



# Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:39 PM GMT

PDB ID : 1GNI  
Title : HUMAN SERUM ALBUMIN COMPLEXED WITH CIS-9-OCTADECENOIC ACID (OLEIC ACID)  
Authors : Petitpas, I.; Gruene, T.; Bhattacharya, A.A.; Curry, S.  
Deposited on : 2001-10-05  
Resolution : 2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (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



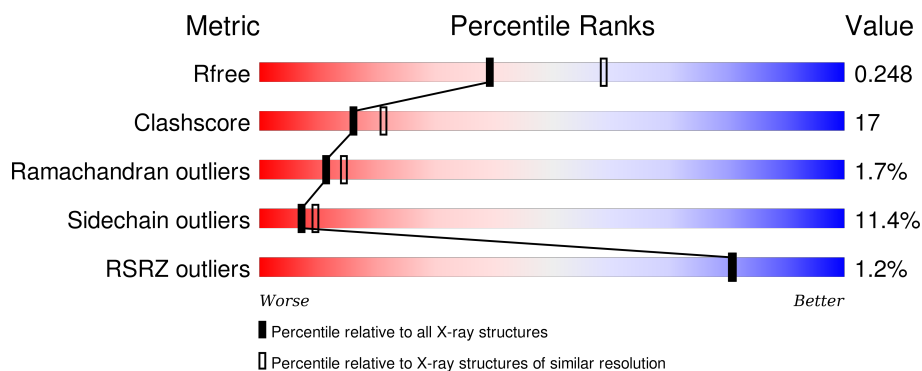
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*


The reported resolution of this entry is 2.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	585	

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
2	OLA	A	1001	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	OLA	A	1002	-	-	-	X
2	OLA	A	1003	-	-	-	X
2	OLA	A	1004[A]	-	-	-	X
2	OLA	A	1004[B]	-	-	-	X
2	OLA	A	1006	-	-	-	X
2	OLA	A	1007	-	-	-	X



## 2 Entry composition [i](#)

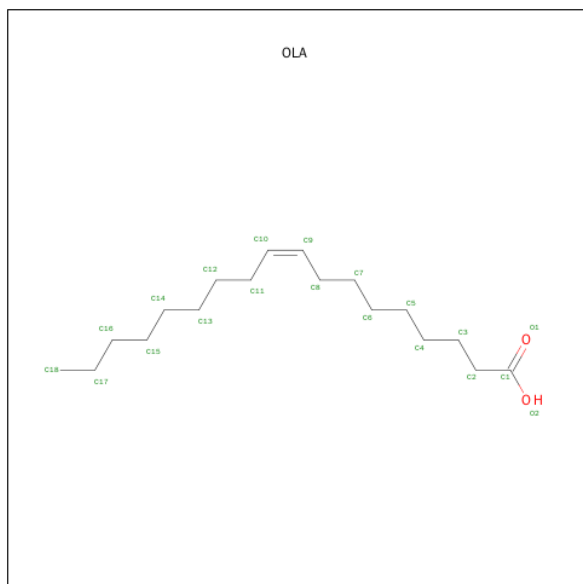
There are 3 unique types of molecules in this entry. The entry contains 4692 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 SERUM ALBUMIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	582	Total	C	N	O	S	0	0	0
			4519	2861	761	856	41			

- Molecule 2 is OLEIC ACID (three-letter code: OLA) (formula:  $C_{18}H_{34}O_2$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			20	18	2		
2	A	1	Total	C	O	0	0
			19	17	2		
2	A	1	Total	C	O	0	0
			20	18	2		
2	A	1	Total	C	O	0	1
			40	36	4		
2	A	1	Total	C	O	0	0
			20	18	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 17 15 2	0	0
2	A	1	Total C 13 13	0	0

- Molecule 3 is water.

