

Full wwPDB X-ray Structure Validation Report (i)

Sep 3, 2023 – 09:03 PM EDT

PDB ID	:	3SQV
Title	:	Crystal Structure of E. coli O157:H7 E3 ubiquitin ligase, NleL, with a human
		E2, UbcH7
Authors	:	Lin, D.Y.; Chen, J.
Deposited on	:	2011-07-06
Resolution	:	3.30 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 (i) 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 (1)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R _{free}	130704	1149 (3.34-3.26)
Clashscore	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 <=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	А	616	% 57%	37%	5% •					
1	В	616	3% 55%	40%						
2	С	156	^{3%} 76%	18%	6%					
2	D	156	3% 74%	22%						

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard



residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	В	9	-	-	-	Х
4	GOL	С	155	-	-	-	Х



2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 10987 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	А	606	Total 4467	C 2828	N 731	O 873	S 35	0	0	0
1	В	606	Total 4450	C 2808	N 731	O 875	S 36	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	167	SER	-	expression tag	UNP Q8X5G6
А	168	ASN	-	expression tag	UNP Q8X5G6
А	169	ALA	-	expression tag	UNP Q8X5G6
В	167	SER	-	expression tag	UNP Q8X5G6
В	168	ASN	-	expression tag	UNP Q8X5G6
В	169	ALA	-	expression tag	UNP Q8X5G6

• Molecule 2 is a protein called Ubiquitin-conjugating enzyme E2 L3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
0	\hat{c}	1.47	Total	С	Ν	0	S	0	0	0
	U	147	959	607	173	178	1	0		
0	Л	159	Total	С	Ν	0	S	0	0	0
	2 D	1.02	1034	657	177	195	5	0		U

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
С	-1	GLY	-	expression tag	UNP P68036
С	0	SER	-	expression tag	UNP P68036
D	-1	GLY	-	expression tag	UNP P68036
D	0	SER	-	expression tag	UNP P68036

• Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	А	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0
3	В	1	$\begin{array}{ccc} \text{Total} & \text{O} & \text{S} \\ 5 & 4 & 1 \end{array}$	0	0





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
4	А	1	$\begin{array}{ccc} \text{Total} \text{C} \text{O} \\ 6 3 3 \end{array}$	0	0
4	С	1	$\begin{array}{ccc} \text{Total} & \text{C} & \text{O} \\ 6 & 3 & 3 \end{array}$	0	0

• Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	А	8	Total O 8 8	0	0
5	В	6	Total O 6 6	0	0



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: secreted effector protein











• Molecule 2: Ubiquitin-conjugating enzyme E2 L3





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	302.31Å 72.01Å 125.67Å	Deperitor
a, b, c, α , β , γ	90.00° 109.22° 90.00°	Depositor
Bosolution(A)	48.08 - 3.30	Depositor
Resolution (A)	48.08 - 3.28	EDS
% Data completeness	99.0 (48.08-3.30)	Depositor
(in resolution range)	98.3 (48.08-3.28)	EDS
R_{merge}	(Not available)	Depositor
R _{sym}	0.14	Depositor
$< I/\sigma(I) > 1$	1.02 (at 3.25 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
D D.	0.266 , 0.298	Depositor
$\mathbf{n}, \mathbf{n}_{free}$	0.250 , 0.289	DCC
R_{free} test set	1935 reflections (4.99%)	wwPDB-VP
Wilson B-factor $(Å^2)$	95.2	Xtriage
Anisotropy	0.426	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.27, 99.4	EDS
L-test for $twinning^2$	$ < L > = 0.45, < L^2 > = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	10987	wwPDB-VP
Average B, all atoms $(Å^2)$	128.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 11.68% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, $\mathrm{SO4}$

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	
	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	А	0.32	0/4569	0.50	3/6223~(0.0%)
1	В	0.32	0/4550	0.51	3/6197~(0.0%)
2	С	0.23	0/983	0.42	0/1358
2	D	0.25	0/1063	0.42	0/1465
All	All	0.31	0/11165	0.49	6/15243~(0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	А	713	ARG	NE-CZ-NH1	-11.21	114.70	120.30
1	В	713	ARG	NE-CZ-NH2	-10.97	114.81	120.30
1	А	713	ARG	NE-CZ-NH2	10.63	125.62	120.30
1	В	713	ARG	NE-CZ-NH1	10.23	125.42	120.30
1	А	713	ARG	CD-NE-CZ	5.20	130.88	123.60
1	В	713	ARG	CD-NE-CZ	5.04	130.66	123.60

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	А	4467	0	3905	228	0



Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	В	4450	0	3859	234	0
2	С	959	0	738	19	0
2	D	1034	0	821	28	0
3	А	30	0	0	0	0
3	В	15	0	0	1	0
4	А	12	0	16	0	0
4	С	6	0	8	0	0
5	А	8	0	0	0	0
5	В	6	0	0	1	0
All	All	10987	0	9347	497	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 (497) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:208:LEU:HD23	1:B:211:LEU:HD11	1.51	0.93
1:A:208:LEU:HD23	1:A:211:LEU:HD11	1.53	0.89
1:B:399:ARG:HG3	1:B:402:VAL:HB	1.55	0.88
1:B:475:ILE:O	1:B:479:MET:HG3	1.74	0.87
1:A:475:ILE:O	1:A:479:MET:HG3	1.75	0.86
1:A:398:PHE:HB2	1:B:558:SER:HB2	1.59	0.82
1:A:766:LYS:O	1:A:770:PRO:HG3	1.80	0.81
1:A:413:HIS:CD2	1:A:414:PRO:HA	2.17	0.80
1:B:766:LYS:O	1:B:770:PRO:HG3	1.83	0.79
1:A:221:VAL:HB	1:A:223:PHE:HE2	1.48	0.79
1:A:711:ILE:HG23	1:A:712:LEU:HD22	1.65	0.78
1:B:413:HIS:CD2	1:B:414:PRO:HA	2.17	0.78
1:B:711:ILE:HG23	1:B:712:LEU:HD22	1.66	0.77
1:A:479:MET:HE1	1:A:550:LEU:HD13	1.65	0.77
1:A:629:LEU:O	1:A:629:LEU:HD12	1.87	0.74
1:B:607:PHE:HD2	1:B:776:TYR:HE1	1.36	0.74
1:A:607:PHE:HD2	1:A:776:TYR:HE1	1.33	0.73
1:B:402:VAL:O	1:B:406:LEU:HD22	1.87	0.73
1:B:554:VAL:O	1:B:557:LEU:HB2	1.89	0.73
1:B:398:PHE:CE2	1:B:400:PRO:HB3	2.25	0.72
1:A:554:VAL:O	1:A:557:LEU:HB2	1.90	0.72
2:D:6:ARG:HH11	2:D:62:PRO:HG3	1.54	0.72
1:B:616:ILE:HD11	1:B:621:LEU:HB3	1.70	0.72
1:A:564:ASN:HD22	1:A:566:MET:HG3	1.54	0.71



