B	177	LEU
1	B	216	MSE
1	B	223	ILE
1	B	231	SER
1	B	238	ILE
1	B	247	ARG
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	325	ARG
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	429	GLN
1	B	434	ASN
1	B	455	ASP

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Mol	Chain	Res	Type
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	513	LEU
1	B	514	PHE
1	B	518	ASP
1	B	532	LEU
1	B	545	LEU
1	B	546	SER
1	B	550	LEU
1	B	552	THR
1	B	564	ASN
1	B	583	GLU
1	B	630	ASN
1	B	632	LYS
1	B	636	VAL
1	B	637	LYS
1	B	660	LEU
1	B	678	THR
1	B	682	GLN
1	B	691	THR
1	B	695	ARG
1	B	717	GLU
1	B	730	ILE
1	B	734	SER
1	B	739	GLU
1	B	745	HIS
1	B	747	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	269	ASN
1	A	300	ASN
1	A	490	GLN
1	A	502	HIS
1	A	511	ASN
1	A	587	HIS

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Mol	Chain	Res	Type
1	A	598	GLN
1	A	622	ASN
1	A	736	GLN
1	B	199	ASN
1	B	240	HIS
1	B	282	GLN
1	B	300	ASN
1	B	322	ASN
1	B	340	ASN
1	B	428	HIS
1	B	431	GLN
1	B	446	GLN
1	B	498	GLN
1	B	508	HIS
1	B	564	ASN
1	B	633	HIS
1	B	673	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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%)	0.36	18 (2%) 54 41	34, 47, 85, 97	0
1	B	600/618 (97%)	0.61	43 (7%) 18 10	41, 58, 94, 116	0
All	All	1205/1236 (97%)	0.48	61 (5%) 32 21	34, 54, 89, 116	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	746	GLY	7.2
1	A	167	PRO	6.0
1	B	570	ALA	5.3
1	B	641	ASP	5.2
1	A	166	SER	4.9
1	B	219	ASP	4.4
1	B	660	LEU	4.1
1	B	707	ASP	4.1
1	B	510	HIS	3.9
1	B	478	CYS	3.8
1	B	702	PHE	3.8
1	B	577	ALA	3.6
1	B	514	PHE	3.6
1	B	513	LEU	3.6
1	B	571	GLY	3.4
1	B	562	TRP	3.3
1	B	515	GLY	3.3
1	A	615	THR	3.3
1	B	512	GLY	3.2
1	B	547	THR	3.2
1	A	747	LEU	3.2
1	A	563	ASP	3.0
1	B	508	HIS	3.0
1	B	516	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	575	SER	2.9
1	B	704	THR	2.9
1	B	744	PHE	2.9
1	A	614	SER	2.9
1	A	578	GLN	2.8
1	A	618	HIS	2.7
1	B	782	ALA	2.6
1	B	737	PHE	2.6
1	A	751	PHE	2.5
1	B	749	GLY	2.5
1	A	311	ASN	2.5
1	B	622	ASN	2.5
1	B	639	ILE	2.5
1	B	703	GLY	2.4
1	A	753	CYS	2.4
1	A	726	LEU	2.4
1	B	530	ASN	2.4
1	B	658	GLY	2.4
1	B	550	LEU	2.3
1	B	532	LEU	2.3
1	B	578	GLN	2.2
1	B	404	ALA	2.2
1	B	406	PRO	2.2
1	B	520	SER	2.2
1	A	668	ILE	2.1
1	B	748	HIS	2.1
1	A	202	PHE	2.1
1	A	313	SER	2.1
1	B	220	GLY	2.1
1	B	694	ALA	2.1
1	A	752	THR	2.1
1	A	577	ALA	2.1
1	B	576	THR	2.0
1	B	372	VAL	2.0
1	B	579	ILE	2.0
1	B	633	HIS	2.0
1	B	413	LEU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.