



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 07:38 AM UTC

PDB ID : 6R7S / pdb_00006r7s
Title : Human Serum Albumin, complexed with Sulfasalazine
Authors : Schreuder, H.A.; Liesum, A.
Deposited on : 2019-03-29
Resolution : 2.21 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

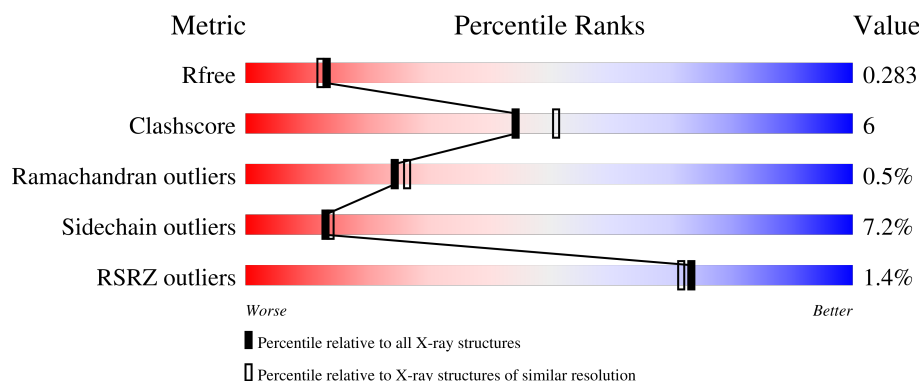
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

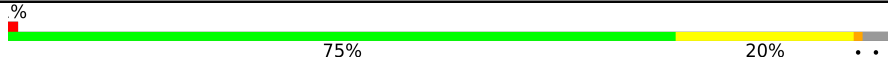
The reported resolution of this entry is 2.21 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	7682 (2.24-2.20)
Clashscore	190562	8402 (2.24-2.20)
Ramachandran outliers	187476	8303 (2.24-2.20)
Sidechain outliers	187428	8304 (2.24-2.20)
RSRZ outliers	180081	7683 (2.24-2.20)

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

Mol	Chain	Length	Quality of chain
1	A	585	

2 Entry composition [i](#)

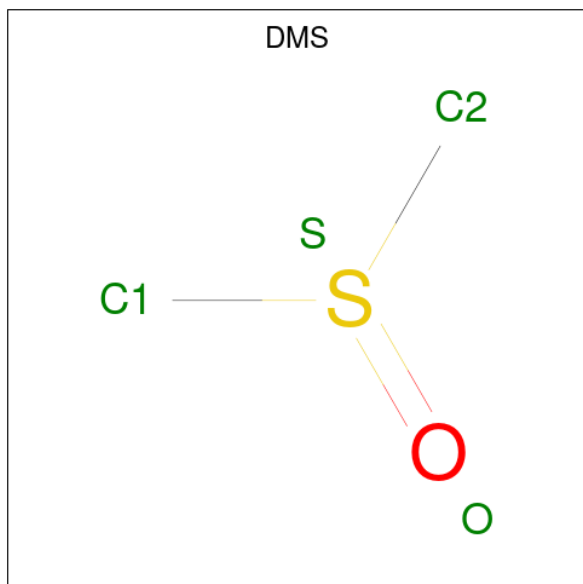
There are 5 unique types of molecules in this entry. The entry contains 4887 atoms, of which 0 are hydrogens and 0 are deuteriums.

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
			Total	C	N	O	S			
1	A	567	4434	2802	749	843	40	0	2	0

- Molecule 2 is DIMETHYL SULFOXIDE (CCD ID: DMS) (formula: C₂H₆OS).