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:401:TYR:O	1:A:405:SER:HB2	1.91	0.71
1:B:305:THR:HG23	1:B:321:GLY:HA3	1.72	0.71
1:A:398:PHE:CE2	1:A:400:PRO:HB3	2.25	0.71
1:A:564:ASN:ND2	1:A:566:MET:HG3	2.06	0.71
2:D:76:HIS:HE1	2:D:112:VAL:HA	1.55	0.71
1:B:401:TYR:O	1:B:405:SER:HB2	1.90	0.71
1:A:402:VAL:O	1:A:406:LEU:HD22	1.90	0.71
1:B:693:PHE:HA	1:B:696:TYR:HD2	1.56	0.71
1:A:693:PHE:HA	1:A:696:TYR:HD2	1.55	0.70
1:B:564:ASN:HD22	1:B:566:MET:HG3	1.55	0.70
1:A:253:LEU:O	1:A:256:CYS:HB2	1.91	0.70
1:B:607:PHE:CD2	1:B:776:TYR:HE1	2.10	0.70
1:B:607:PHE:HD2	1:B:776:TYR:CE1	2.10	0.70
1:B:564:ASN:ND2	1:B:566:MET:HG3	2.07	0.69
1:A:320:LEU:HD23	1:A:339:CYS:SG	2.33	0.69
1:A:594:ILE:HD13	1:A:594:ILE:H	1.58	0.69
2:C:76:HIS:HE1	2:C:112:VAL:HA	1.56	0.69
1:A:305:THR:HG23	1:A:321:GLY:HA3	1.73	0.69
1:A:218:LEU:O	1:A:221:VAL:HG23	1.93	0.69
1:B:629:LEU:HD12	1:B:629:LEU:O	1.93	0.68
1:B:724:TYR:HE2	1:B:728:PRO:HB3	1.58	0.68
1:A:607:PHE:CD2	1:A:776:TYR:HE1	2.11	0.67
1:A:607:PHE:HD2	1:A:776:TYR:CE1	2.11	0.67
1:A:724:TYR:HE2	1:A:728:PRO:HB3	1.59	0.67
1:B:594:ILE:HD13	1:B:594:ILE:H	1.59	0.67
2:C:63:PHE:O	2:C:64:LYS:HD2	1.94	0.67
1:B:416:LEU:HA	1:B:422:GLN:NE2	2.10	0.66
2:C:76:HIS:CD2	2:C:77:PRO:HD2	2.30	0.66
1:B:724:TYR:CE2	1:B:728:PRO:HB3	2.31	0.66
1:A:526:ASP:OD2	1:A:529:ASP:HA	1.95	0.65
2:D:51:PHE:HZ	2:D:144:THR:HG23	1.60	0.65
2:D:76:HIS:CD2	2:D:77:PRO:HD2	2.30	0.65
1:A:724:TYR:CE2	1:A:728:PRO:HB3	2.32	0.65
1:B:253:LEU:O	1:B:256:CYS:HB2	1.96	0.65
1:A:597:ILE:N	1:A:598:PRO:HD2	2.12	0.65
1:B:516:CYS:HB2	2:D:9:LYS:HE3	1.77	0.65
1:A:257:ASN:C	1:A:257:ASN:HD22	1.99	0.65
2:D:55:ILE:HD11	2:D:57:PHE:CE1	2.32	0.65
1:A:307:ALA:O	1:A:339:CYS:HB2	1.97	0.65
1:A:673:VAL:HG12	1:A:674:LEU:HD23	1.77	0.65
1:B:479:MET:HE1	1:B:550:LEU:HD13	1.79	0.65



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:416:LEU:HA	1:A:422:GLN:NE2	2.13	0.64
1:B:353:VAL:HG13	1:B:364:ILE:HG22	1.78	0.64
1:B:438:SER:HA	1:B:470:TYR:CE1	2.33	0.64
1:B:597:ILE:N	1:B:598:PRO:HD2	2.12	0.64
1:B:257:ASN:C	1:B:257:ASN:HD22	2.01	0.64
1:A:438:SER:HA	1:A:470:TYR:CE1	2.33	0.63
1:B:522:PRO:HG2	1:B:524:TRP:HE1	1.63	0.63
1:A:674:LEU:CD2	1:A:685:ILE:HD12	2.29	0.62
1:A:651:TRP:HA	1:A:654:PHE:HD2	1.63	0.62
1:A:654:PHE:HD1	1:A:664:HIS:CE1	2.17	0.62
1:A:680:ARG:O	1:A:684:GLU:HG3	1.98	0.62
1:B:320:LEU:HD23	1:B:339:CYS:SG	2.39	0.62
1:A:654:PHE:CD1	1:A:664:HIS:CE1	2.88	0.62
1:A:353:VAL:HG13	1:A:364:ILE:HG22	1.82	0.62
1:B:651:TRP:HA	1:B:654:PHE:HD2	1.64	0.62
1:B:307:ALA:O	1:B:339:CYS:HB2	2.00	0.61
1:A:271:LEU:H	1:A:271:LEU:HD12	1.65	0.61
1:B:505:TYR:N	1:B:506:PRO:HD2	2.15	0.61
1:B:271:LEU:HD12	1:B:271:LEU:H	1.65	0.61
2:C:70:PHE:HD2	2:C:79:ILE:HG21	1.65	0.61
1:B:331:SER:CB	1:B:389:LYS:NZ	2.63	0.61
1:B:625:PHE:HE2	1:B:651:TRP:HH2	1.48	0.61
1:B:654:PHE:HD1	1:B:664:HIS:CE1	2.19	0.61
1:A:481:GLY:HA3	1:A:491:PHE:CD2	2.35	0.61
1:B:654:PHE:CD1	1:B:664:HIS:CE1	2.89	0.60
2:C:70:PHE:HE2	2:C:79:ILE:HD13	1.66	0.60
1:A:505:TYR:N	1:A:506:PRO:HD2	2.15	0.60
1:A:594:ILE:HD13	1:A:594:ILE:N	2.15	0.60
1:A:309:ILE:O	1:A:341:ILE:HA	2.02	0.60
2:C:70:PHE:CE2	2:C:79:ILE:HD13	2.37	0.59
1:A:529:ASP:HB2	1:A:550:LEU:HB3	1.84	0.59
1:B:404:MET:O	1:B:408:ASP:OD2	2.20	0.59
1:A:251:SER:O	1:A:270:ALA:HB1	2.03	0.59
1:A:232:ASP:OD1	1:A:234:ARG:HG2	2.03	0.59
1:A:513:PHE:HB2	1:A:547:MET:HE1	1.83	0.59
1:A:398:PHE:O	1:A:399:ARG:C	2.41	0.59
1:A:565:TRP:HB3	1:A:588:PHE:CE2	2.37	0.59
1:B:387:ILE:HG23	1:B:424:TRP:CE2	2.39	0.58
1:B:594:ILE:HD13	1:B:594:ILE:N	2.17	0.58
1:B:171:GLN:N	1:B:199:GLU:O	2.36	0.58
1:B:244:GLU:O	1:B:245:ASN:HB2	2.03	0.58