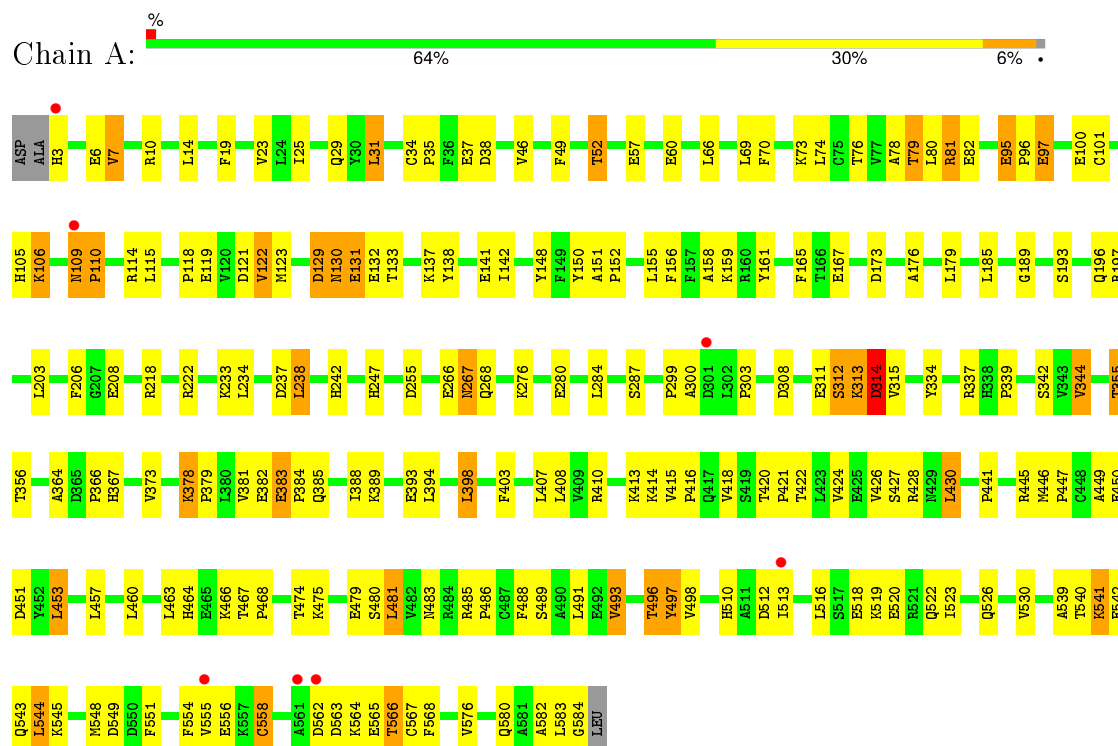
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	24	Total O 24 24	0	0



### 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 ( $\text{RSRZ} > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

#### • Molecule 1: SERUM ALBUMIN





## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	188.39Å 38.92Å 95.48Å 90.00° 104.86° 90.00°	Depositor
Resolution (Å)	32.80 – 2.40 34.54 – 2.38	Depositor EDS
% Data completeness (in resolution range)	95.2 (32.80-2.40) 93.1 (34.54-2.38)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.91 (at 2.36Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.209 , 0.242 0.216 , 0.248	Depositor DCC
$R_{free}$ test set	1229 reflections (4.81%)	DCC
Wilson B-factor (Å <sup>2</sup> )	50.8	Xtriage
Anisotropy	0.285	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 50.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 25711 reflections (0.004%)	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	4692	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.17% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.



## 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: OLA

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	0/4609	0.63	1/6238 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	313	LYS	N-CA-C	-5.78	95.40	111.00

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	A	4519	0	4326	156	0
2	A	149	0	237	19	0
3	A	24	0	0	3	0
All	All	4692	0	4563	156	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 17.