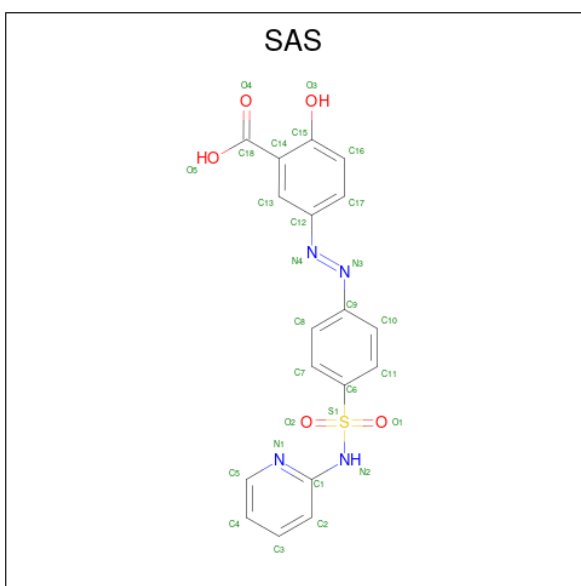
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O	S		
2	A	1	4	2	1	1	0	0
2	A	1	4	2	1	1	0	0

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	O	S		0	0
			5	4	1			

- Molecule 4 is 2-HYDROXY-(5-([4-(2-PYRIDINYLAMINO)SULFONYL]PHENYL)AZO) BENZOIC ACID (CCD ID: SAS) (formula: C₁₈H₁₄N₄O₅S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			28	18	4	5	1		
4	A	1	Total	C	N	O	S	0	0
			28	18	4	5	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			28	18	4	5	1		

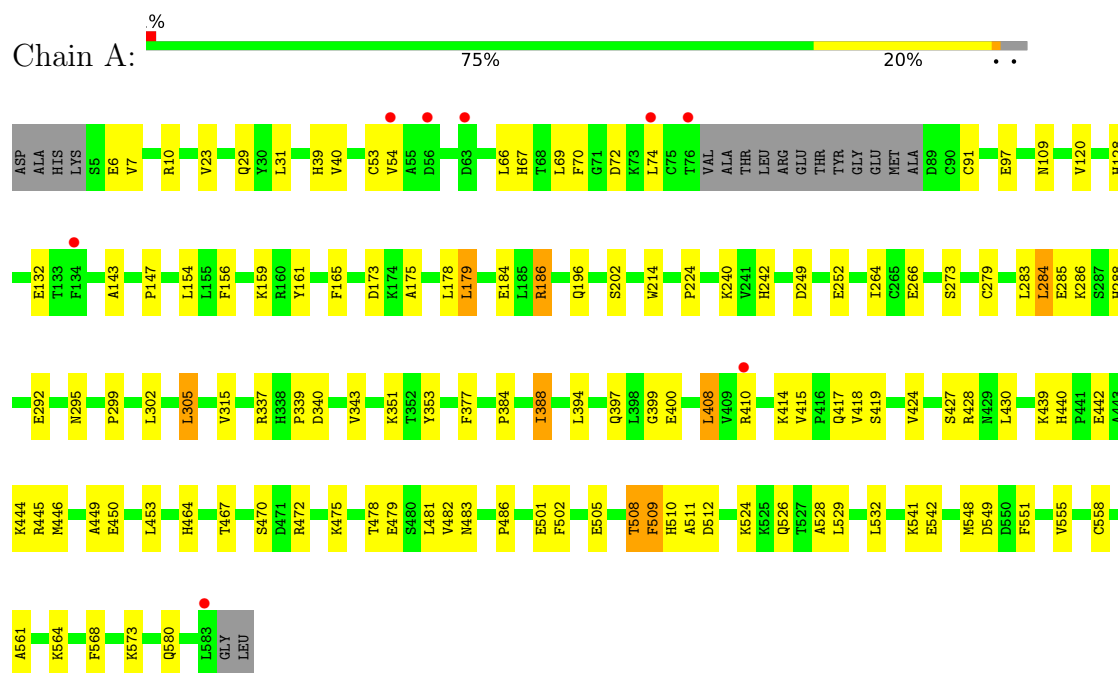
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	356	Total	O	0	0
			356	356		