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:A:529:ASP:CB	1:A:550:LEU:HD23	2.32	0.58
1:A:769:PHE:N	1:A:769:PHE:CD1	2.67	0.58
1:B:263:LEU:HB3	1:B:266:CYS:SG	2.44	0.58
1:A:383:ALA:HB2	1:A:415:TYR:HE1	1.69	0.58
1:B:565:TRP:HB3	1:B:588:PHE:CE2	2.39	0.58
1:A:188:LEU:O	1:A:192:ARG:HD2	2.04	0.57
1:B:232:ASP:OD1	1:B:234:ARG:HG2	2.04	0.57
1:B:522:PRO:HG2	1:B:524:TRP:NE1	2.19	0.57
1:B:454:LEU:HA	1:B:487:MET:HE1	1.86	0.57
1:B:652:ASN:N	1:B:653:PRO:HD2	2.19	0.57
1:A:616:ILE:HD11	1:A:621:LEU:HB3	1.86	0.57
1:B:529:ASP:CB	1:B:550:LEU:HD23	2.34	0.57
1:B:587:LEU:HD11	1:B:592:PHE:HE2	1.69	0.57
1:A:263:LEU:HB3	1:A:266:CYS:SG	2.44	0.57
1:B:243:LEU:N	1:B:243:LEU:HD12	2.20	0.57
1:B:779:VAL:HG12	1:B:782:ARG:CZ	2.34	0.57
2:C:101:THR:O	2:C:104:VAL:HG12	2.04	0.57
1:A:433:PHE:HD2	1:A:456:ALA:HA	1.70	0.57
1:B:398:PHE:O	1:B:399:ARG:C	2.41	0.57
1:B:607:PHE:HB2	1:B:776:TYR:CE1	2.39	0.57
1:B:383:ALA:HB2	1:B:415:TYR:HE1	1.69	0.57
1:B:680:ARG:O	1:B:684:GLU:HG3	2.04	0.57
1:A:213:LEU:HD12	1:A:216:LEU:CD1	2.35	0.56
1:A:479:MET:CE	1:A:550:LEU:HD13	2.33	0.56
1:A:652:ASN:N	1:A:653:PRO:HD2	2.19	0.56
1:A:221:VAL:HB	1:A:223:PHE:CE2	2.35	0.56
1:A:386:LEU:O	1:A:389:LYS:HB2	2.05	0.56
1:A:387:ILE:HG23	1:A:424:TRP:CE2	2.40	0.56
1:A:626:ILE:HA	1:A:629:LEU:HD23	1.86	0.56
1:A:779:VAL:HG12	1:A:782:ARG:CZ	2.35	0.56
1:A:298:ILE:HD12	1:B:298:ILE:HD12	1.86	0.56
1:A:472:SER:CB	1:A:594:ILE:HD12	2.36	0.56
2:D:101:THR:O	2:D:104:VAL:HG12	2.05	0.56
1:B:588:PHE:O	1:B:593:PRO:HA	2.06	0.56
1:A:211:LEU:HD23	1:A:211:LEU:H	1.71	0.56
1:A:243:LEU:HD23	1:A:248:PHE:HZ	1.71	0.56
1:A:587:LEU:HD11	1:A:592:PHE:HE2	1.71	0.56
1:B:529:ASP:HB2	1:B:550:LEU:HB3	1.87	0.56
1:A:558:SER:HB2	1:B:398:PHE:HB2	1.86	0.55
1:A:654:PHE:CD1	1:A:664:HIS:HE1	2.23	0.55
1:B:309:ILE:O	1:B:341:ILE:HA	2.06	0.55



	A i a	Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:331:SER:CB	1:B:389:LYS:HZ3	2.18	0.55
1:A:453:LEU:HD22	1:A:484:ARG:HE	1.71	0.55
1:B:243:LEU:HD23	1:B:248:PHE:HZ	1.72	0.55
1:B:695:LYS:HD3	1:B:781:TRP:CE3	2.42	0.55
1:A:695:LYS:HD3	1:A:781:TRP:CE3	2.41	0.55
1:B:326:LEU:O	1:B:381:ARG:HD3	2.06	0.55
1:A:472:SER:HB3	1:A:594:ILE:HD12	1.89	0.55
1:B:211:LEU:HD23	1:B:211:LEU:H	1.71	0.55
1:B:213:LEU:HD12	1:B:216:LEU:CD1	2.37	0.55
1:A:684:GLU:HG2	1:A:769:PHE:CD2	2.42	0.55
1:B:433:PHE:HD2	1:B:456:ALA:HA	1.70	0.55
1:B:677:MET:SD	1:B:685:ILE:HD11	2.47	0.55
2:D:51:PHE:CZ	2:D:144:THR:HG23	2.41	0.55
1:B:594:ILE:H	1:B:594:ILE:CD1	2.17	0.54
1:A:243:LEU:N	1:A:243:LEU:HD12	2.23	0.54
1:A:242:VAL:HG23	1:A:242:VAL:O	2.07	0.54
1:A:304:LEU:HD23	1:A:309:ILE:HG21	1.90	0.54
1:B:242:VAL:HG23	1:B:242:VAL:O	2.07	0.54
1:B:361:ASN:OD1	1:B:362:LYS:HG2	2.07	0.54
1:A:212:SER:C	1:A:213:LEU:HD22	2.28	0.54
1:B:212:SER:C	1:B:213:LEU:HD22	2.27	0.54
1:B:251:SER:O	1:B:270:ALA:HB1	2.07	0.54
1:B:453:LEU:HD22	1:B:484:ARG:HE	1.72	0.54
1:A:244:GLU:O	1:A:245:ASN:HB2	2.07	0.54
1:A:681:LYS:O	1:A:685:ILE:HG13	2.08	0.54
1:B:654:PHE:CD1	1:B:664:HIS:HE1	2.25	0.54
1:B:607:PHE:HB2	1:B:776:TYR:CD1	2.42	0.53
1:A:404:MET:O	1:A:408:ASP:OD2	2.26	0.53
1:A:588:PHE:O	1:A:593:PRO:HA	2.07	0.53
1:A:559:PRO:HG3	1:A:601:LYS:HD3	1.89	0.53
1:B:248:PHE:HB2	1:B:268:ILE:HA	1.91	0.53
1:B:398:PHE:HE2	1:B:400:PRO:HB3	1.73	0.53
1:A:361:ASN:OD1	1:A:362:LYS:HG2	2.09	0.53
1:A:320:LEU:HD12	1:A:320:LEU:H	1.73	0.53
1:B:234:ARG:NH2	1:B:252:ILE:HG21	2.24	0.53
1:B:320:LEU:HD13	1:B:375:TYR:CD1	2.44	0.53
1:A:454:LEU:HA	1:A:487:MET:HE1	1.90	0.53
1:B:595:PHE:H	1:B:595:PHE:HD2	1.55	0.53
1:B:692:VAL:HG12	1:B:696:TYR:CE2	2.44	0.53
1:A:674:LEU:HD22	1:A:685:ILE:HD12	1.91	0.52
1:B:481:GLY:HA3	1:B:491:PHE:CD2	2.44	0.52