All (156) 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:313:LYS:O	1:A:314:ASP:HB2	1.53	1.06
1:A:356:THR:HG21	1:A:373:VAL:HG21	1.51	0.91
1:A:339:PRO:HG3	3:A:2007:HOH:O	1.73	0.85
1:A:356:THR:HG21	1:A:373:VAL:CG2	2.08	0.84
1:A:378:LYS:O	1:A:382:GLU:HG3	1.79	0.82
1:A:342:SER:HB3	1:A:446:MET:HG2	1.63	0.81
1:A:267:ASN:HD22	1:A:267:ASN:N	1.85	0.74
1:A:383:GLU:HG3	1:A:384:PRO:HD3	1.68	0.73
1:A:60:GLU:H	1:A:60:GLU:CD	1.91	0.73
1:A:313:LYS:O	1:A:314:ASP:CB	2.35	0.72
1:A:424:VAL:O	1:A:428:ARG:HG3	1.89	0.71
1:A:95:GLU:HB3	1:A:96:PRO:HD3	1.73	0.71
1:A:418:VAL:HG21	2:A:1004[A]:OLA:H121	1.71	0.71
1:A:7:VAL:HG22	3:A:2001:HOH:O	1.91	0.70
1:A:155:LEU:HD22	1:A:159:LYS:HE2	1.74	0.69
1:A:566:THR:HG23	1:A:567:CYS:H	1.58	0.68
1:A:119:GLU:HB2	1:A:122:VAL:CG2	2.24	0.68
1:A:564:LYS:O	1:A:566:THR:N	2.27	0.67
1:A:519:LYS:O	1:A:523:ILE:HG12	1.96	0.65
1:A:383:GLU:HG3	1:A:384:PRO:CD	2.25	0.65
1:A:118:PRO:HD2	1:A:123:MET:CE	2.27	0.65
1:A:218:ARG:HE	1:A:222:ARG:HH12	1.43	0.65
1:A:344:VAL:HG22	1:A:450:GLU:OE1	1.97	0.65
1:A:312:SER:O	1:A:315:VAL:HG23	1.97	0.65
1:A:150:TYR:H	1:A:196:GLN:HE22	1.45	0.64
1:A:206:PHE:CZ	1:A:481:LEU:HD23	2.33	0.64
1:A:101:CYS:O	1:A:105:HIS:HD2	1.81	0.64
1:A:25:ILE:O	1:A:29:GLN:HG3	1.98	0.63
1:A:142:ILE:HD13	2:A:1001:OLA:H111	1.81	0.63
1:A:95:GLU:O	1:A:96:PRO:C	2.37	0.63
1:A:378:LYS:HB3	1:A:379:PRO:HD3	1.80	0.62
1:A:381:VAL:O	1:A:385:GLN:HG3	1.99	0.62
1:A:388:ILE:HG23	2:A:1003:OLA:H183	1.82	0.62
1:A:118:PRO:HD2	1:A:123:MET:HE3	1.81	0.61
1:A:576:VAL:HG12	1:A:580:GLN:NE2	2.14	0.61
1:A:138:TYR:O	1:A:142:ILE:HD12	2.01	0.60
1:A:19:PHE:O	1:A:23:VAL:HG23	2.02	0.60
1:A:148:TYR:HH	1:A:193:SER:HG	1.50	0.60
1:A:516:LEU:HD22	1:A:520:GLU:HB3	1.83	0.60
1:A:540:THR:HG22	1:A:541:LYS:N	2.17	0.60
1:A:562:ASP:O	1:A:563:ASP:HB3	2.02	0.59
1:A:115:LEU:HD11	1:A:141:GLU:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:446:MET:HB3	1:A:447:PRO:HD3	1.85	0.58
1:A:426:VAL:HG21	1:A:460:LEU:HD11	1.85	0.58
1:A:123:MET:HE2	2:A:1001:OLA:H51	1.86	0.58
1:A:299:PRO:O	1:A:300:ALA:HB3	2.04	0.58
1:A:119:GLU:O	1:A:122:VAL:HG23	2.04	0.57
1:A:566:THR:HG23	1:A:567:CYS:N	2.18	0.57
1:A:496:THR:HG22	1:A:497:TYR:N	2.19	0.57
1:A:408:LEU:HD13	1:A:427:SER:CB	2.35	0.57
1:A:109:ASN:N	1:A:110:PRO:HD3	2.20	0.57
1:A:398:LEU:HD12	1:A:403:PHE:HA	1.87	0.56