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: Serum albumin



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.30Å 85.11Å 60.12Å 90.00° 99.89° 90.00°	Depositor
Resolution (Å)	48.62 – 2.21 48.62 – 2.21	Depositor EDS
% Data completeness (in resolution range)	62.1 (48.62-2.21) 62.3 (48.62-2.21)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.72 (at 2.20Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.177 , 0.275 0.179 , 0.283	Depositor DCC
R_{free} test set	1367 reflections (4.61%)	wwPDB-VP
Wilson B-factor (Å ²)	43.4	Xtriage
Anisotropy	0.026	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 70.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.033 for l,-k,h	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4887	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, SAS, DMS

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	0.89	2/4521 (0.0%)	1.55	43/6117 (0.7%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	415	VAL	CA-C	6.17	1.59	1.52
1	A	179	LEU	CA-C	5.51	1.58	1.52

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	481	LEU	CA-C-N	7.34	130.51	120.46
1	A	481	LEU	C-N-CA	7.34	130.51	120.46
1	A	353	TYR	CA-C-N	6.88	129.80	120.38
1	A	353	TYR	C-N-CA	6.88	129.80	120.38
1	A	53	CYS	N-CA-C	-6.79	104.87	113.43
1	A	377	PHE	CA-CB-CG	6.55	120.35	113.80
1	A	481	LEU	N-CA-C	-6.30	103.07	111.96
1	A	399	GLY	N-CA-C	6.22	123.33	115.42
1	A	502	PHE	CA-CB-CG	6.17	119.97	113.80
1	A	526	GLN	CA-C-N	5.71	127.93	120.28
1	A	526	GLN	C-N-CA	5.71	127.93	120.28
1	A	478	THR	CA-C-N	5.67	128.15	120.38
1	A	478	THR	C-N-CA	5.67	128.15	120.38
1	A	509	PHE	CA-CB-CG	5.59	119.39	113.80
1	A	541	LYS	CA-C-N	5.50	128.09	120.29
1	A	541	LYS	C-N-CA	5.50	128.09	120.29
1	A	510	HIS	CA-C-N	5.49	127.91	120.38
1	A	510	HIS	C-N-CA	5.49	127.91	120.38
1	A	388	ILE	CA-C-N	5.36	127.73	120.65

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	388	ILE	C-N-CA	5.36	127.73	120.65
1	A	305	LEU	CA-C-N	5.25	127.32	120.28
1	A	305	LEU	C-N-CA	5.25	127.32	120.28
1	A	340	ASP	CA-C-N	5.25	130.47	122.65
1	A	340	ASP	C-N-CA	5.25	130.47	122.65
1	A	288	HIS	CA-C-N	5.23	127.55	120.44
1	A	288	HIS	C-N-CA	5.23	127.55	120.44
1	A	72	ASP	CA-CB-CG	5.21	117.81	112.60
1	A	249	ASP	CA-C-N	5.21	127.78	120.28
1	A	249	ASP	C-N-CA	5.21	127.78	120.28
1	A	161	TYR	CA-C-N	5.17	127.52	120.54
1	A	161	TYR	C-N-CA	5.17	127.52	120.54
1	A	561	ALA	CA-C-N	5.17	127.16	120.44
1	A	561	ALA	C-N-CA	5.17	127.16	120.44
1	A	284	LEU	CA-C-N	5.13	127.15	120.28
1	A	284	LEU	C-N-CA	5.13	127.15	120.28
1	A	128	HIS	CA-C-N	5.12	127.40	120.38
1	A	128	HIS	C-N-CA	5.12	127.40	120.38
1	A	549	ASP	CA-C-N	5.08	127.09	120.28
1	A	549	ASP	C-N-CA	5.08	127.09	120.28
1	A	173	ASP	CA-C-N	5.03	127.27	120.38
1	A	173	ASP	C-N-CA	5.03	127.27	120.38
1	A	240	LYS	CA-C-N	5.00	127.05	120.60
1	A	240	LYS	C-N-CA	5.00	127.05	120.60

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	A	4434	0	4256	52	0
2	A	8	0	12	6	0
3	A	5	0	0	0	0
4	A	84	0	36	5	0
5	A	356	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4887	0	4304	53	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 6.