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:681:LYS:O	1:B:685:ILE:HG13	2.09	0.52
1:A:171:GLN:N	1:A:199:GLU:O	2.42	0.52
1:A:234:ARG:NH2	1:A:252:ILE:HG21	2.25	0.52
2:D:0:SER:HB2	2:D:59:ALA:HB1	1.91	0.52
1:A:176:LEU:HB3	1:A:180:GLU:HB3	1.91	0.52
1:A:248:PHE:HB2	1:A:268:ILE:HA	1.91	0.52
1:A:692:VAL:HG12	1:A:696:TYR:CE2	2.44	0.52
1:B:626:ILE:HA	1:B:629:LEU:HD23	1.91	0.52
2:D:109:ILE:O	2:D:112:VAL:HG22	2.10	0.52
1:A:257:ASN:C	1:A:257:ASN:ND2	2.64	0.51
1:A:673:VAL:HG12	1:A:674:LEU:CD2	2.40	0.51
1:B:304:LEU:HD23	1:B:309:ILE:HG21	1.90	0.51
1:B:479:MET:CE	1:B:550:LEU:HD13	2.41	0.51
1:B:188:LEU:HD11	1:B:192:ARG:NH1	2.25	0.51
1:B:386:LEU:O	1:B:389:LYS:HB2	2.11	0.51
1:B:425:LEU:O	1:B:426:GLU:C	2.49	0.51
1:A:484:ARG:HG2	1:A:487:MET:SD	2.49	0.51
2:C:38:LEU:HD23	2:C:51:PHE:O	2.10	0.51
1:A:594:ILE:H	1:A:594:ILE:CD1	2.17	0.51
1:B:176:LEU:HB3	1:B:180:GLU:HB3	1.91	0.51
1:B:515:LEU:O	1:B:516:CYS:HB2	2.10	0.51
1:A:392:LEU:HD23	1:A:395:LEU:HD12	1.93	0.51
1:B:320:LEU:HD12	1:B:320:LEU:H	1.75	0.51
1:B:479:MET:HE3	1:B:534:TRP:CD1	2.46	0.51
2:C:109:ILE:O	2:C:112:VAL:HG22	2.10	0.51
1:A:271:LEU:HD12	1:A:271:LEU:N	2.25	0.51
1:A:565:TRP:HB3	1:A:588:PHE:CZ	2.46	0.51
1:A:272:PHE:CG	1:A:297:PRO:HG3	2.45	0.51
1:A:515:LEU:O	1:A:516:CYS:HB2	2.11	0.51
1:A:530:LEU:HA	1:A:549:SER:OG	2.11	0.51
1:A:595:PHE:H	1:A:595:PHE:HD2	1.59	0.51
1:A:492:ARG:HG2	1:A:524:TRP:CE2	2.46	0.51
1:A:659:GLU:HG2	1:A:660:LEU:H	1.76	0.51
1:B:189:SER:O	1:B:192:ARG:HG2	2.11	0.51
1:B:271:LEU:HD12	1:B:271:LEU:N	2.26	0.51
1:B:362:LYS:HE3	5:B:783:HOH:O	2.10	0.50
1:B:484:ARG:HG2	1:B:487:MET:SD	2.51	0.50
2:D:87:LEU:HD12	2:D:88:PRO:HD2	1.91	0.50
1:A:467:MET:HB3	1:A:498:TYR:HD1	1.76	0.50
1:B:458:MET:HG2	1:B:490:ARG:NH2	2.26	0.50
1:B:392:LEU:HD23	1:B:395:LEU:HD12	1.92	0.50



		Interatomic	Clash
Atom-1	Atom-2	distance (Å)	overlap (Å)
1:B:686:LEU:HB3	1:B:723:ALA:HB2	1.93	0.50
1:B:659:GLU:HG2	1:B:660:LEU:H	1.75	0.50
1:A:441:ASN:HA	1:A:473:SER:HB2	1.94	0.50
1:B:488:GLN:HG3	3:B:3:SO4:O4	2.12	0.50
1:B:272:PHE:CG	1:B:297:PRO:HG3	2.47	0.50
1:B:565:TRP:HB3	1:B:588:PHE:CZ	2.47	0.50
1:A:208:LEU:HA	1:A:211:LEU:HD21	1.94	0.50
1:A:429:CYS:SG	1:A:455:GLN:HG2	2.52	0.50
1:A:695:LYS:HA	1:A:758:THR:HG21	1.94	0.49
1:A:710:GLU:HA	1:A:713:ARG:HH21	1.77	0.49
1:B:257:ASN:C	1:B:257:ASN:ND2	2.65	0.49
2:D:55:ILE:HD11	2:D:57:PHE:CZ	2.47	0.49
1:B:221:VAL:CB	1:B:223:PHE:HE2	2.25	0.49
1:B:741:LEU:C	1:B:743:ARG:H	2.16	0.49
1:B:208:LEU:HA	1:B:211:LEU:HD21	1.94	0.49
1:A:425:LEU:O	1:A:426:GLU:C	2.50	0.49
1:B:433:PHE:CD2	1:B:456:ALA:HA	2.48	0.49
1:B:530:LEU:HA	1:B:549:SER:OG	2.11	0.49
1:A:263:LEU:HD12	1:A:263:LEU:N	2.27	0.49
1:A:741:LEU:C	1:A:743:ARG:H	2.16	0.49
1:B:311:PRO:HB3	1:B:364:ILE:HB	1.95	0.49
1:B:376:ASN:HA	1:B:379:LYS:HD3	1.95	0.49
2:D:21:ASN:CB	2:D:109:ILE:HD13	2.42	0.49
1:A:684:GLU:HG2	1:A:769:PHE:HD2	1.76	0.49
1:A:728:PRO:C	1:A:730:VAL:H	2.16	0.49
1:A:211:LEU:HD12	1:A:213:LEU:HD21	1.95	0.49
1:B:441:ASN:HA	1:B:473:SER:HB2	1.94	0.49
1:B:569:PHE:CE2	2:D:63:PHE:HE1	2.31	0.49
1:B:717:ASN:O	1:B:721:GLU:HG3	2.13	0.49
1:A:176:LEU:O	1:A:181:LEU:HD23	2.13	0.48
1:B:263:LEU:N	1:B:263:LEU:HD12	2.28	0.48
1:B:194:GLY:O	1:B:195:GLU:HG3	2.13	0.48
1:B:263:LEU:HB2	1:B:282:LEU:HD23	1.94	0.48
1:B:272:PHE:CD1	1:B:272:PHE:N	2.81	0.48
1:B:479:MET:HE1	1:B:550:LEU:CD1	2.42	0.48
2:D:38:LEU:HD22	2:D:50:ALA:HB3	1.95	0.48
1:A:283:LYS:O	1:A:284:ASN:HB2	2.13	0.48
1:A:376:ASN:HA	1:A:379:LYS:HD3	1.94	0.48
1:A:203:TYR:C	1:A:206:CYS:SG	2.92	0.48
1:A:607:PHE:HB2	1:A:776:TYR:CD1	2.48	0.48
1:B:580:PHE:HB3	1:B:632:ASN:HB3	1.96	0.48