1:A:540:THR:HG22	1:A:542:GLU:H	1.69	0.56
1:A:378:LYS:CB	1:A:379:PRO:HD3	2.35	0.56
1:A:238:LEU:HD22	1:A:242:HIS:CD2	2.40	0.56
1:A:510:HIS:HB2	1:A:512:ASP:OD1	2.06	0.56
1:A:173:ASP:OD1	1:A:176:ALA:HB2	2.06	0.56
1:A:513:ILE:HA	1:A:516:LEU:HD12	1.86	0.56
1:A:475:LYS:O	1:A:479:GLU:HB2	2.06	0.56
1:A:558:CYS:HB3	1:A:568:PHE:CE1	2.40	0.55
1:A:129:ASP:O	1:A:131:GLU:N	2.39	0.55
1:A:308:ASP:HB2	3:A:2015:HOH:O	2.06	0.55
1:A:119:GLU:HB2	1:A:122:VAL:HG22	1.88	0.55
1:A:418:VAL:HG21	2:A:1004[B]:OLA:H72	1.88	0.54
1:A:49:PHE:O	1:A:52:THR:HB	2.08	0.54
1:A:383:GLU:HG3	1:A:384:PRO:N	2.21	0.54
1:A:138:TYR:HB3	2:A:1001:OLA:H82	1.90	0.54
1:A:449:ALA:O	1:A:453:LEU:HB2	2.08	0.54
1:A:130:ASN:HB3	1:A:133:THR:HG23	1.89	0.54
1:A:410:ARG:O	1:A:414:LYS:HG3	2.09	0.53
1:A:10:ARG:NH2	1:A:255:ASP:OD1	2.41	0.53
1:A:37:GLU:CD	1:A:37:GLU:H	2.12	0.53
1:A:151:ALA:HB3	1:A:152:PRO:HD3	1.92	0.52
1:A:389:LYS:O	1:A:393:GLU:HG3	2.09	0.52
1:A:428:ARG:NH2	1:A:522:GLN:OE1	2.43	0.51
1:A:551:PHE:O	1:A:554:PHE:HB3	2.10	0.51
1:A:148:TYR:HH	1:A:197:ARG:HH21	1.59	0.51
1:A:238:LEU:HD22	1:A:242:HIS:HD2	1.76	0.51
1:A:355:THR:HG22	1:A:356:THR:N	2.26	0.51
1:A:540:THR:HB	1:A:543:GLN:HG3	1.92	0.51
1:A:266:GLU:C	1:A:267:ASN:HD22	2.13	0.51
1:A:564:LYS:C	1:A:566:THR:H	2.14	0.51
1:A:287:SER:HB2	2:A:1007:OLA:H51	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:GLY:HA3	2:A:1001:OLA:H162	1.93	0.50
1:A:311:GLU:O	1:A:367:HIS:NE2	2.44	0.50
1:A:539:ALA:HA	1:A:543:GLN:OE1	2.11	0.50
1:A:466:LYS:O	1:A:468:PRO:HD3	2.11	0.50
1:A:95:GLU:HB3	1:A:96:PRO:CD	2.42	0.50
1:A:158:ALA:HA	2:A:1001:OLA:H10	1.94	0.50
1:A:234:LEU:O	1:A:238:LEU:HB2	2.12	0.50
1:A:70:PHE:CZ	1:A:74:LEU:HD21	2.46	0.49
1:A:545:LYS:HA	1:A:548:MET:HE3	1.93	0.49
1:A:413:LYS:HB3	1:A:493:VAL:HG12	1.94	0.49
1:A:79:THR:O	1:A:82:GLU:N	2.44	0.49
1:A:218:ARG:HE	1:A:222:ARG:NH1	2.10	0.49
1:A:483:ASN:C	1:A:486:PRO:HD2	2.33	0.49
1:A:516:LEU:HD22	1:A:520:GLU:CB	2.42	0.49
1:A:544:LEU:O	1:A:548:MET:HG3	2.12	0.48
1:A:563:ASP:OD1	1:A:566:THR:HG21	2.14	0.48
1:A:420:THR:N	1:A:421:PRO:HD2	2.29	0.48
1:A:422:THR:HG21	2:A:1004[A]:OLA:H171	1.97	0.47
1:A:418:VAL:CG2	2:A:1004[A]:OLA:H121	2.44	0.47
1:A:422:THR:HG21	2:A:1004[B]:OLA:H32	1.97	0.47
1:A:479:GLU:HG2	1:A:480:SER:H	1.79	0.47
1:A:485:ARG:HB3	1:A:486:PRO:HD3	1.97	0.46