All (53) 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:475:LYS:O	1:A:479:GLU:HB2	1.83	0.76
1:A:418:VAL:HG13	2:A:602:DMS:H23	1.66	0.74
1:A:464:HIS:HE1	1:A:470:SER:H	1.37	0.72
1:A:264:ILE:CD1	4:A:604:SAS:H16	2.21	0.71
1:A:91:CYS:HA	5:A:755:HOH:O	1.93	0.67
1:A:419:SER:H	2:A:602:DMS:H12	1.60	0.66
1:A:384:PRO:O	1:A:388:ILE:HG12	1.97	0.64
1:A:464:HIS:CE1	1:A:470:SER:H	2.17	0.62
1:A:509:PHE:HA	2:A:601:DMS:H13	1.82	0.61
1:A:305:LEU:HG	1:A:337:ARG:HH11	1.66	0.60
1:A:97:GLU:HA	5:A:847:HOH:O	2.02	0.60
1:A:512:ASP:OD1	2:A:601:DMS:H22	2.02	0.60
1:A:305:LEU:HG	1:A:337:ARG:NH1	2.18	0.58
1:A:6:GLU:HG2	1:A:66:LEU:HG	1.86	0.56
1:A:224:PRO:HB2	1:A:299:PRO:HD3	1.89	0.55
1:A:159:LYS:HD2	1:A:284:LEU:HD12	1.88	0.54
1:A:156:PHE:HE1	1:A:285:GLU:HG3	1.74	0.53
1:A:29:GLN:HG2	1:A:147:PRO:HA	1.92	0.52
1:A:179:LEU:HD12	5:A:912:HOH:O	2.10	0.51
1:A:186:ARG:HB2	5:A:1023:HOH:O	2.10	0.51
1:A:196:GLN:HE22	1:A:242:HIS:CE1	2.28	0.51
2:A:602:DMS:H13	5:A:1018:HOH:O	2.12	0.49
1:A:449:ALA:O	1:A:453:LEU:HG	2.13	0.49
1:A:558:CYS:O	1:A:564:LYS:HG2	2.13	0.48
1:A:410[A]:ARG:HG3	1:A:414:LYS:HE2	1.96	0.46
1:A:29:GLN:HG3	1:A:143:ALA:HB1	1.97	0.46
1:A:529:LEU:HD13	1:A:548:MET:HE3	1.98	0.46
1:A:23:VAL:HG22	1:A:70:PHE:CZ	2.51	0.45
1:A:551:PHE:HB3	4:A:606:SAS:C16	2.47	0.45
1:A:165:PHE:CZ	1:A:178:LEU:HD21	2.52	0.45
1:A:31:LEU:HB2	1:A:39:HIS:HE1	1.82	0.44
1:A:501:GLU:HB3	5:A:716:HOH:O	2.17	0.44
1:A:214:TRP:CD1	1:A:343:VAL:HG11	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:483:ASN:O	1:A:486:PRO:HD2	2.18	0.44
1:A:10:ARG:HG3	1:A:66:LEU:HD11	2.00	0.43
1:A:388:ILE:HG21	1:A:445:ARG:HB3	2.00	0.43
1:A:302:LEU:HD23	1:A:302:LEU:HA	1.90	0.43
1:A:427:SER:HA	1:A:430:LEU:HD12	2.01	0.43
1:A:279:CYS:HA	1:A:286:LYS:HD2	2.01	0.43
1:A:528:ALA:HB2	4:A:606:SAS:H10	2.00	0.43
1:A:408:LEU:HD23	1:A:427:SER:HB2	2.01	0.42
1:A:417:GLN:HB2	1:A:470:SER:HB2	2.01	0.42
1:A:23:VAL:HG22	1:A:70:PHE:HZ	1.84	0.41
1:A:295:ASN:HD22	1:A:339:PRO:HB3	1.84	0.41
1:A:66:LEU:HD22	1:A:70:PHE:HE1	1.85	0.41
1:A:410[B]:ARG:CZ	4:A:605:SAS:H2	2.50	0.41
1:A:439:LYS:HG3	1:A:440:HIS:CD2	2.55	0.41
1:A:511:ALA:HA	1:A:568:PHE:HE1	1.86	0.41
1:A:120:VAL:HG21	1:A:175:ALA:HA	2.03	0.41
1:A:264:ILE:HD11	4:A:604:SAS:H16	2.02	0.41
1:A:351:LYS:HD3	5:A:829:HOH:O	2.20	0.41
1:A:424:VAL:O	1:A:428:ARG:HG3	2.20	0.41
1:A:508:THR:O	2:A:601:DMS:H13	2.21	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	565/585 (97%)	532 (94%)	30 (5%)	3 (0%)	24 26