		Interatomic	Clash	
Atom-1	Atom-2	distance (\AA)	overlap (Å)	
2:D:58:PRO:HD2	2:D:61:TYR:HB2	1.95	0.48	
1:A:433:PHE:CD2	1:A:456:ALA:HA	2.49	0.48	
1:B:309:ILE:HD12	1:B:315:LEU:HD21	1.96	0.48	
1:A:221:VAL:CB	1:A:223:PHE:HE2	2.22	0.48	
1:A:607:PHE:HB2	1:A:776:TYR:CE1	2.49	0.48	
1:B:259:CYS:O	1:B:260:TYR:HB2	2.13	0.48	
1:A:576:VAL:HG11	2:C:98:ALA:HB2	1.96	0.48	
1:B:616:ILE:HD13	1:B:622:LYS:HA	1.96	0.48	
1:B:728:PRO:C	1:B:730:VAL:H	2.16	0.48	
1:A:192:ARG:HA	1:A:192:ARG:NE	2.28	0.47	
1:A:579:THR:O	1:A:582:TYR:HB2	2.14	0.47	
1:B:211:LEU:HD12	1:B:213:LEU:HD21	1.96	0.47	
1:A:326:LEU:O	1:A:381:ARG:HD3	2.14	0.47	
1:B:472:SER:CB	1:B:594:ILE:HD12	2.44	0.47	
1:A:544:MET:HE3	1:A:571:TYR:O	2.14	0.47	
1:B:549:SER:O	1:B:552:HIS:N	2.48	0.47	
2:D:34:THR:C	2:D:35:TRP:HD1	2.18	0.47	
1:A:263:LEU:HB2	1:A:282:LEU:HD23	1.96	0.47	
1:A:492:ARG:HG2	1:A:524:TRP:CD2	2.48	0.47	
1:B:191:ASN:OD1	1:B:191:ASN:N	2.44	0.47	
1:A:529:ASP:HB3	1:A:550:LEU:HD23	1.97	0.47	
1:B:559:PRO:HG3	1:B:601:LYS:HD3	1.96	0.47	
2:D:61:TYR:CD1	2:D:62:PRO:HA	2.49	0.47	
1:B:540:GLN:HG2	1:B:541:ASP:N	2.29	0.47	
1:B:619:ASN:C	1:B:621:LEU:N	2.68	0.47	
1:B:390:ILE:HD12	1:B:424:TRP:CH2	2.49	0.47	
1:B:182:THR:O	1:B:186:ILE:HG23	2.15	0.47	
1:B:312:GLY:N	1:B:367:THR:OG1	2.47	0.47	
1:A:259:CYS:O	1:A:260:TYR:HB2	2.13	0.47	
1:A:540:GLN:HG2	1:A:541:ASP:N	2.28	0.47	
1:B:283:LYS:O	1:B:284:ASN:HB2	2.15	0.47	
1:A:234:ARG:O	1:A:235:MET:HB2	2.15	0.46	
1:A:717:ASN:O	1:A:721:GLU:HG3	2.15	0.46	
1:B:256:CYS:SG	1:B:257:ASN:N	2.88	0.46	
1:A:688:CYS:O	1:A:692:VAL:HG23	2.16	0.46	
1:B:579:THR:O	1:B:582:TYR:HB2	2.15	0.46	
2:C:61:TYR:CD1	2:C:62:PRO:HA	2.50	0.46	
1:A:390:ILE:HD12	1:A:424:TRP:CH2	2.51	0.46	
1:A:516:CYS:C	1:A:518:GLY:H	2.18	0.46	
1:A:765:ALA:HA	1:A:769:PHE:HE1	1.80	0.46	
1:A:176:LEU:HB3	1:A:180:GLU:HG2	1.97	0.46	