1:A:10:ARG:HG3	1:A:66:LEU:HD11	1.97	0.46
1:A:583:LEU:HD12	2:A:1005:OLA:H182	1.96	0.46
1:A:554:PHE:O	1:A:558:CYS:HB2	2.15	0.46
1:A:367:HIS:ND1	1:A:367:HIS:O	2.37	0.46
1:A:407:LEU:HD13	1:A:430:LEU:HB3	1.97	0.46
1:A:233:LYS:NZ	1:A:237:ASP:OD2	2.44	0.46
1:A:488:PHE:HB3	2:A:1004[B]:OLA:H141	1.98	0.45
1:A:383:GLU:CG	1:A:384:PRO:HD3	2.41	0.45
1:A:453:LEU:HA	1:A:453:LEU:HD12	1.86	0.45
1:A:394:LEU:CD1	1:A:398:LEU:HD21	2.47	0.45
1:A:267:ASN:ND2	1:A:267:ASN:N	2.58	0.45
1:A:441:PRO:O	1:A:445:ARG:HG3	2.17	0.45
1:A:489:SER:HA	2:A:1004[B]:OLA:H183	1.98	0.44
1:A:430:LEU:HD12	1:A:430:LEU:HA	1.81	0.44
1:A:268:GLN:HE22	1:A:276:LYS:HA	1.83	0.44
1:A:97:GLU:HG2	1:A:97:GLU:H	1.32	0.44
1:A:545:LYS:HA	1:A:548:MET:CE	2.48	0.44
1:A:69:LEU:HB3	2:A:1002:OLA:C17	2.48	0.43
1:A:118:PRO:HD2	1:A:123:MET:HE1	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:GLU:HG2	1:A:167:GLU:O	2.18	0.43
1:A:161:TYR:O	1:A:165:PHE:HD1	2.02	0.43
1:A:420:THR:HG23	1:A:530:VAL:HB	2.00	0.43
1:A:582:ALA:C	1:A:584:GLY:H	2.21	0.43
1:A:156:PHE:HZ	1:A:284:LEU:O	2.01	0.43
1:A:79:THR:O	1:A:81:ARG:N	2.51	0.43
1:A:155:LEU:O	1:A:155:LEU:HD23	2.18	0.43
1:A:60:GLU:N	1:A:60:GLU:CD	2.68	0.42
1:A:408:LEU:HD13	1:A:427:SER:HB2	2.00	0.42
1:A:398:LEU:HD12	1:A:403:PHE:CA	2.49	0.42
1:A:491:LEU:HA	1:A:491:LEU:HD23	1.85	0.42
1:A:426:VAL:CG2	1:A:460:LEU:HD11	2.47	0.42
1:A:6:GLU:OE1	1:A:66:LEU:HG	2.19	0.42
1:A:583:LEU:O	1:A:584:GLY:C	2.57	0.42
1:A:100:GLU:OE2	1:A:247:HIS:CE1	2.73	0.42
1:A:562:ASP:O	1:A:563:ASP:CB	2.67	0.42
1:A:31:LEU:CD1	1:A:74:LEU:HD12	2.49	0.42
1:A:29:GLN:O	1:A:106:LYS:HD2	2.20	0.42
1:A:416:PRO:HB2	1:A:497:TYR:CD1	2.55	0.42
1:A:460:LEU:HD21	2:A:1004[B]:OLA:H82	2.02	0.41
1:A:513:ILE:CD1	1:A:555:VAL:HG13	2.50	0.41
1:A:206:PHE:CE1	1:A:481:LEU:HD23	2.55	0.41
1:A:299:PRO:O	1:A:300:ALA:CB	2.68	0.41
1:A:513:ILE:HD11	1:A:568:PHE:HZ	1.86	0.41
1:A:540:THR:CG2	1:A:541:LYS:N	2.84	0.41
1:A:46:VAL:HG11	2:A:1002:OLA:H162	2.03	0.41
1:A:364:ALA:O	1:A:366:PRO:HD3	2.21	0.41
1:A:408:LEU:HD21	1:A:526:GLN:HB3	2.03	0.41
1:A:34:CYS:HA	1:A:35:PRO:HD3	1.90	0.41
1:A:109:ASN:N	1:A:109:ASN:ND2	2.69	0.40
1:A:449:ALA:HB2	2:A:1003:OLA:H171	2.04	0.40
1:A:464:HIS:HE1	1:A:474:THR:OG1	2.04	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	580/585 (99%)	529 (91%)	41 (7%)	10 (2%)	11 14