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	400	GLU

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Mol	Chain	Res	Type
1	A	442	GLU
1	A	315	VAL

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	473/511 (93%)	439 (93%)	34 (7%)	13	14

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	VAL
1	A	40	VAL
1	A	54	VAL
1	A	67	HIS
1	A	69	LEU
1	A	74	LEU
1	A	109	ASN
1	A	132	GLU
1	A	154	LEU
1	A	184	GLU
1	A	186	ARG
1	A	202	SER
1	A	252	GLU
1	A	266	GLU
1	A	273	SER
1	A	283	LEU
1	A	292	GLU
1	A	394	LEU
1	A	397	GLN
1	A	408	LEU
1	A	444	LYS
1	A	446	MET
1	A	450	GLU
1	A	467	THR

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Mol	Chain	Res	Type
1	A	472	ARG
1	A	482	VAL
1	A	505	GLU
1	A	508	THR
1	A	524	LYS
1	A	532	LEU
1	A	542	GLU
1	A	555	VAL
1	A	573	LYS
1	A	580	GLN

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

Mol	Chain	Res	Type
1	A	99	ASN
1	A	109	ASN
1	A	130	ASN
1	A	196	GLN
1	A	221	GLN
1	A	247	HIS
1	A	267	ASN
1	A	397	GLN
1	A	464	HIS
1	A	510	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

6 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	DMS	A	602	-	3,3,3	0.41	0	3,3,3	0.38	0
4	SAS	A	606	-	30,30,30	0.72	2 (6%)	42,42,42	1.04	3 (7%)
4	SAS	A	604	-	30,30,30	0.30	0	42,42,42	0.70	3 (7%)
4	SAS	A	605	-	30,30,30	0.32	0	42,42,42	0.43	0
2	DMS	A	601	-	3,3,3	0.43	0	3,3,3	0.51	0
3	SO4	A	603	-	4,4,4	0.21	0	6,6,6	0.13	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	SAS	A	604	-	-	3/20/20/20	0/3/3/3
4	SAS	A	606	-	-	7/20/20/20	0/3/3/3
4	SAS	A	605	-	-	6/20/20/20	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	606	SAS	O5-C18	-2.67	1.22	1.30
4	A	606	SAS	O4-C18	2.37	1.29	1.22

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	606	SAS	O4-C18-C14	-3.89	112.67	121.97
4	A	606	SAS	O5-C18-C14	3.23	124.47	115.28
4	A	606	SAS	C1-N2-S1	2.31	130.14	124.83
4	A	604	SAS	C8-C9-N3	2.10	131.82	120.26

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	604	SAS	C1-N2-S1	2.09	129.64	124.83
4	A	604	SAS	C10-C9-N3	-2.06	108.97	120.26