	ti a	Interatomic	Clash overlap (Å)	
Atom-1	Atom-2	distance (Å)		
1:A:778:PRO:HG2	1:A:781:TRP:CE3	2.51	0.46	
1:B:176:LEU:O	1:B:181:LEU:HD23	2.15	0.46	
1:A:504:VAL:HG22	1:A:537:LEU:HD11	1.98	0.46	
1:B:277:PHE:O	1:B:278:SER:C	2.54	0.46	
1:B:203:TYR:C	1:B:206:CYS:SG	2.94	0.46	
1:B:529:ASP:HB3	1:B:550:LEU:HD23	1.98	0.46	
1:A:218:LEU:HB3	1:A:221:VAL:HG21	1.98	0.45	
1:A:265:ASN:HA	1:A:284:ASN:O	2.17	0.45	
1:A:413:HIS:CG	1:A:414:PRO:HA	2.51	0.45	
1:B:176:LEU:HB2	1:B:181:LEU:CD2	2.46	0.45	
2:D:75:TYR:HB2	2:D:143:PHE:CD2	2.51	0.45	
1:A:258:PHE:O	1:A:259:CYS:C	2.55	0.45	
1:B:682:GLN:O	1:B:686:LEU:HD13	2.16	0.45	
1:A:583:SER:HA	1:A:631:SER:OG	2.15	0.45	
1:A:634:SER:C	1:A:636:TYR:H	2.19	0.45	
2:D:34:THR:O	2:D:35:TRP:HD1	1.99	0.45	
1:A:218:LEU:C	1:A:221:VAL:HG23	2.36	0.45	
1:A:272:PHE:N	1:A:272:PHE:CD1	2.83	0.45	
1:A:309:ILE:HD12	1:A:315:LEU:HD21	1.98	0.45	
1:A:398:PHE:HE2	1:A:400:PRO:HB3	1.74	0.45	
1:B:232:ASP:OD1	1:B:232:ASP:C	2.55	0.45	
1:B:376:ASN:HA	1:B:379:LYS:CD	2.46	0.45	
1:B:688:CYS:O	1:B:692:VAL:HG23	2.17	0.45	
1:A:263:LEU:O	1:A:266:CYS:SG	2.67	0.45	
1:B:258:PHE:HB2	1:B:276:ASN:O	2.16	0.45	
1:B:265:ASN:HA	1:B:284:ASN:O	2.17	0.45	
1:A:460:PHE:CE2	1:A:474:PHE:HD1	2.35	0.45	
1:A:176:LEU:HB2	1:A:181:LEU:CD2	2.47	0.45	
1:B:538:SER:HA	1:B:591:SER:O	2.17	0.45	
1:B:778:PRO:HG2	1:B:781:TRP:CE3	2.51	0.45	
1:B:597:ILE:N	1:B:598:PRO:CD	2.80	0.45	
1:A:228:LEU:O	1:A:231:THR:HB	2.17	0.44	
1:B:777:TYR:HE2	1:B:781:TRP:HB2	1.82	0.44	
1:A:228:LEU:HD12	1:A:228:LEU:N	2.31	0.44	
1:B:176:LEU:HD13	1:B:180:GLU:HG2	1.99	0.44	
1:B:569:PHE:CE2	2:D:63:PHE:CE1	3.05	0.44	
1:A:176:LEU:HD13	1:A:180:GLU:HG2	2.00	0.44	
1:A:442:ASN:HB3	1:A:593:PRO:HB2	1.99	0.44	
1:A:595:PHE:CD2	1:A:595:PHE:N	2.85	0.44	
1:B:513:PHE:HB2	1:B:547:MET:HE1	1.99	0.44	
1:B:595:PHE:CD2	1:B:595:PHE:N	2.83	0.44	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:311:PRO:HB3	1:A:364:ILE:HB	1.98	0.44	
1:A:251:SER:C	1:A:270:ALA:HB1	2.38	0.44	
1:A:479:MET:HE1	1:A:550:LEU:CD1	2.40	0.44	
1:B:467:MET:HB3	1:B:498:TYR:HD1	1.83	0.44	
2:C:34:THR:C	2:C:35:TRP:HD1	2.21	0.44	
2:C:58:PRO:HD2	2:C:61:TYR:HB2	1.99	0.44	
1:A:564:ASN:HD21	1:A:566:MET:HB2	1.82	0.44	
1:A:616:ILE:HD13	1:A:622:LYS:HA	2.00	0.44	
1:B:472:SER:HB3	1:B:594:ILE:HD12	1.99	0.44	
1:B:176:LEU:HB3	1:B:180:GLU:HG2	1.98	0.44	
1:B:228:LEU:N	1:B:228:LEU:HD12	2.33	0.44	
1:B:507:VAL:CG1	1:B:547:MET:HE3	2.48	0.44	
1:A:232:ASP:OD1	1:A:232:ASP:C	2.56	0.44	
1:A:616:ILE:HG12	1:A:617:SER:N	2.33	0.44	
1:B:457:GLY:O	1:B:461:GLU:HG3	2.18	0.44	
1:A:439:TRP:HH2	1:B:557:LEU:O	1.99	0.44	
1:A:549:SER:O	1:A:552:HIS:N	2.51	0.44	
1:A:777:TYR:HE2	1:A:781:TRP:HB2	1.82	0.44	
1:B:228:LEU:O	1:B:231:THR:HB	2.17	0.44	
1:B:556:MET:HB3	1:B:565:TRP:CD1	2.53	0.44	
1:A:674:LEU:HD21	1:A:685:ILE:HD12	2.00	0.43	
1:A:419:ALA:O	1:A:421:ILE:N	2.52	0.43	
1:B:429:CYS:SG	1:B:455:GLN:HG2	2.58	0.43	
1:A:376:ASN:HA	1:A:379:LYS:CD	2.48	0.43	
1:A:185:LEU:O	1:A:188:LEU:HB3	2.18	0.43	
1:A:189:SER:O	1:A:192:ARG:HG2	2.17	0.43	
2:C:76:HIS:HB3	2:C:79:ILE:HG13	2.00	0.43	
1:A:238:LEU:HB2	1:A:257:ASN:O	2.19	0.43	
1:A:426:GLU:HB3	1:A:427:PRO:CD	2.49	0.43	
1:A:277:PHE:O	1:A:278:SER:C	2.57	0.43	
1:B:460:PHE:CE2	1:B:474:PHE:HD1	2.37	0.43	
1:B:444:ILE:HD11	1:B:557:LEU:HD13	2.01	0.43	
1:B:564:ASN:HD21	1:B:566:MET:HB2	1.84	0.43	
1:B:724:TYR:HD1	1:B:737:TYR:CE1	2.37	0.43	
1:A:342:ASP:O	1:A:343:LEU:HD23	2.18	0.43	
1:A:538:SER:HA	1:A:591:SER:O	2.18	0.43	
1:B:258:PHE:O	1:B:259:CYS:C	2.57	0.43	
1:B:633:LYS:HD2	2:D:93:GLU:HG3	1.99	0.43	
1:B:222:ASN:HA	1:B:242:VAL:HG22	2.01	0.43	
1:B:238:LEU:HD13	1:B:258:PHE:CE1	2.54	0.43	
1:B:555:ASP:C	1:B:557:LEU:H	2.22	0.43	



		Interatomic	Clash	
Atom-1	Atom-2	distance (Å)	overlap (Å)	
1:A:222:ASN:HA	1:A:242:VAL:HG22	2.01	0.42	
1:A:258:PHE:HB2	1:A:276:ASN:O	2.18	0.42	
1:B:279:ASN:HA	1:B:301:GLU:O	2.20	0.42	
1:A:182:THR:O	1:A:186:ILE:HG23	2.19	0.42	
1:A:557:LEU:O	1:B:439:TRP:HH2	2.03	0.42	
1:B:398:PHE:CD2	1:B:400:PRO:HB3	2.54	0.42	
1:B:544:MET:HE3	1:B:571:TYR:O	2.19	0.42	
1:B:211:LEU:HD23	1:B:211:LEU:N	2.34	0.42	
1:B:331:SER:CB	1:B:389:LYS:HZ1	2.33	0.42	
1:B:675:LYS:O	1:B:676:ASP:HB2	2.19	0.42	
1:A:565:TRP:O	1:A:568:PHE:HE2	2.03	0.42	
1:B:413:HIS:CG	1:B:414:PRO:HA	2.53	0.42	
1:B:565:TRP:O	1:B:568:PHE:HE2	2.02	0.42	
1:A:622:LYS:C	1:A:624:ARG:H	2.23	0.42	
1:B:194:GLY:C	1:B:195:GLU:HG3	2.40	0.42	
1:A:549:SER:O	1:A:550:LEU:C	2.57	0.42	
1:A:597:ILE:N	1:A:598:PRO:CD	2.81	0.42	
1:A:658:TRP:HH2	1:A:710:GLU:OE2	2.02	0.42	
1:B:263:LEU:O	1:B:266:CYS:SG	2.68	0.42	
1:B:396:ALA:O	1:B:397:ALA:C	2.57	0.42	
1:B:580:PHE:HB3	1:B:632:ASN:CB	2.49	0.42	
1:B:619:ASN:O	1:B:621:LEU:N	2.52	0.42	
2:D:117:PRO:O	2:D:120:PRO:HD3	2.20	0.42	
1:B:487:MET:HE2	1:B:491:PHE:CE2	2.55	0.42	
1:B:254:ASN:O	1:B:256:CYS:N	2.53	0.42	
1:B:426:GLU:N	1:B:427:PRO:HD2	2.35	0.42	
1:B:597:ILE:HD13	1:B:597:ILE:HA	1.75	0.42	
2:C:117:PRO:O	2:C:120:PRO:HD3	2.20	0.42	
1:A:221:VAL:CG1	1:A:223:PHE:CE2	3.03	0.42	
1:B:251:SER:C	1:B:270:ALA:HB1	2.40	0.42	
1:B:426:GLU:HB3	1:B:427:PRO:CD	2.50	0.42	
1:B:499:LEU:HA	1:B:504:VAL:HG11	2.02	0.42	
1:B:549:SER:O	1:B:550:LEU:C	2.57	0.42	
1:B:576:VAL:HG11	2:D:98:ALA:HB2	2.01	0.42	
1:B:616:ILE:HG12	1:B:617:SER:N	2.34	0.42	
1:A:202:ASN:OD1	1:A:202:ASN:C	2.58	0.41	
1:A:472:SER:HB3	1:A:594:ILE:CD1	2.49	0.41	
1:A:724:TYR:HD1	1:A:737:TYR:CE1	2.37	0.41	
1:A:754:THR:O	1:A:758:THR:HG23	2.20	0.41	
1:B:203:TYR:O	1:B:223:PHE:HA	2.19	0.41	
1:B:560:ASN:OD1	1:B:560:ASN:N	2.52	0.41	



		Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
1:A:254:ASN:O	1:A:256:CYS:N	2.53	0.41
1:A:256:CYS:SG	1:A:257:ASN:N	2.93	0.41
1:A:299:LEU:HD11	1:A:313:MET:CE	2.50	0.41
1:A:597:ILE:HD13	1:A:597:ILE:HA	1.78	0.41
1:A:211:LEU:HD23	1:A:211:LEU:N	2.34	0.41
1:A:238:LEU:HD13	1:A:258:PHE:CE1	2.55	0.41
1:A:321:GLY:H	1:A:338:GLY:HA3	1.85	0.41
1:A:398:PHE:CD2	1:A:400:PRO:HB3	2.55	0.41
1:B:487:MET:CE	1:B:491:PHE:CE2	3.03	0.41
1:B:565:TRP:HB3	1:B:588:PHE:HE2	1.83	0.41
1:B:580:PHE:CD2	1:B:632:ASN:ND2	2.88	0.41
1:B:652:ASN:N	1:B:653:PRO:CD	2.84	0.41
1:B:658:TRP:HH2	1:B:710:GLU:OE2	2.03	0.41
1:A:499:LEU:HA	1:A:504:VAL:HG11	2.02	0.41
1:B:300:ASN:OD1	1:B:300:ASN:N	2.54	0.41
1:B:325:GLU:O	1:B:326:LEU:C	2.59	0.41
1:B:462:ARG:O	1:B:464:PRO:HD3	2.21	0.41
1:A:453:LEU:HD21	1:A:481:GLY:HA2	2.01	0.41
1:A:565:TRP:HB3	1:A:588:PHE:HE2	1.82	0.41
1:A:594:ILE:C	1:A:596:SER:H	2.24	0.41
1:A:387:ILE:C	1:A:389:LYS:H	2.24	0.41
1:A:560:ASN:OD1	1:A:560:ASN:N	2.53	0.41
1:B:238:LEU:HB2	1:B:257:ASN:O	2.21	0.41
1:B:408:ASP:HA	1:B:451:GLY:HA3	2.02	0.41
1:B:487:MET:CE	1:B:491:PHE:HE2	2.34	0.41
1:B:557:LEU:HD23	1:B:557:LEU:HA	1.88	0.41
1:B:622:LYS:C	1:B:624:ARG:H	2.23	0.41
2:C:33:LEU:O	2:C:57:PHE:O	2.39	0.41
2:D:136:PHE:O	2:D:140:ALA:HB2	2.21	0.41
1:A:505:TYR:O	1:A:506:PRO:C	2.59	0.41
1:A:554:VAL:O	1:A:555:ASP:C	2.59	0.41
1:A:565:TRP:O	1:A:568:PHE:CE2	2.74	0.41
1:B:222:ASN:HA	1:B:242:VAL:CG2	2.51	0.41
1:A:271:LEU:H	1:A:271:LEU:CD1	2.32	0.41
1:A:421:ILE:O	1:A:424:TRP:HB3	2.21	0.41
1:A:507:VAL:CG1	1:A:547:MET:HE3	2.51	0.41
1:A:684:GLU:CG	1:A:769:PHE:HD2	2.34	0.41
1:B:353:VAL:HG13	1:B:364:ILE:CG2	2.48	0.41
1:B:505:TYR:O	1:B:506:PRO:C	2.58	0.41
1:B:544:MET:HE3	1:B:572:LYS:HA	2.03	0.41
2:D:101:THR:HA	2:D:104:VAL:HG12	2.02	0.41



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	$distance (\text{\AA})$	overlap (Å)
1:A:365:LEU:O	1:A:369:ASN:HB2	2.21	0.41
1:A:516:CYS:HB2	2:C:9:LYS:HE3	2.02	0.41
2:D:57:PHE:HA	2:D:58:PRO:HD3	1.83	0.41
1:A:412:ILE:HA	1:A:416:LEU:HD21	2.03	0.40
1:A:652:ASN:N	1:A:653:PRO:CD	2.84	0.40
1:B:421:ILE:O	1:B:424:TRP:HB3	2.21	0.40
1:B:453:LEU:HD21	1:B:481:GLY:HA2	2.03	0.40
1:B:616:ILE:HD13	1:B:622:LYS:CA	2.51	0.40
1:B:708:SER:HA	1:B:709:PRO:HD3	1.92	0.40
1:A:460:PHE:CD2	1:A:474:PHE:HD1	2.39	0.40
1:B:234:ARG:O	1:B:235:MET:HB2	2.21	0.40
1:B:272:PHE:H	1:B:272:PHE:HD1	1.67	0.40
2:C:34:THR:O	2:C:35:TRP:HD1	2.03	0.40
2:C:78:ASN:HD22	2:C:111:LEU:HD11	1.86	0.40
1:A:203:TYR:O	1:A:223:PHE:HA	2.22	0.40
1:A:765:ALA:HA	1:A:769:PHE:CE1	2.56	0.40
1:B:584:LEU:HD23	1:B:584:LEU:HA	1.82	0.40
2:D:67:LYS:HG2	2:D:69:THR:HG23	2.02	0.40
1:A:673:VAL:C	1:A:674:LEU:HD23	2.42	0.40
1:B:271:LEU:H	1:B:271:LEU:CD1	2.33	0.40
1:A:214:VAL:H	1:A:214:VAL:HG12	1.58	0.40
1:B:724:TYR:CD1	1:B:737:TYR:CE1	3.10	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	Perce	entiles
1	А	602/616~(98%)	480 (80%)	115 (19%)	7 (1%)	13	42
1	В	602/616~(98%)	485 (81%)	112 (19%)	5 (1%)	19	51
2	С	143/156~(92%)	122 (85%)	19~(13%)	2 (1%)	11	38



Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	D	150/156~(96%)	127 (85%)	21 (14%)	2(1%)	12 40
All	All	1497/1544 (97%)	1214 (81%)	267~(18%)	16 (1%)	14 45

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	615	LEU
1	В	615	LEU
2	С	31	ASN
2	D	31	ASN
1	А	190	ALA
1	А	274	ASN
1	А	305	THR
1	А	344	SER
1	В	190	ALA
1	В	305	THR
1	В	344	SER
1	В	374	LYS
1	А	420	ASN
2	С	92	ALA
2	D	92	ALA
1	А	559	PRO

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent side chain 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	А	433/548~(79%)	394 (91%)	39~(9%)	9 32
1	В	429/548~(78%)	389~(91%)	40 (9%)	9 30
2	С	64/139~(46%)	63~(98%)	1 (2%)	62 79
2	D	79/139~(57%)	77~(98%)	2(2%)	47 72
All	All	1005/1374~(73%)	923~(92%)	82 (8%)	11 36

All (82) residues with a non-rotameric sidechain are listed below:



Mol	Chain	Res	Type
1	А	186	ILE
1	А	192	ARG
1	А	193	THR
1	А	206	CYS
1	А	208	LEU
1	А	211	LEU
1	А	214	VAL
1	А	231	THR
1	А	257	ASN
1	А	265	ASN
1	А	272	PHE
1	А	293	ILE
1	А	320	LEU
1	А	323	VAL
1	А	353	VAL
1	А	358	THR
1	А	386	LEU
1	А	406	LEU
1	А	408	ASP
1	А	428	ILE
1	А	439	TRP
1	А	446	MET
1	А	529	ASP
1	А	536	LEU
1	А	544	MET
1	А	549	SER
1	А	553	MET
1	А	576	VAL
1	А	594	ILE
1	А	603	PHE
1	А	629	LEU
1	A	630	ASN
1	А	632	ASN
1	A	658	TRP
1	А	701	MET
1	А	724	TYR
1	А	736	TYR
1	А	753	CYS
1	А	769	PHE
1	В	186	ILE
1	В	191	ASN
1	В	206	CYS
1	В	208	LEU



Mol	Chain	Res	Type
1	В	211	LEU
1	В	214	VAL
1	В	231	THR
1	В	257	ASN
1	В	265	ASN
1	В	272	PHE
1	В	293	ILE
1	В	320	LEU
1	В	323	VAL
1	В	353	VAL
1	В	358	THR
1	В	386	LEU
1	В	406	LEU
1	В	408	ASP
1	В	428	ILE
1	В	439	TRP
1	В	445	MET
1	В	446	MET
1	В	529	ASP
1	В	536	LEU
1	В	544	MET
1	В	549	SER
1	В	553	MET
1	В	576	VAL
1	В	594	ILE
1	В	603	PHE
1	В	629	LEU
1	В	630	ASN
1	В	658	TRP
1	В	676	ASP
1	В	701	MET
1	В	706	TYR
1	В	724	TYR
1	В	736	TYR
1	В	739	ASP
1	В	753	CYS
2	С	42	ASP
2	D	0	SER
2	D	55	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:



Mol	Chain	Res	Type
1	А	413	HIS
1	А	422	GLN
1	А	564	ASN
1	А	664	HIS
1	В	413	HIS
1	В	564	ASN
1	В	664	HIS
2	С	56	ASN
2	С	76	HIS
2	D	76	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

12 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).

Mal	Mol Type	Chain	Dec	Link	Bond lengths			Bond angles		
INIOI	Type	Unain	nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	В	9	-	4,4,4	0.14	0	$6,\!6,\!6$	0.08	0
3	SO4	А	2	-	4,4,4	0.13	0	6,6,6	0.15	0
3	SO4	А	5	-	4,4,4	0.14	0	6,6,6	0.05	0
3	SO4	А	4	-	4,4,4	0.13	0	6,6,6	0.14	0
3	SO4	В	1	-	4,4,4	0.15	0	6,6,6	0.12	0



Mal	Turne	Chain	Dec	Link	B	Bond lengths			Bond angles		
IVIOI	туре	Unain	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2	
3	SO4	В	3	-	4,4,4	0.14	0	6,6,6	0.29	0	
4	GOL	А	1	-	$5,\!5,\!5$	0.38	0	5,5,5	0.34	0	
3	SO4	А	8	-	4,4,4	0.14	0	6,6,6	0.07	0	
4	GOL	А	783	-	$5,\!5,\!5$	0.38	0	5,5,5	0.32	0	
3	SO4	A	6	-	4,4,4	0.14	0	6,6,6	0.06	0	
4	GOL	С	155	-	$5,\!5,\!5$	0.36	0	5,5,5	0.27	0	
3	SO4	А	7	-	4,4,4	0.13	0	6,6,6	0.08	0	

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	А	1	-	-	2/4/4/4	-
4	GOL	С	155	-	-	2/4/4/4	-
4	GOL	А	783	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	А	1	GOL	O1-C1-C2-C3
4	А	783	GOL	O1-C1-C2-C3
4	С	155	GOL	O1-C1-C2-O2
4	С	155	GOL	O1-C1-C2-C3
4	А	783	GOL	O1-C1-C2-O2
4	А	1	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	3	SO4	1	0



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} 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	$\mathbf{OWAB}(\mathrm{\AA}^2)$	Q<0.9
1	А	606/616~(98%)	-0.17	8 (1%) 77 77	55, 114, 194, 302	0
1	В	606/616~(98%)	-0.16	18 (2%) 50 49	57, 113, 187, 413	0
2	С	147/156~(94%)	0.17	5 (3%) 45 43	108, 178, 282, 417	0
2	D	152/156~(97%)	-0.16	4 (2%) 56 53	94, 149, 214, 339	0
All	All	1511/1544 (97%)	-0.13	35 (2%) 60 59	55, 122, 215, 417	0

All (35) RSRZ outliers are listed below:

Mol	Chain	\mathbf{Res}	Type	RSRZ
2	С	21	ASN	5.6
1	А	328	SER	5.5
1	В	327	PHE	5.3
1	В	325	GLU	5.3
1	В	651	TRP	4.5
1	В	331	SER	4.3
1	В	639	ILE	3.6
1	В	527	ASP	3.4
1	А	676	ASP	3.3
1	В	640	ALA	3.0
2	С	70	PHE	3.0
1	А	625	PHE	2.7
2	D	137	CYS	2.7
1	В	174	ALA	2.6
2	С	119	HIS	2.6
2	С	130	SER	2.5
2	С	42	ASP	2.5
1	В	731	PHE	2.4
1	А	651	TRP	2.4
1	В	625	PHE	2.3
1	А	562	SER	2.3



Mol	Chain	Res	Type	RSRZ
1	В	528	SER	2.3
1	В	265	ASN	2.3
1	В	727	ASP	2.3
1	В	326	LEU	2.2
1	В	638	MET	2.2
2	D	75	TYR	2.2
1	В	175	CYS	2.1
1	А	520	GLY	2.1
2	D	115	PRO	2.1
1	В	178	LYS	2.1
1	В	590	GLU	2.1
1	А	729	GLN	2.0
2	D	73	LYS	2.0
1	А	615	LEU	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides 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, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	$B-factors(Å^2)$	Q<0.9
4	GOL	С	155	6/6	0.78	0.46	$157,\!157,\!157,\!157$	0
3	SO4	В	9	5/5	0.79	0.42	219,219,219,219	0
4	GOL	А	783	6/6	0.81	0.43	125, 125, 125, 125, 125	0
3	SO4	А	5	5/5	0.81	0.51	241,241,241,241	0
3	SO4	А	7	5/5	0.87	0.29	187,187,187,187	0
4	GOL	А	1	6/6	0.88	0.22	134,134,134,134	0
3	SO4	А	8	5/5	0.90	0.10	203,203,203,203	0
3	SO4	А	4	5/5	0.92	0.14	$152,\!152,\!152,\!152$	0
3	SO4	A	6	5/5	0.92	0.19	179,179,179,179	0



Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	SO4	В	1	5/5	0.95	0.15	141,141,141,141	0
3	SO4	В	3	5/5	0.96	0.12	118,118,118,118	0
3	SO4	А	2	5/5	0.97	0.10	$131,\!131,\!131,\!131$	0

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6.5 Other polymers (i)

There are no such residues in this entry.