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	80	LEU
1	A	130	ASN
1	A	497	TYR
1	A	565	GLU
1	A	314	ASP
1	A	303	PRO
1	A	110	PRO
1	A	78	ALA
1	A	129	ASP
1	A	95	GLU

### 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	475/511 (93%)	421 (89%)	54 (11%)	7 9

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	HIS
1	A	7	VAL
1	A	14	LEU
1	A	31	LEU
1	A	38	ASP
1	A	52	THR
1	A	57	GLU

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Mol	Chain	Res	Type
1	A	73	LYS
1	A	76	THR
1	A	79	THR
1	A	81	ARG
1	A	97	GLU
1	A	106	LYS
1	A	109	ASN
1	A	114	ARG
1	A	121	ASP
1	A	122	VAL
1	A	131	GLU
1	A	132	GLU
1	A	137	LYS
1	A	179	LEU
1	A	185	LEU
1	A	203	LEU
1	A	208	GLU
1	A	238	LEU
1	A	267	ASN
1	A	280	GLU
1	A	312	SER
1	A	314	ASP
1	A	334	TYR
1	A	337	ARG
1	A	344	VAL
1	A	355	THR
1	A	378	LYS
1	A	383	GLU
1	A	398	LEU
1	A	415	VAL
1	A	430	LEU
1	A	451	ASP
1	A	453	LEU
1	A	457	LEU
1	A	463	LEU
1	A	467	THR
1	A	481	LEU
1	A	493	VAL
1	A	496	THR
1	A	498	VAL
1	A	518	GLU
1	A	541	LYS

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Mol	Chain	Res	Type
1	A	544	LEU
1	A	549	ASP
1	A	556	GLU
1	A	558	CYS
1	A	566	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	105	HIS
1	A	109	ASN
1	A	146	HIS
1	A	196	GLN
1	A	242	HIS
1	A	247	HIS
1	A	267	ASN
1	A	268	GLN
1	A	318	ASN
1	A	510	HIS
1	A	580	GLN

### 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](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and



the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	OLA	A	1001	-	16,19,19	0.42	0	16,19,19	0.70	1 (6%)
2	OLA	A	1002	-	15,18,19	0.46	0	15,18,19	0.67	1 (6%)
2	OLA	A	1003	-	16,19,19	0.45	0	16,19,19	0.74	0
2	OLA	A	1004[A]	-	16,19,19	0.47	0	16,19,19	0.65	1 (6%)
2	OLA	A	1004[B]	-	16,19,19	0.50	0	16,19,19	0.74	1 (6%)
2	OLA	A	1005	-	16,19,19	0.45	0	16,19,19	0.68	1 (6%)
2	OLA	A	1006	-	13,16,19	0.66	0	13,16,19	0.75	1 (7%)
2	OLA	A	1007	-	12,12,19	0.35	0	10,11,19	0.52	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OLA	A	1001	-	-	0/15/17/17	0/0/0/0
2	OLA	A	1002	-	-	0/14/16/17	0/0/0/0
2	OLA	A	1003	-	-	0/15/17/17	0/0/0/0
2	OLA	A	1004[A]	-	-	0/15/17/17	0/0/0/0
2	OLA	A	1004[B]	-	-	0/15/17/17	0/0/0/0
2	OLA	A	1005	-	-	0/15/17/17	0/0/0/0
2	OLA	A	1006	-	-	0/12/14/17	0/0/0/0
2	OLA	A	1007	-	-	0/10/10/17	0/0/0/0

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1006	OLA	C4-C3-C2	-2.28	104.26	113.90
2	A	1001	OLA	C4-C3-C2	-2.14	104.86	113.90
2	A	1004[B]	OLA	C4-C3-C2	-2.09	105.07	113.90
2	A	1004[A]	OLA	C4-C3-C2	-2.07	105.13	113.90
2	A	1005	OLA	C4-C3-C2	-2.06	105.20	113.90
2	A	1002	OLA	C4-C3-C2	-2.02	105.37	113.90



There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	OLA	5	0
2	A	1002	OLA	2	0
2	A	1003	OLA	2	0
2	A	1004[A]	OLA	3	0
2	A	1004[B]	OLA	5	0
2	A	1005	OLA	1	0
2	A	1007	OLA	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<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	582/585 (99%)	-0.10	7 (1%) 81 81	31, 55, 84, 108	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	562	ASP	5.0
1	A	3	HIS	4.7
1	A	561	ALA	4.7
1	A	301	ASP	3.9
1	A	513	ILE	2.8
1	A	109	ASN	2.6
1	A	555	VAL	2.0

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

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

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.



Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
2	OLA	A	1001	20/20	0.61	0.44	12.06	80,87,102,103	0
2	OLA	A	1004[A]	20/20	0.70	0.31	5.51	44,55,65,65	20
2	OLA	A	1004[B]	20/20	0.70	0.31	5.21	58,61,62,62	20
2	OLA	A	1007	13/20	0.87	0.28	4.78	64,66,68,70	0
2	OLA	A	1006	17/20	0.80	0.31	4.41	49,58,83,83	0
2	OLA	A	1002	19/20	0.91	0.23	3.30	50,62,76,76	0
2	OLA	A	1003	20/20	0.93	0.28	2.88	45,58,60,62	0
2	OLA	A	1005	20/20	0.93	0.20	1.72	59,61,70,72	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.