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	604	SAS	C1-N2-S1-O2
4	A	604	SAS	C1-N2-S1-C6
4	A	605	SAS	C7-C6-S1-N2
4	A	605	SAS	C11-C6-S1-N2
4	A	606	SAS	C7-C6-S1-O1
4	A	606	SAS	C11-C6-S1-O1
4	A	606	SAS	C7-C6-S1-N2
4	A	606	SAS	C11-C6-S1-N2
4	A	604	SAS	C1-N2-S1-O1
4	A	606	SAS	C1-N2-S1-O1
4	A	606	SAS	C1-N2-S1-O2
4	A	605	SAS	C11-C6-S1-O1
4	A	605	SAS	C7-C6-S1-O1
4	A	606	SAS	C1-N2-S1-C6
4	A	605	SAS	C7-C6-S1-O2
4	A	605	SAS	C11-C6-S1-O2

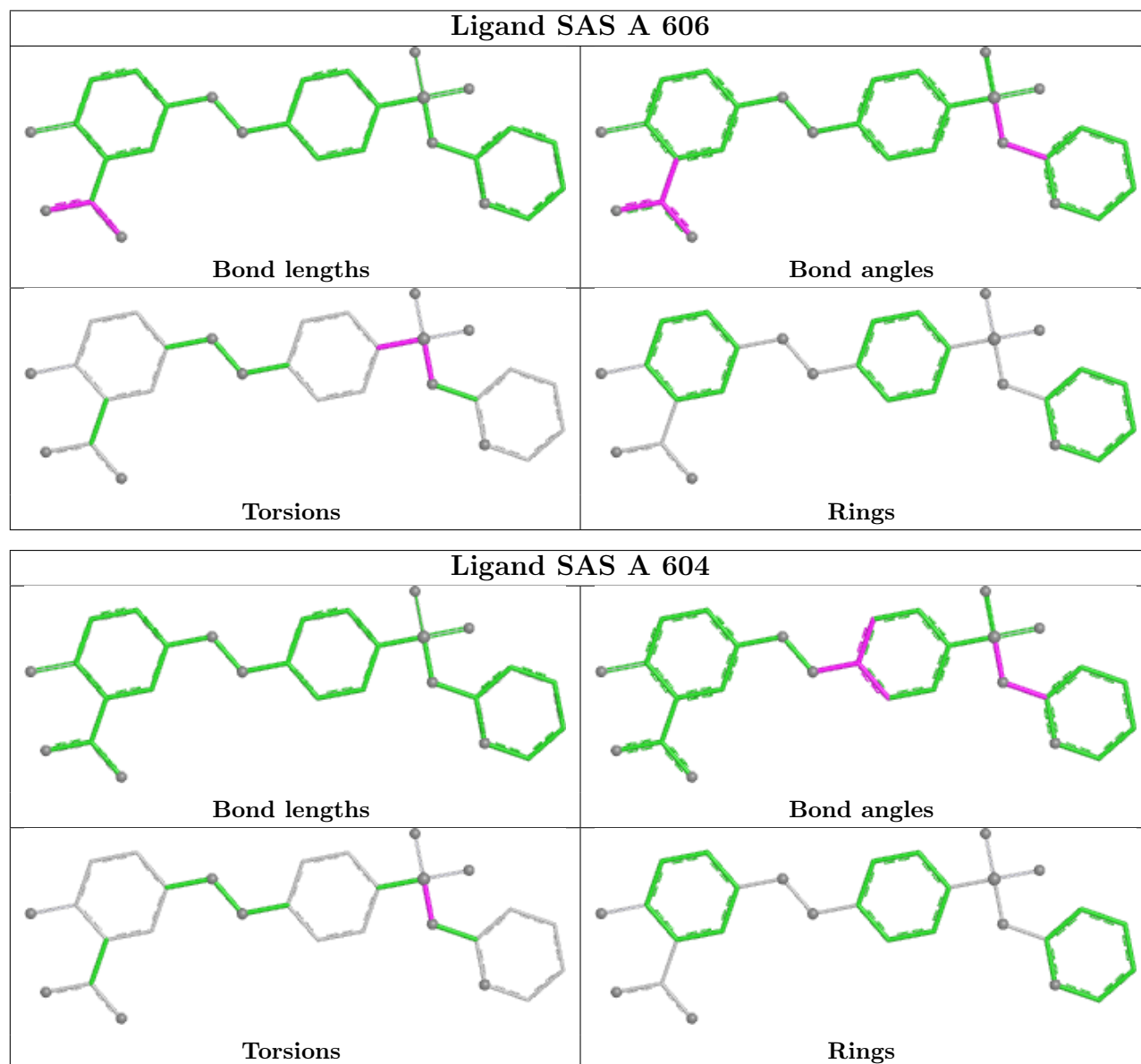
There are no ring outliers.

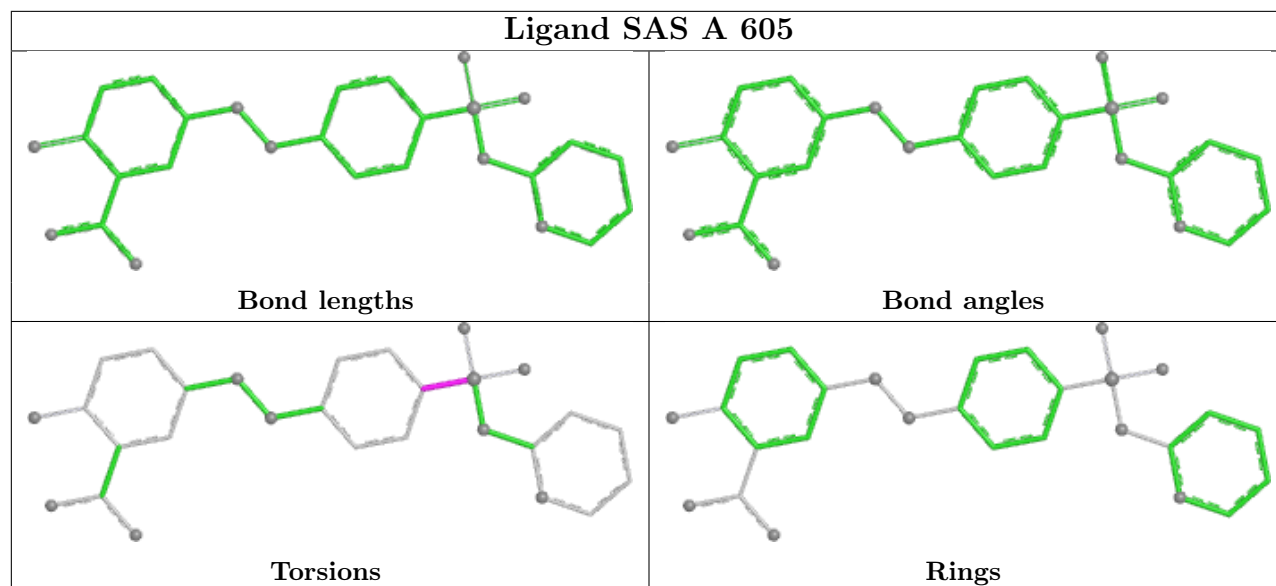
5 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	602	DMS	3	0
4	A	606	SAS	2	0
4	A	604	SAS	2	0
4	A	605	SAS	1	0
2	A	601	DMS	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the

average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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, 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	567/585 (96%)	0.12	8 (1%) 73 72	20, 51, 87, 119	2 (0%)

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	74	LEU	3.2
1	A	54	VAL	2.8
1	A	56	ASP	2.6
1	A	63	ASP	2.6
1	A	583	LEU	2.6
1	A	410[A]	ARG	2.4
1	A	76	THR	2.4
1	A	134	PHE	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

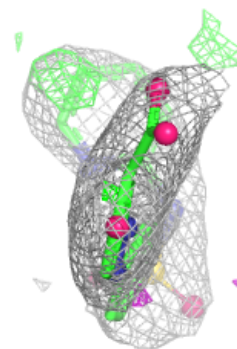
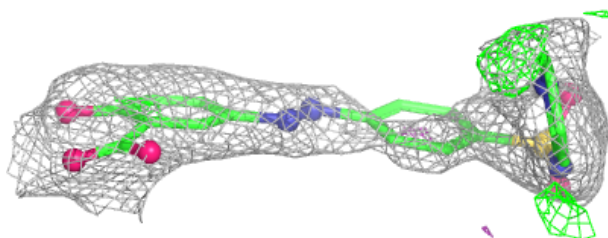
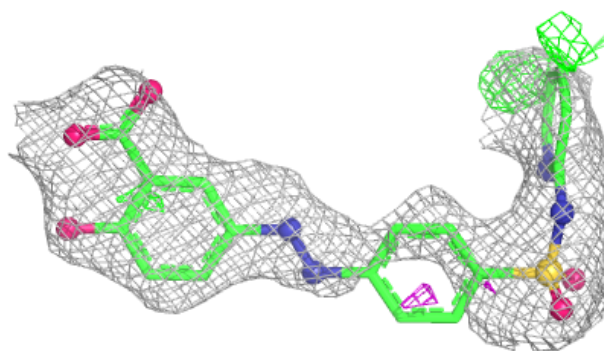
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	SAS	A	605	28/28	0.85	0.15	30,59,74,75	28
2	DMS	A	602	4/4	0.89	0.21	100,100,100,100	0
3	SO4	A	603	5/5	0.90	0.08	119,120,121,121	0
4	SAS	A	606	28/28	0.90	0.11	32,45,79,80	28
2	DMS	A	601	4/4	0.95	0.11	59,60,60,62	4
4	SAS	A	604	28/28	0.95	0.08	29,45,56,58	28

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

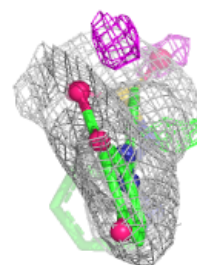
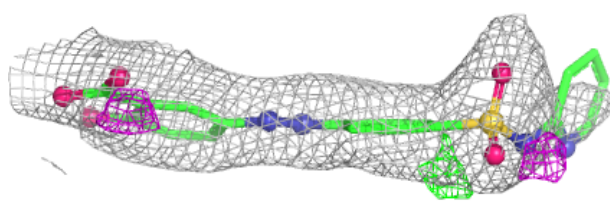
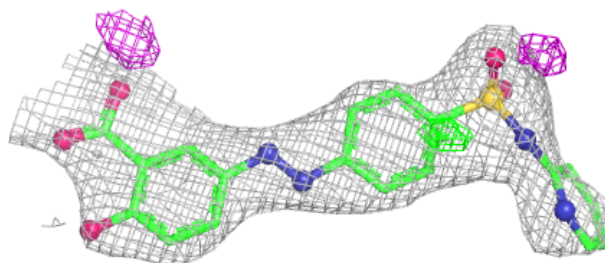
Electron density around SAS A 605:

2mF_o-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

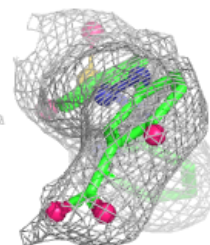
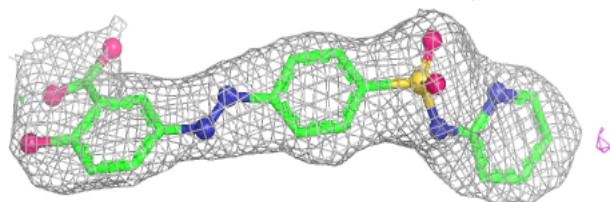
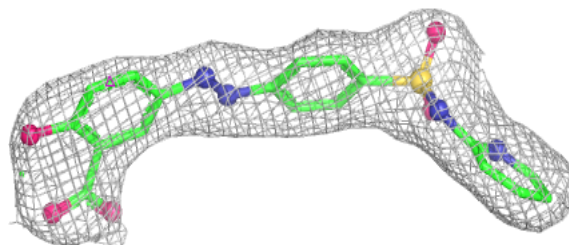


Electron density around SAS A 606:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around SAS A 604:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.